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Pro	Thr	Ile	Val	Arg	His	Ile	Val	Arg	Pro	Lys	Ser	Ala	Glu	Pro	Pro		
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Glu	Ser	His	Gln	Lys	Ser	His	Gly	Pro	Gly	Ser	Asp	Leu	Glu	Asn	Phe		
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Pro	Pro	Leu	Gly	Ser	Leu	Leu	Lys	Asp	Ala	Leu	His	Lys	Gln	Ala	Ser		
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Glu Lys Leu Asp Ser Lys Leu Ala Asn Ile Asp Tyr Leu Arg Lys Lys	
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Arg Gly Val Glu Pro Lys Pro Glu Ala Leu Leu Ala Arg Arg Ser Leu	
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Gln Pro Pro Gly Ile Glu Ser Glu Lys Ser Glu Lys Leu Ser Ser Phe	
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Pro Ser Leu Gln Lys Asp Gly Ala Lys Glu Pro Glu Arg Lys Glu Gln	
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Pro Leu Gln Arg His Pro Ser Ser Ile Pro Pro Pro Pro Leu Thr Ala	
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Ser Ser Ser His Lys Pro Arg Pro Gly Pro Asp Pro Gly Pro Pro Lys	
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His Pro Lys Pro Ser Thr Val Lys Asp Cys Pro Thr Leu Cys Lys Gln	
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Pro Ala Glu Gly Asp Lys Leu Glu Ala Gly Leu Ser Phe Val His Ser	
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Thr Glu Ala Asp Lys Pro Asn Gly Met Lys Arg Ser Pro Ser Ala Thr	
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Cys Ser Ser Ser Phe Pro Glu Thr Arg Ala Gly Val Arg Glu Ala Ser	
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Ala Ala Ser Ser Asp Thr Ser Ser Ala Lys Ala Ala Gly Gly Met Leu	
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Gly Glu Gly Arg Thr His Met Thr Lys Ser Asp Ser Leu Pro Ser Phe	
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Val Gly Glu Thr Lys Gly Lys Asp Pro Ala Pro Ala Gln Pro Pro Pro	
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 Asn Pro Ala Pro Ser Pro Pro Leu Arg Ser Pro Gly Lys Gly Arg Leu
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 Ala Ser Pro Ile Leu Pro Gln Arg Ser Gly Asn Ile Pro Glu Ala Pro
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 Arg Arg Tyr Asp Pro Gly Val Arg Ile Gly Leu Gly Gly Ala Ala Ala
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 Leu Leu Ser Ala Phe Arg Cys His Ala Thr Ala Ser Pro Ser His Pro
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 Ser Leu Ser Thr Ser Gly Arg Asp Cys Arg Val Met Arg Tyr Ser Val
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 Gly Asp Gly Arg Thr Gly Asp Gly Asp Asn Arg Asn His Ile His Asp
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 Gly Asp His Gly Arg Gly Glu Glu Pro Ile Ala Pro Pro Leu Ala Pro
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 Arg Thr Arg Lys Pro Pro Leu Arg Pro Gly Asp Arg Ala Pro Val Cys
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Gly Glu Lys Lys Thr Leu Ile Val Leu Thr Asn Val Thr Lys Asn Ile
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Leu Gln Leu Ser Arg Leu Leu Glu Ser Asn Arg Lys Leu Glu Asp Gln
      580                      585                      590

gtt cag cgt tgt atc tgg ttc cag cag ctg ctg ctt tcc tta aca atg      1824
Val Gln Arg Cys Ile Trp Phe Gln Gln Leu Leu Ser Leu Thr Met
      595                      600                      605

ctc ttg ctt gct ttt gtc acc tct ttc ttc tat tta ttg tac agt taa      1872
Leu Leu Leu Ala Phe Val Thr Ser Phe Phe Tyr Leu Leu Tyr Ser *
      610                      615                      620

agaagtgggtg ccgggtagga accacgggttc cttcgtccat tagttggaaa aagtaacaga      1932

cctaaaactc taccaagcta ctaaaaacat tgcacatctg tgcttcctaa aaggaaatat      1992

gcagcacgtg gaggggaaca catacatgtc ttgaaaataa actgctagaa taaagaaatg      2052

ctggagaaat tgaaaaaaaa aaaaaa      2077

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<210> 639
 <211> 601
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (89)..(448)

<400> 639

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atttgccct cgaggccaag aattcgccac gagggggcgt aagacgggga gaggggcagc      60
tccgagtaca cggagaagaa ctggaaac   atg caa aaa ctc caa aca cgg tcc      112
                                   1       5
                                   Met Gln Lys Leu Gln Thr Arg Ser

cct gcc atg tcc ctg tct gac cca ggc ctg ggg tac cac ccc acg tgc      160
Pro Ala Met Ser Leu Ser Asp Pro Gly Leu Gly Tyr His Pro Thr Cys
   10              15              20

tgg acc cta cgc tgg cca ccc ctg tgc tcc ctc cac gcc ctc cac gtg      208
Trp Thr Leu Arg Trp Pro Pro Leu Cys Ser Leu His Ala Leu His Val
   25              30              35              40

ttc cac tgc ctc ttc tct tct cgc ttg gga act cca gtc tca cct cgg      256
Phe His Cys Leu Phe Ser Ser Arg Leu Gly Thr Pro Val Ser Pro Arg
              45              50              55

ctt gca atg gac ccc aac tgc tcc tgc gag gct ggt ggc tcc tgc gcc      304
Leu Ala Met Asp Pro Asn Cys Ser Cys Glu Ala Gly Gly Ser Cys Ala
              60              65              70

tgc gcc ggc tcc tgc aag tgc aaa aag tgc aaa tgc acc tcc tgc aag      352
Cys Ala Gly Ser Cys Lys Cys Lys Lys Cys Lys Cys Thr Ser Cys Lys
              75              80              85

aag agc tgc tgc tcc tgt tgc ccc ctg ggc tgt gcc aag tgt gcc cag      400
Lys Ser Cys Cys Ser Cys Cys Pro Leu Gly Cys Ala Lys Cys Ala Gln
              90              95              100

ggc tgc atc tgc aaa ggg ggc tca gag aag tgc agc tgc tgt gcc tga      448
Gly Cys Ile Cys Lys Gly Ala Ser Glu Lys Cys Ser Cys Cys Ala *
105              110              115              120

tgtcgggaca gccctgctgt cagatgaaaa cagaatgaca cgtaaaatcc aggatttttt      508
tttttctaca actccgactc atttgctaca ttcttttttt ttctgtgaaa tatgtgaata      568
ataattaaac acttagactt gaaaaaaaaa aaa                                601

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<210> 640

<211> 1856

<212> DNA

<213> Homo sapiens

<220>

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<222> (1061)..(1780)

<220>

<221> misc_feature

<222> (1)...(1856)

<223> n = a,t,c or g

<400> 640

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ccgcgctttt tgcccgtaaa gcgccggtga cgcttgagat tggttttggc atgggggcgt      60

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cgctgggtggc aatgggctaaa gatcgccctg agcaggactt cctcggcatt gaagtgcatt	120
caccgggcggt tgggtgcgtgc ctggcttctg cgcatagaaga aggtttaagc aacctgcgcg	180
tgatgtgtca cgatgcggtt gaagtgcgtc ataaaatgat tcctgacaat tcattgcgca	240
tgggtgcagct ctttttccct gacccgtggc acaaagcgcg ccataataaa cgccgtatcg	300
ttcaggtgcc gtttgccgaa ctggtaaaaa gcaaaactgca gctggggggc gtattccata	360
tggcgaccga ctgggaacct tatgcggaac atatgcttga agtgatgtct tctattgacg	420
gttataaaaa cctgtcagag agcaatgatt acgtaccgcg tccggcatca cgtccggtga	480
cgaaatttga acaacgtggt catcgtcttg gtcacggagt atgggactta atgttcgaga	540
gggtgaaata atggcaaaga accgtagccg tcgtctgcgt aaaaaaatgc acatcgacga	600
attccaggaa ttaggatttt cgggtggcatg gcgattcccg gaaggtagat cggaagaaca	660
gattgataaa accgttgatg attttattaa cgaggttatc gaaccgaaca aactggcctt	720
tgacggcagc gggttatctgg cctgggaagg tctgatctgc atgcaggaaa tcggcaaatg	780
caccgaagaa catcaggcga ttgtgcgtaa gtggctggaa gagcgcaaac tggatgaggt	840
acgccccagc gaacttttcg acgtttggtg ggactaagaa agcatacggg cgatgacaaa	900
tgcaaaactg cctgatgcgc tacgcttatac aggcctggaa agatgcacga tcgagtaggc	960
gggataaggt gtttacgccg catccggcat ggaaaacgcg tactttgtta tcaatctggg	1020
gccagcaaat gctggcctga ttttttcttg agggaagact atg atg cgc aaa atg	1075
Met Met Arg Lys Met	
1 5	
ctg ctg gcg gca gca ctt tca gtg acg gca atg acc gct cac gcc gac	1123
Leu Leu Ala Ala Ala Leu Ser Val Thr Ala Met Thr Ala His Ala Asp	
10 15 20	
tac cag tgc agc gtc acg ccg cgt gac gat gtg att gtc agc ccg caa	1171
Tyr Gln Cys Ser Val Thr Pro Arg Asp Asp Val Ile Val Ser Pro Gln	
25 30 35	
acc gtg cag gtg aag ggc gaa aac ggc aat ctg gtg atc acg cca gac	1219
Thr Val Gln Val Lys Gly Glu Asn Gly Asn Leu Val Ile Thr Pro Asp	
40 45 50	
ggc aac gtg atg tat aac ggt aag caa tat tcc ctg aat gcc gcc cag	1267
Gly Asn Val Met Tyr Asn Gly Lys Gln Tyr Ser Leu Asn Ala Ala Gln	
55 60 65	
cgc gag cag gcg aag gat tat cag gct gaa cta cgc agc acg ctg ccg	1315
Arg Glu Gln Ala Lys Asp Tyr Gln Ala Glu Leu Arg Ser Thr Leu Pro	
70 75 80 85	
tgg att gat gaa ggc gcg aaa agc cgc gtc gag aaa gcc cgt att gct	1363
Trp Ile Asp Glu Gly Ala Lys Ser Arg Val Glu Lys Ala Arg Ile Ala	
90 95 100	
ctg gat aaa att atc gtt cag gag atg ggc gaa agc agc aaa atg cgc	1411
Leu Asp Lys Ile Ile Val Gln Glu Met Gly Glu Ser Ser Lys Met Arg	
105 110 115	

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agc cgt ctg acc aaa ctt gat gcg cag ctg aaa gag cag atg aac cgc      1459
Ser Arg Leu Thr Lys Leu Asp Ala Gln Leu Lys Glu Gln Met Asn Arg
      120                      125                      130

att att gaa acg cgc agc gat ggc ctg acg ttt cac tat aaa gcc att      1507
Ile Ile Glu Thr Arg Ser Asp Gly Leu Thr Phe His Tyr Lys Ala Ile
      135                      140                      145

gat cag gtt cgc gcc gaa ggc cag caa tta gtg aat cag gca atg ggt      1555
Asp Gln Val Arg Ala Glu Gly Gln Gln Leu Val Asn Gln Ala Met Gly
      150                      155                      160                      165

gga att tta cag gac agc att aat gaa atg ggc gcg aaa gcg gtg ctg      1603
Gly Ile Leu Gln Asp Ser Ile Asn Glu Met Gly Ala Lys Ala Val Leu
      170                      175                      180

aaa agc ggc ggt aac cca tta cag aat gtg ctg gga agc ctg ggg ggg      1651
Lys Ser Gly Gly Asn Pro Leu Gln Asn Val Leu Gly Ser Leu Gly Gly
      185                      190                      195

ctg caa tcc tca atc caa acc gag tgg aaa aag cag gaa aaa gat ttc      1699
Leu Gln Ser Ser Ile Gln Thr Glu Trp Lys Lys Gln Glu Lys Asp Phe
      200                      205                      210

cag cag ttt ggc aaa gat gtt tgt agc cgc gtt gtg act ctg gaa gat      1747
Gln Gln Phe Gly Lys Asp Val Cys Ser Arg Val Val Thr Leu Glu Asp
      215                      220                      225

agc cgc aaa gcc ctg gtc ggg aat tta aaa taa tcctctat tttaagacgg      1798
Ser Arg Lys Ala Leu Val Gly Asn Leu Lys *
      230                      235                      240

cataatactt ttttatgccg nttaattctt cgttttgtta cctgcctcta acttttga      1856

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<210> 641
 <211> 2659
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (230) .. (2164)

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tcccttctct gagacgggga ccaggggatg gcagccatgc acctgacagc ctggccccag      120
gaacctattg tttcagaagt cggtgacctt tgaggacgtg gctgtgtact tcacccaggc      180
ggaatgggat ggccgtgtccc ctgcacagag gacctgtac agggatgtg      atg ctg      235
                                Met Leu
                                1

gag aat tat ggg aat gtg gca tcc ctg gga ttt cca ctt ctc aaa cct      283
Glu Asn Tyr Gly Asn Val Ala Ser Leu Gly Phe Pro Leu Leu Lys Pro
      5                      10                      15

gct gtg atc tca caa ctg gag gga gga agt gag ctg ggg ggc tca tct      331
Ala Val Ile Ser Gln Leu Glu Gly Gly Ser Glu Leu Gly Gly Ser Ser

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20	25	30	
cca ctg gct gca gga aca ggc ctc cag ggc ctc cag act gta gat att			379
Pro Leu Ala Ala Gly Thr Gly Leu Gln Gly Leu Gln Thr Val Asp Ile			
35	40	45	50
cag act gac aat gat ttg aca aag gaa atg tat gaa gga aaa gag aat			427
Gln Thr Asp Asn Asp Leu Thr Lys Glu Met Tyr Glu Gly Lys Glu Asn			
	55	60	65
gta tca ttt gaa ctt caa aga gac ttt tcc cag gaa aca gac ttt tca			475
Val Ser Phe Glu Leu Gln Arg Asp Phe Ser Gln Glu Thr Asp Phe Ser			
	70	75	80
gaa gcc tct ctt cta gag aaa caa cag gaa gtc cac tca gca gga aat			523
Glu Ala Ser Leu Leu Glu Lys Gln Gln Glu Val His Ser Ala Gly Asn			
	85	90	95
ata aag aag gag aag agc aac acc att gat gga aca gtg aaa gat gag			571
Ile Lys Lys Glu Lys Ser Asn Thr Ile Asp Gly Thr Val Lys Asp Glu			
	100	105	110
aca agc ccc gtg gag gag tgt ttt ttt agt caa agt tca aac tca tat			619
Thr Ser Pro Val Glu Glu Cys Phe Phe Ser Gln Ser Ser Asn Ser Tyr			
	115	120	125
cag tgt cat acc atc act gga gag cag ccc tct ggg tgt aca gga ttg			667
Gln Cys His Thr Ile Thr Gly Glu Gln Pro Ser Gly Cys Thr Gly Leu			
	135	140	145
ggg aaa tcc atc agc ttt gat aca aaa ctc gtg aag cat gaa ata att			715
Gly Lys Ser Ile Ser Phe Asp Thr Lys Leu Val Lys His Glu Ile Ile			
	150	155	160
aat tct gag gaa aga cct ttc aaa tgt gaa gaa tta gta gag ccc ttt			763
Asn Ser Glu Glu Arg Pro Phe Lys Cys Glu Glu Leu Val Glu Pro Phe			
	165	170	175
agg tgt gac tct caa ctt att caa cat caa gag aac aac act gag gaa			811
Arg Cys Asp Ser Gln Leu Ile Gln His Gln Glu Asn Asn Thr Glu Glu			
	180	185	190
aag cct tat cag tgt tct gag tgt ggc aaa gct ttc agc att aat gag			859
Lys Pro Tyr Gln Cys Ser Glu Cys Gly Lys Ala Phe Ser Ile Asn Glu			
	195	200	205
aaa tta att tgg cat cag aga ctt cac agt ggg gag aaa ccc ttc aaa			907
Lys Leu Ile Trp His Gln Arg Leu His Ser Gly Glu Lys Pro Phe Lys			
	215	220	225
tgt gtg gag tgt ggg aaa agc ttc agc tac agt tcc cat tat atc aca			955
Cys Val Glu Cys Gly Lys Ser Phe Ser Tyr Ser Ser His Tyr Ile Thr			
	230	235	240
cat cag aca atc cac agt ggg gag aag ccc tat cag tgt aag atg tgt			1003
His Gln Thr Ile His Ser Gly Glu Lys Pro Tyr Gln Cys Lys Met Cys			
	245	250	255
ggg aag gcc ttc agt gtt aat gga agc cta agt agg cat cag aga atc			1051
Gly Lys Ala Phe Ser Val Asn Gly Ser Leu Ser Arg His Gln Arg Ile			
	260	265	270
cat acg gga gag aag ccc tat cag tgc aag gaa tgt gga aat ggc ttc			1099
His Thr Gly Glu Lys Pro Tyr Gln Cys Lys Glu Cys Gly Asn Gly Phe			

275	280	285	290	
agc tgt agt tct gca tat att aca cat cag aga gtc cac act gga gag				1147
Ser Cys Ser Ser Ala Tyr Ile Thr His Gln Arg Val His Thr Gly Glu				
295		300	305	
aaa cct tac gag tgt aat gac tgt ggg aaa gcg ttc aat gtt aat gca				1195
Lys Pro Tyr Glu Cys Asn Asp Cys Gly Lys Ala Phe Asn Val Asn Ala				
310		315	320	
aaa tta att caa cat cag aga atc cat act gga gag aaa cct tat gaa				1243
Lys Leu Ile Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu				
325		330	335	
tgt aat gaa tgt gga aaa ggc ttc agg tgc agc tcc cag ctt agg cag				1291
Cys Asn Glu Cys Gly Lys Gly Phe Arg Cys Ser Ser Gln Leu Arg Gln				
340		345	350	
cat cag agc atc cac aca gga gaa aag ccc tat cag tgt aaa gag tgt				1339
His Gln Ser Ile His Thr Gly Glu Lys Pro Tyr Gln Cys Lys Glu Cys				
355		360	365	370
gga aaa ggc ttc aat aat aat aca aaa ctc att cag cat cag aga atc				1387
Gly Lys Gly Phe Asn Asn Asn Thr Lys Leu Ile Gln His Gln Arg Ile				
375		380	385	
cac aca ggt gag aaa ccc tat gaa tgc act gaa tgt gga aaa gcc ttc				1435
His Thr Gly Glu Lys Pro Tyr Glu Cys Thr Glu Cys Gly Lys Ala Phe				
390		395	400	
agt gtc aaa ggg aag tta atc caa cac cag aga att cac aca ggc gag				1483
Ser Val Lys Gly Lys Leu Ile Gln His Gln Arg Ile His Thr Gly Glu				
405		410	415	
aaa ccc tat gag tgt aat gaa tgc ggg aaa gcc ttc aga tgt aac tcc				1531
Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe Arg Cys Asn Ser				
420		425	430	
caa ttt cgg cag cat ctg aga att cac act ggg gag aag ccc tat gag				1579
Gln Phe Arg Gln His Leu Arg Ile His Thr Gly Glu Lys Pro Tyr Glu				
435		440	445	450
tgt aat gag tgt gga aag gcc ttc agc gtt aat ggg aaa cta atg cgg				1627
Cys Asn Glu Cys Gly Lys Ala Phe Ser Val Asn Gly Lys Leu Met Arg				
455		460	465	
cat cag aga att cac act ggg gag aaa cct ttt gaa tgt aat gag tgt				1675
His Gln Arg Ile His Thr Gly Glu Lys Pro Phe Glu Cys Asn Glu Cys				
470		475	480	
ggg aga tgc ttt act tct aaa aga aac cta ctt gat cat cac cga atc				1723
Gly Arg Cys Phe Thr Ser Lys Arg Asn Leu Leu Asp His His Arg Ile				
485		490	495	
cat act gga gaa aag ccc tat caa tgt aag gaa tgt ggg aaa gcc ttc				1771
His Thr Gly Glu Lys Pro Tyr Gln Cys Lys Glu Cys Gly Lys Ala Phe				
500		505	510	
agt atc aat gcc aaa cta act agg cat cag agg ata cat act ggg gag				1819
Ser Ile Asn Ala Lys Leu Thr Arg His Gln Arg Ile His Thr Gly Glu				
515		520	525	530
aaa cct ttc aaa tgt atg gaa tgt gag aaa gca ttc agc tgt agt tct				1867
Lys Pro Phe Lys Cys Met Glu Cys Glu Lys Ala Phe Ser Cys Ser Ser				

535	540	545	
aac tat att gtg cac cag aga atc cat aca gga gag aaa ccc ttt cag			1915
Asn Tyr Ile Val His Gln Arg Ile His Thr Gly Glu Lys Pro Phe Gln			
550	555	560	
tgt aag gag tgt gga aaa gcc ttc cat gtt aat gcc cat tta att cgg			1963
Cys Lys Glu Cys Gly Lys Ala Phe His Val Asn Ala His Leu Ile Arg			
565	570	575	
cat cag aga agc cac act ggg gag aaa ccc ttc aga tgt gtg gaa tgt			2011
His Gln Arg Ser His Thr Gly Glu Lys Pro Phe Arg Cys Val Glu Cys			
580	585	590	
ggc aaa ggc ttc agc ttt agt tct gac tac att ata cat cag aca gtc			2059
Gly Lys Gly Phe Ser Phe Ser Ser Asp Tyr Ile Ile His Gln Thr Val			
595	600	605	610
cac act tgg aag aaa ccc tat atg tgt agt gtg tgt ggg aaa gca ttc			2107
His Thr Trp Lys Lys Pro Tyr Met Cys Ser Val Cys Gly Lys Ala Phe			
615	620	625	
agg ttt agc ttc cag ctc agt cag cat cag agt gtc cat agt gaa gga			2155
Arg Phe Ser Phe Gln Leu Ser Gln His Gln Ser Val His Ser Glu Gly			
630	635	640	
aaa tcc taa taatgag aaagatatag aaaactctta aggttaatgc caaaatggat			2211
Lys Ser *			
645			
caagtatcat cagattcatc cattgaaaaa cctccaagag ggcatgaata tggcagagtc			2271
ttcatatgga aacagtttttt attctattca gtttaaatca ggaaaggatg accagttaaa			2331
gagaaacatc caaaaatagc tttgttttgt accaacagga attagaaaat ataataaaaa			2391
gatttcgttc ccagcagcat caagaaaagt agattttcta gaaataaaca gttatggagg			2451
acttgatagg agaaatttaa gtcttcaactg agggccactt tacaaaggaa atttgaataa			2511
atggagagag agagaagcct tgttggttga taggaaaacc cgtactaaag atactctacc			2571
tacattaatt tatttgttta atttttgaca acaagcatgt attacttttg aaaagatgaa			2631
aaataaagat ttatttaaaa aaaaaaaaa			2659

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 <212> DNA
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<220>
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 <222> (53) .. (352)

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	Met	
	1	
cac gcg tac gta agc ttg gat cct cta gag cgg ccg cct act act act		103

His Ala Tyr Val Ser Leu Asp Pro Leu Glu Arg Pro Pro Thr Thr Thr
 5 10 15
 aaa ttc gcg gcc gcg tcc gac cgc cgc cgc gcc gcc atc atg gac acc 151
 Lys Phe Ala Ala Ala Ser Asp Arg Arg Arg Ala Ala Ile Met Asp Thr
 20 25 30
 agc cgt gtg cag cct atc aag ctg gcc agg gtc acc aag gtc ctg ggc 199
 Ser Arg Val Gln Pro Ile Lys Leu Ala Arg Val Thr Lys Val Leu Gly
 35 40 45
 agg acc ggt tct cag gga cag tgc acg cag gtg cgc gtg gaa ttc atg 247
 Arg Thr Gly Ser Gln Gly Gln Cys Thr Gln Val Arg Val Glu Phe Met
 50 55 60 65
 gac gac acg agc cga tcc atc atc cgc aat gta aaa ggc ccc gtg cgc 295
 Asp Asp Thr Ser Arg Ser Ile Ile Arg Asn Val Lys Gly Pro Val Arg
 70 75 80
 gag ggc gac gtg ctc acc ctt ttg gag tca gag cga gaa gcc cgg agg 343
 Glu Gly Asp Val Leu Thr Leu Leu Glu Ser Glu Arg Glu Ala Arg Arg
 85 90 95
 ttg cgc tga gcttggc tgcctgctgg gtcttgatg tcgggttcga ccacttgcc 399
 Leu Arg *
 100
 gatgggaatg gtctgtcaca atctgctcct tttttttgtc cgccacacgt aactgagatg 459
 ctcccttataa taaagcgttt gtgtttcaag ttaactcaga aaaaaaaaaa a 510

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 <212> DNA
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 <222> (67) .. (948)

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 caccaa atg gcg gat gac gcc ggt gca gcg ggg ggg ccc ggg ggc cct 108
 Met Ala Asp Asp Ala Gly Ala Ala Gly Gly Pro Gly Gly Pro
 1 5 10
 ggt ggc cct ggg atg ggg aac cgc ggt ggc ttc cgc gga ggt ttc ggc 156
 Gly Gly Pro Gly Met Gly Asn Arg Gly Gly Phe Arg Gly Gly Phe Gly
 15 20 25 30
 agt ggc atc cgg ggc cgg ggt cgc ggc cgt gga cgg ggc cgg ggc cga 204
 Ser Gly Ile Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
 35 40 45
 ggc cgc gga gct cgc gga ggc aag gcc gag gat aag gag tgg atg ccc 252
 Gly Arg Gly Ala Arg Gly Gly Lys Ala Glu Asp Lys Glu Trp Met Pro
 50 55 60
 gtc acc aag ttg ggc cgc ttg gtc aag gac atg aag atc aag tcc ctg 300
 Val Thr Lys Leu Gly Arg Leu Val Lys Asp Met Lys Ile Lys Ser Leu

65	70	75	
gag gag atc tat ctc ttc tcc ctg ccc att aag gaa tca gag atc att Glu Glu Ile Tyr Leu Phe Ser Leu Pro Ile Lys Glu Ser Glu Ile Ile 80 85 90			348
gat ttc ttc ctg ggg gcc tct ctc aag gat gag gtt ttg aag att atg Asp Phe Phe Leu Gly Ala Ser Leu Lys Asp Glu Val Leu Lys Ile Met 95 100 105 110			396
cca gtg cag aag cag acc cgt gcc ggc cag cgc acc agg ttc aag gca Pro Val Gln Lys Gln Thr Arg Ala Gly Gln Arg Thr Arg Phe Lys Ala 115 120 125			444
ttt gtt gct atc ggg gac tac aat ggc cac gtc ggt ctg ggt gtt aag Phe Val Ala Ile Gly Asp Tyr Asn Gly His Val Gly Leu Gly Val Lys 130 135 140			492
tgc tcc aag gag gtg gcc acc gcc atc cgt ggg gcc atc atc ctg gcc Cys Ser Lys Glu Val Ala Thr Ala Ile Arg Gly Ala Ile Ile Leu Ala 145 150 155			540
aag ctc tcc atc gtc ccc gtg cgc aga ggc tac tgg ggg aac aag atc Lys Leu Ser Ile Val Pro Val Arg Arg Gly Tyr Trp Gly Asn Lys Ile 160 165 170			588
ggc aag ccc cac act gtc cct tgc aag gtg aca ggc cgc tgc ggc tct Gly Lys Pro His Thr Val Pro Cys Lys Val Thr Gly Arg Cys Gly Ser 175 180 185 190			636
gtg ctg gta cgc ctc atc cct gca ccc agg ggc act ggc atc gtc tcc Val Leu Val Arg Leu Ile Pro Ala Pro Arg Gly Thr Gly Ile Val Ser 195 200 205			684
gca cct gtg cct aag aag ctg ctc atg atg gct ggt atc gat gac tgc Ala Pro Val Pro Lys Lys Leu Leu Met Met Ala Gly Ile Asp Asp Cys 210 215 220			732
tac acc tca gcc cgg ggc tgc act gcc acc ctg ggc aac ttc gcc aag Tyr Thr Ser Ala Arg Gly Cys Thr Ala Thr Leu Gly Asn Phe Ala Lys 225 230 235			780
gcc acc ttt gat gcc att tct aag acc tac agc tac ctg acc ccc gac Ala Thr Phe Asp Ala Ile Ser Lys Thr Tyr Ser Tyr Leu Thr Pro Asp 240 245 250			828
ctc tgg aag gag act gta ttc acc aag tct ccc tat cag gag ttc act Leu Trp Lys Glu Thr Val Phe Thr Lys Ser Pro Tyr Gln Glu Phe Thr 255 260 265 270			876
gac cac ctc gtc aag acc cac acc aga gtc tcc gtg cag cgg act cag Asp His Leu Val Lys Thr His Thr Arg Val Ser Val Gln Arg Thr Gln 275 280 285			924
gct cca gct gtg gct aca aca tag gggttttata caagaaaaat aaagtgaatt Ala Pro Ala Val Ala Thr Thr * 290			978
aagcgtgaaa aaaaaaaaaa			997

<211> 3323
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (162)..(3323)

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 ccgcgcgcgc atcctccgct tgtgctaccg ccgcgggcgc tgggcccgtc tgctgggtccg 120
 gcatgagacc gtgagacgag agacgggtcg gggccgccga c atg ttt ggc cgc 173
 Met Phe Gly Arg
 1
 tcg cgg agc tgg gtg ggc ggg ggc cat ggc aag act tcc cgc aac atc 221
 Ser Arg Ser Trp Val Gly Gly Gly His Gly Lys Thr Ser Arg Asn Ile
 5 10 15 20
 cac tcc ttg gac cac ctc aag tat ctg tac cac gtt ttg acc aaa aac 269
 His Ser Leu Asp His Leu Lys Tyr Leu Tyr His Val Leu Thr Lys Asn
 25 30 35
 acc aca gtc aca gaa cag aac cgg aac ctg cta gtg gag acc atc cgt 317
 Thr Thr Val Thr Glu Gln Asn Arg Asn Leu Leu Val Glu Thr Ile Arg
 40 45 50
 tcc atc act gag atc ctg atc tgg gga gat caa aat gac agc tct gta 365
 Ser Ile Thr Glu Ile Leu Ile Trp Gly Asp Gln Asn Asp Ser Ser Val
 55 60 65
 ttt gac ttc ttc ctg gag aag aat atg ttt gtt ttc ttc ttg aac atc 413
 Phe Asp Phe Phe Leu Glu Lys Asn Met Phe Val Phe Phe Leu Asn Ile
 70 75 80
 ttg cgg caa aag tcg ggc cgt tac gtg tgc gtt cag ctg ctg cag acc 461
 Leu Arg Gln Lys Ser Gly Arg Tyr Val Cys Val Gln Leu Leu Gln Thr
 85 90 95 100
 ttg aac atc ctc ttt gag aac atc agt cac gag acc tca ctt tat tat 509
 Leu Asn Ile Leu Phe Glu Asn Ile Ser His Glu Thr Ser Leu Tyr Tyr
 105 110 115
 ttg ctc tca aat aac tac gta aat tct atc atc gtt cat aaa ttt gac 557
 Leu Leu Ser Asn Asn Tyr Val Asn Ser Ile Ile Val His Lys Phe Asp
 120 125 130
 ttt tct gat gag gag att atg gcc tat tat ata tcg ttc ctg aaa aca 605
 Phe Ser Asp Glu Glu Ile Met Ala Tyr Tyr Ile Ser Phe Leu Lys Thr
 135 140 145
 ctt tcg tta aaa ctc aac aac cac act gtc cat ttc ttt tat aat gag 653
 Leu Ser Leu Lys Leu Asn Asn His Thr Val His Phe Phe Tyr Asn Glu
 150 155 160
 cac acc aat gac ttt gcc ctg tac aca gaa gcc atc aag ttt ttc aac 701
 His Thr Asn Asp Phe Ala Leu Tyr Thr Glu Ala Ile Lys Phe Phe Asn
 165 170 175 180
 cac cct gaa agc atg gtt aga att gct gta aga acc ata act ttg aat 749
 His Pro Glu Ser Met Val Arg Ile Ala Val Arg Thr Ile Thr Leu Asn
 185 190 195

gtc tat aaa gtg tca ttg gat aac cag gcc atg ctg cac tac atc cga Val Tyr Lys Val Ser Leu Asp Asn Gln Ala Met Leu His Tyr Ile Arg 200 205 210	797
gat aaa act gct gtt cct tac ttc tcc aat ttg gtc tgg ttc att ggg Asp Lys Thr Ala Val Pro Tyr Phe Ser Asn Leu Val Trp Phe Ile Gly 215 220 225	845
agc cat gtg atc gaa ctc gat gac tgc gtg cag act gat gag gag cat Ser His Val Ile Glu Leu Asp Asp Cys Val Gln Thr Asp Glu Glu His 230 235 240	893
cgg aat cgg ggt aaa ctg agt gat ctg gtg gca gag cac cta gac cac Arg Asn Arg Gly Lys Leu Ser Asp Leu Val Ala Glu His Leu Asp His 245 250 255 260	941
ctg cac tat ctc aat gac atc ctg atc atc aac tgt gag ttc ctc aac Leu His Tyr Leu Asn Asp Ile Leu Ile Ile Asn Cys Glu Phe Leu Asn 265 270 275	989
gat gtg ctc act gac cac ctg ctc aac agg ctc ttc ctg ccc ctc tac Asp Val Leu Thr Asp His Leu Leu Asn Arg Leu Phe Leu Pro Leu Tyr 280 285 290	1037
gtg tac tca ctg gag aac cag gac aag gga gga gaa cgg ccg aaa att Val Tyr Ser Leu Glu Asn Gln Asp Lys Gly Gly Glu Arg Pro Lys Ile 295 300 305	1085
agc ctg ccg gtg tct ctt tat ctt ctg tca cag gtc ttc tta att ata Ser Leu Pro Val Ser Leu Tyr Leu Leu Ser Gln Val Phe Leu Ile Ile 310 315 320	1133
cat cat gca ccg ctg gtg aac tcg tta gct gaa gtc att ctg aat ggt His His Ala Pro Leu Val Asn Ser Leu Ala Glu Val Ile Leu Asn Gly 325 330 335 340	1181
gat ctg tct gag atg tac gct aag act gaa cag gat att cag aga agt Asp Leu Ser Glu Met Tyr Ala Lys Thr Glu Gln Asp Ile Gln Arg Ser 345 350 355	1229
tct gcc aag ccc agc att cgg tgc ttc att aaa ccc acc gag aca ctc Ser Ala Lys Pro Ser Ile Arg Cys Phe Ile Lys Pro Thr Glu Thr Leu 360 365 370	1277
gag cgg tcc ctt gag atg aac aag cac aag ggc aag agg cgg gtg caa Glu Arg Ser Leu Glu Met Asn Lys His Lys Gly Lys Arg Arg Val Gln 375 380 385	1325
aag aga ccc aac tac aaa aac gtt ggg gaa gaa gaa gat gag gag aaa Lys Arg Pro Asn Tyr Lys Asn Val Gly Glu Glu Glu Asp Glu Glu Lys 390 395 400	1373
ggg ccc acc gag gat gcc caa gaa gac gcc gag aag gct aaa ggt aca Gly Pro Thr Glu Asp Ala Gln Glu Asp Ala Glu Lys Ala Lys Gly Thr 405 410 415 420	1421
gag ggt ggt tca aaa ggc atc aag acg agt ggg gag agt gaa gag atc Glu Gly Gly Ser Lys Gly Ile Lys Thr Ser Gly Glu Ser Glu Glu Ile 425 430 435	1469
gag atg gtg atc atg gag cgt agc aag ctc tca gag ctg gcc gcc agc Glu Met Val Ile Met Glu Arg Ser Lys Leu Ser Glu Leu Ala Ala Ser 440 445 450	1517

acc tcc gtg cag gag cag aac acc acg gac gag gag aaa agc gcc gcc	1565
Thr Ser Val Gln Glu Gln Asn Thr Thr Asp Glu Glu Lys Ser Ala Ala	
455 460 465	
gcc acc tgc tct gag agc acg caa tgg agc aga ccc ttc ctg gat atg	1613
Ala Thr Cys Ser Glu Ser Thr Gln Trp Ser Arg Pro Phe Leu Asp Met	
470 475 480	
gtg tac cac gcg ctg gac agc ccg gat gat gat tac cat gcc ctg ttc	1661
Val Tyr His Ala Leu Asp Ser Pro Asp Asp Asp Tyr His Ala Leu Phe	
485 490 495 500	
gtg ctc tgc ctc ctc tat gcc atg tct cat aat aaa ggc atg gat cct	1709
Val Leu Cys Leu Tyr Ala Met Ser His Asn Lys Gly Met Asp Pro	
505 510 515	
gaa aaa tta gag cga atc cag ctc ccc gtg cca aat gcg gcc gag aag	1757
Glu Lys Leu Glu Arg Ile Gln Leu Pro Val Pro Asn Ala Ala Glu Lys	
520 525 530	
acc acc tac aac cac ccg cta gct gaa aga ctc atc agg atc atg aac	1805
Thr Thr Tyr Asn His Pro Leu Ala Glu Arg Leu Ile Arg Ile Met Asn	
535 540 545	
aac gct gcc cag cca gat ggg aag atc cgg ctg gcg acg ctg gag ctg	1853
Asn Ala Ala Gln Pro Asp Gly Lys Ile Arg Leu Ala Thr Leu Glu Leu	
550 555 560	
agc tgc ctg ctt ctg aag cag caa gtc ctg atg agt gct ggc tgc atc	1901
Ser Cys Leu Leu Leu Lys Gln Gln Val Leu Met Ser Ala Gly Cys Ile	
565 570 575 580	
atg aag gac gtg cac ctg gcc tgc ctg gag ggt gcg aga gaa gaa agt	1949
Met Lys Asp Val His Leu Ala Cys Leu Glu Gly Ala Arg Glu Glu Ser	
585 590 595	
gtt cac ctt gta cga cat ttt tat aag gga gaa gac att ttt ttg gac	1997
Val His Leu Val Arg His Phe Tyr Lys Gly Glu Asp Ile Phe Leu Asp	
600 605 610	
atg ttt gaa gat gag tat agg agc atg aca atg aag ccc atg aac gtg	2045
Met Phe Glu Asp Glu Tyr Arg Ser Met Thr Met Lys Pro Met Asn Val	
615 620 625	
gaa tat ctc atg atg gac gcc tcc atc ctg ctg ccc cca aca ggc acg	2093
Glu Tyr Leu Met Met Asp Ala Ser Ile Leu Leu Pro Pro Thr Gly Thr	
630 635 640	
cca ctg acg ggc att gac ttc gtg aag cgg ctg ccg tgt ggc gat gtg	2141
Pro Leu Thr Gly Ile Asp Phe Val Lys Arg Leu Pro Cys Gly Asp Val	
645 650 655 660	
gag aag acc cgg cgg gcc atc cgg gtg ttc ttc atg ctg cgt tcc ctg	2189
Glu Lys Thr Arg Ala Ile Arg Val Phe Phe Met Leu Arg Ser Leu	
665 670 675	
tca ctg caa ttg cga ggg gag cct gag aca cag ttg ccg ctg act cgg	2237
Ser Leu Gln Leu Arg Gly Glu Pro Glu Thr Gln Leu Pro Leu Thr Arg	
680 685 690	
gag gag gac ctg atc aag act gat gat gtc ctg gat ctg aat aac agc	2285
Glu Glu Asp Leu Ile Lys Thr Asp Asp Val Leu Asp Leu Asn Asn Ser	
695 700 705	

gac ttg att gca tgt aca gtg atc acc aag gat ggc ggc atg gtc cag Asp Leu Ile Ala Cys Thr Val Ile Thr Lys Asp Gly Gly Met Val Gln 710 715 720	2333
cga ttc ctg gct gtg gat att tac cag atg agt ttg gtg gag cct gat Arg Phe Leu Ala Val Asp Ile Tyr Gln Met Ser Leu Val Glu Pro Asp 725 730 735 740	2381
gtg tcc agg ctt ggc tgg gga gtg gtc aag ttt gca ggc cta ttg cag Val Ser Arg Leu Gly Trp Gly Val Val Lys Phe Ala Gly Leu Leu Gln 745 750 755	2429
gac atg cag gtg act ggc gtg gag gac gac agc cgt gcc ctg aac atc Asp Met Gln Val Thr Gly Val Glu Asp Asp Ser Arg Ala Leu Asn Ile 760 765 770	2477
acc atc cac aag cct gcg tcc agc ccc cat tcc aag ccc ttc ccc atc Thr Ile His Lys Pro Ala Ser Ser Pro His Ser Lys Pro Phe Pro Ile 775 780 785	2525
ctc cag gcc acc ttc atc ttc tca gac cac atc cgc tgc atc atc gcc Leu Gln Ala Thr Phe Ile Phe Ser Asp His Ile Arg Cys Ile Ile Ala 790 795 800	2573
aag cag cgc ctg gcc aaa ggc cgc atc cag gca agg cgc atg aag atg Lys Gln Arg Leu Ala Lys Gly Arg Ile Gln Ala Arg Arg Met Lys Met 805 810 815 820	2621
cag aga ata gct gcc ctc ctg gac ctc cca atc cag ccc acc act gaa Gln Arg Ile Ala Ala Leu Leu Asp Leu Pro Ile Gln Pro Thr Thr Glu 825 830 835	2669
gtc ctg ggg ttt gga ctc ggc tcc tcc acc tcc act cag cac ctg cct Val Leu Gly Phe Gly Leu Gly Ser Ser Thr Ser Thr Gln His Leu Pro 840 845 850	2717
ttc cgc ttc tac gac cag ggg cgc cgg ggc agc agc gac ccc aca gtg Phe Arg Phe Tyr Asp Gln Gly Arg Arg Gly Ser Ser Asp Pro Thr Val 855 860 865	2765
cag cgc tcc gtg ttt gca tcg gtg gac aag gtg cca ggc ttc gcc gtg Gln Arg Ser Val Phe Ala Ser Val Asp Lys Val Pro Gly Phe Ala Val 870 875 880	2813
gcc cag tgc ata aac cag cac agc tcc ccg tcc ctg tcc tca cag tcg Ala Gln Cys Ile Asn Gln His Ser Ser Pro Ser Leu Ser Ser Gln Ser 885 890 895 900	2861
cca ccc tcc gcc agc ggg agc ccc agc ggc agc ggg agc acc agc cac Pro Pro Ser Ala Ser Gly Ser Pro Ser Gly Ser Gly Ser Thr Ser His 905 910 915	2909
tgc gac tct gga ggc acc agc tcg tcc tcc acc ccc tcc aca gcc cag Cys Asp Ser Gly Gly Thr Ser Ser Ser Ser Thr Pro Ser Thr Ala Gln 920 925 930	2957
agt cca gca gat gcc ccc atg agt cca gaa ctg cct aag cct cac ctt Ser Pro Ala Asp Ala Pro Met Ser Pro Glu Leu Pro Lys Pro His Leu 935 940 945	3005
cct gac cag ttg gta atc gtc aac gaa acg gaa gca gac tct aag ccc Pro Asp Gln Leu Val Ile Val Asn Glu Thr Glu Ala Asp Ser Lys Pro 950 955 960	3053


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agc aag aac gtg gcc agg agc gca gcc gtg gag aca gcc agc ctg tcc      3101
Ser Lys Asn Val Ala Arg Ser Ala Ala Val Glu Thr Ala Ser Leu Ser
965                      970                      975                      980

ccc agc ctc gtc cct gcc cgg cag ccc acc att tcc ctg ctc tgc gag      3149
Pro Ser Leu Val Pro Ala Arg Gln Pro Thr Ile Ser Leu Leu Cys Glu
                      985                      990                      995

gac acg gct gac acg ctg agc gtc gaa tgc ctg acc ctt gtc ccc cca      3197
Asp Thr Ala Asp Thr Leu Ser Val Glu Ser Leu Thr Leu Val Pro Pro
                      1000                      1005                      1010

gtt gac ccc cac agc ctc cgc agc ctc acc ggc atg ccc ccg ctg tcc      3245
Val Asp Pro His Ser Leu Arg Ser Leu Thr Gly Met Pro Pro Leu Ser
                      1015                      1020                      1025

acg ccg gct gcc gcc tgc aca gag ccc gtg ggc gaa gag gct gca tgt      3293
Thr Pro Ala Ala Ala Cys Thr Glu Pro Val Gly Glu Glu Ala Ala Cys
                      1030                      1035                      1040

gct gag cct gtg ggc acc gct gag gac tga      3323
Ala Glu Pro Val Gly Thr Ala Glu Asp *
1045                      1050

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<210> 645
<211> 843
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (388)..(507)

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acgatcgctt attaatattgg tttttaagtc cagatgaaga accttgaaaa tagccaaaga      120
gccaaaaata ctgagtaact tcacattcag agggactgtt tcttctctct atatatagca      180
agtcaaaaat agacatctcg gattctgggc cccagcattc atctttgtac tcaccttctt      240
tcaaatacca ccatttacac cctcggagcc cctgttttat ctgctttag atttctctga      300
cacctgccaa ttggcagctc cagctcctcc tcaacatttt tactctttca ttaaggtgta      360
aggagaattc aacaccattg ggcacaa      atg cat gaa tgc aat gtc cat aca      411
                                Met His Glu Cys Asn Val His Thr
                                1                      5

tac gcc tct tta ttt tgc ctt ttt ctg ctt cat act ggt aag ctt tgc      459
Tyr Ala Ser Leu Phe Cys Leu Phe Leu Leu His Thr Gly Lys Leu Cys
                      10                      15                      20

tgt cta aat tct cac cgg cac ttt cat tgc ata aaa tat tcc aaa tga      507
Cys Leu Asn Ser His Arg His Phe His Cys Ile Lys Tyr Ser Lys *
                      25                      30                      35                      40

ggccatgctc agcgttcaga actactccct gtaccaccag ccatatttca acaatgtggg      567

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aaccgtttcc tatagactgg ggtctggagt tctcagtgac aaggagaata atgtaaacad 627
aagatgacga tgataatgaa gaaatactct ggacggcttt tatcacctag gatccacagg 687
aagcctgcc aagagggcaga agcacattcc atcagcagag ggcacattat caatgcagcc 747
agaccttcac ttataacat ttaatatgga aataccggac gcgtgggtcg acccggaat 807
tccggaacgg tactcccagg cgtacggctt cataaa 843

<210> 646
<211> 1465
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (251)..(931)

<400> 646
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ggcatgggtgg catgtgcctg tagtcccagc tactcgggag gcgggggcgt gggagtcgct 120
tgagcctggg aggtgtaggt tgcagtgagc cgggatcgca ccactgcact ccagcctggg 180
caacggctgg ctacgcgttta aacttaagct tccggaattc cgggtcgac gatttcgtcc 240
gcggacgaag atg gcg acc gcc atg tac ttg gag cac tat ctg gac agt 289
Met Ala Thr Ala Met Tyr Leu Glu His Tyr Leu Asp Ser
1 5 10
atc gag aac ctt ccc tgc gaa ctt cag agg aac ttc cag ctg atg cga 337
Ile Glu Asn Leu Pro Cys Glu Leu Gln Arg Asn Phe Gln Leu Met Arg
15 20 25
gag ctg gac cag agg acg gaa gat aag aaa gca gag att gac atc ctg 385
Glu Leu Asp Gln Arg Thr Glu Asp Lys Lys Ala Glu Ile Asp Ile Leu
30 35 40 45
gct gca gag tac atc tcc acg gtg aag acg ctg tct cca gac cag cgc 433
Ala Ala Glu Tyr Ile Ser Thr Val Lys Thr Leu Ser Pro Asp Gln Arg
50 55 60
gtg gag cgc ctg cag aag atc cag aac gcc tac agc aag tgc aag gaa 481
Val Glu Arg Leu Gln Lys Ile Gln Asn Ala Tyr Ser Lys Cys Lys Glu
65 70 75
tac agt gac gac aaa gtg cag ctg gcc atg cag acc tac gag atg gtg 529
Tyr Ser Asp Asp Lys Val Gln Leu Ala Met Gln Thr Tyr Glu Met Val
80 85 90
gat aaa cac att cga agg ctt gat gca gac ctg gcg cgc ttt gaa gca 577
Asp Lys His Ile Arg Arg Leu Asp Ala Asp Leu Ala Arg Phe Glu Ala
95 100 105
gat ctg aag gac aag atg gag ggc agt gat ttt gaa agc tcc gga ggg 625
Asp Leu Lys Asp Lys Met Glu Gly Ser Asp Phe Glu Ser Ser Gly Gly
110 115 120 125

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cga ggg tta aaa aaa ggc ctg cgt cag aaa gaa aaa aga ggg tcc cgg      673
Arg Gly Leu Lys Lys Gly Leu Arg Gln Lys Glu Lys Arg Gly Ser Arg
              130              135              140

ggc cga ggc agg agg aca tca gag gaa gac aca cca aag aaa aag aag      721
Gly Arg Gly Arg Arg Thr Ser Glu Glu Asp Thr Pro Lys Lys Lys Lys
              145              150              155

cac aaa gga ggg tct gag ttc act gac acc atc ctg tcc gtg cac ccc      769
His Lys Gly Gly Ser Glu Phe Thr Asp Thr Ile Leu Ser Val His Pro
              160              165              170

tct gat gtg ctg gac atg ccc gtg gac cca aac gaa ccc acg tac tgc      817
Ser Asp Val Leu Asp Met Pro Val Asp Pro Asn Glu Pro Thr Tyr Cys
              175              180              185

ctg tgc cac cag gtc tcc tat ggg gag atg att ggc tgt gac aat cca      865
Leu Cys His Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Asn Pro
              190              195              200              205

gac tgt cca att gag tgg ttt cac ttt gcc tgc gtg gac ctt acc acg      913
Asp Cys Pro Ile Glu Trp Phe His Phe Ala Cys Val Asp Leu Thr Thr
              210              215              220

aaa ccc aaa gga aaa tga tttcat ttaaataaaa acctgtagtc tgggcaacat      967
Lys Pro Lys Gly Lys *
              225

cgggagaccc caactctaca aaaaatacaa aaattagtgct ctgtcctctt agccacagtg      1027

tgtgtgtgcc cactagggac aggaggatgg tgagcaacgt gttgttgaca gaggccaatg      1087

tagaccactc ttttaagtagc tagatttctg tatatctgtc agttatttta tgtgtcaaca      1147

tatagtgtgc atatattcat tgtaattat gtggccacat ttattaaata gacatgtcat      1207

ttaacttgaa gttttttgag atactttatt taaagcattc tcccactgac accctccctg      1267

ccaaagggtgt tgtataccct ccaaagagat cgtagcatta cctcagagga gtggcattta      1327

gagtaaagag aaaatgctca aatgccacgt agcctctctc cagatgatct ctgagaggga      1387

gggtcaaaga gtaaaagttt tgggcacgaa tggcgaaacg aaatcgtcga gccggcaatt      1447

ccggatcggc caagcagt      1465

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<210> 647
 <211> 5804
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (88) .. (3927)

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<400> 647
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tacttggtca ctggagagag tgggcac      atg cct gcc gtg cgg gtt tgg gac      111
Met Pro Ala Val Arg Val Trp Asp
              1              5

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gtg gca gag cac agc cag gtg gcc gag ctg cag gag cac aag tat ggt	159
Val Ala Glu His Ser Gln Val Ala Glu Leu Gln Glu His Lys Tyr Gly	
10 15 20	
gtg gct tgt gtg gcc ttc tct cct agc gcc aag tac att gtc tct gtg	207
Val Ala Cys Val Ala Phe Ser Pro Ser Ala Lys Tyr Ile Val Ser Val	
25 30 35 40	
ggc tac cag cat gac atg atc gtc aac gtg tgg gcc tgg aag aaa aac	255
Gly Tyr Gln His Asp Met Ile Val Asn Val Trp Ala Trp Lys Lys Asn	
45 50 55	
att gtg gtg gcc tcc aac aag gtg tcc agt cgg gtg aca gca gtg tcc	303
Ile Val Val Ala Ser Asn Lys Val Ser Ser Arg Val Thr Ala Val Ser	
60 65 70	
ttc tct gag gat tgc agc tac ttt gtc act gca ggc aac cga cac atc	351
Phe Ser Glu Asp Cys Ser Tyr Phe Val Thr Ala Gly Asn Arg His Ile	
75 80 85	
aaa ttc tgg tat ctc gat gac agc aag acc tca aag gtg aat gcc act	399
Lys Phe Trp Tyr Leu Asp Asp Ser Lys Thr Ser Lys Val Asn Ala Thr	
90 95 100	
gtg ccc ttg ctg ggc cgc tca ggg ctg ctg gga gag cta cgg aac aac	447
Val Pro Leu Leu Gly Arg Ser Gly Leu Leu Gly Glu Leu Arg Asn Asn	
105 110 115 120	
cta ttc act gat gtg gcc tgt ggc aga gga aaa aag gcg gac agt acc	495
Leu Phe Thr Asp Val Ala Cys Gly Arg Gly Lys Lys Ala Asp Ser Thr	
125 130 135	
ttc tgc atc acg tcc tca ggg ctg ctg tgc gag ttc agt gat cga agg	543
Phe Cys Ile Thr Ser Ser Gly Leu Leu Cys Glu Phe Ser Asp Arg Arg	
140 145 150	
ctt ttg gac aag tgg gtg gag ctg agg gtc tac ccc gag gtg aag gat	591
Leu Leu Asp Lys Trp Val Glu Leu Arg Val Tyr Pro Glu Val Lys Asp	
155 160 165	
agt aac cag gcc tgc ctg ccc ccc agt tcc ttt att acc tgc tcc tca	639
Ser Asn Gln Ala Cys Leu Pro Pro Ser Ser Phe Ile Thr Cys Ser Ser	
170 175 180	
gac aac acc atc cgc ctg tgg aac aca gag agc tcc ggg gtg cat ggc	687
Asp Asn Thr Ile Arg Leu Trp Asn Thr Glu Ser Ser Gly Val His Gly	
185 190 195 200	
tcc acc ctc cac cga aac atc ctc agc agt gac ctc att aaa atc atc	735
Ser Thr Leu His Arg Asn Ile Leu Ser Ser Asp Leu Ile Lys Ile Ile	
205 210 215	
tat gtg gat ggg aac acc cag gcc ctg ctg gac aca gag ctg cct gga	783
Tyr Val Asp Gly Asn Thr Gln Ala Leu Leu Asp Thr Glu Leu Pro Gly	
220 225 230	
gga gac aaa gct gat gca tcc ctg ttg gat ccc cgc gtg ggc atc cgc	831
Gly Asp Lys Ala Asp Ala Ser Leu Leu Asp Pro Arg Val Gly Ile Arg	
235 240 245	
tcg gtg tgt gtc agc ccc aat gga cag cat cta gca tca ggg gac cgt	879
Ser Val Cys Val Ser Pro Asn Gly Gln His Leu Ala Ser Gly Asp Arg	
250 255 260	

atg ggc aca ctt agg gtg cac gaa ctt cag tcc ctg agt gag atg ctg	927
Met Gly Thr Leu Arg Val His Glu Leu Gln Ser Leu Ser Glu Met Leu	
265 270 275 280	
aag gtg gag gcc cat gac tct gag att ctg tgc ctg gag tat tct aag	975
Lys Val Glu Ala His Asp Ser Glu Ile Leu Cys Leu Glu Tyr Ser Lys	
285 290 295	
cca gac aca ggt ctg aaa ctg cta gca tgc gcg agc cgg gac cgg ctg	1023
Pro Asp Thr Gly Leu Lys Leu Leu Ala Ser Ala Ser Arg Asp Arg Leu	
300 305 310	
atc cat gtg ctg gat gcc ggg cgg gag tac agc cta cag cag acg ctg	1071
Ile His Val Leu Asp Ala Gly Arg Glu Tyr Ser Leu Gln Gln Thr Leu	
315 320 325	
gac gaa cac tca tcc tcc atc act gct gtc aag ttt gca gcc agt gat	1119
Asp Glu His Ser Ser Ser Ile Thr Ala Val Lys Phe Ala Ala Ser Asp	
330 335 340	
ggg caa gtc cgc atg atc agc tgt gga gca gac aag agc atc tac ttc	1167
Gly Gln Val Arg Met Ile Ser Cys Gly Ala Asp Lys Ser Ile Tyr Phe	
345 350 355 360	
cgc act gcg cag aag tct gga gat gga gtg cag ttc aca cgg aca cac	1215
Arg Thr Ala Gln Lys Ser Gly Asp Gly Val Gln Phe Thr Arg Thr His	
365 370 375	
cac gtg gtg cgg aag acg acc ctc tat gac atg gat gtg gag ccc agc	1263
His Val Val Arg Lys Thr Thr Leu Tyr Asp Met Asp Val Glu Pro Ser	
380 385 390	
tgg aag tac acg gct atc ggc tgc cag gac cga aat att cgg ata ttt	1311
Trp Lys Tyr Thr Ala Ile Gly Cys Gln Asp Arg Asn Ile Arg Ile Phe	
395 400 405	
aac atc agc agt gga aag cag aag aag ctg ttt aaa ggg tca cag ggt	1359
Asn Ile Ser Ser Gly Lys Gln Lys Lys Leu Phe Lys Gly Ser Gln Gly	
410 415 420	
gag gac ggc aca ctc att aag gtg cag aca gac ccc tca ggg atc tac	1407
Glu Asp Gly Thr Leu Ile Lys Val Gln Thr Asp Pro Ser Gly Ile Tyr	
425 430 435 440	
att gcc acc agc tgt tct gac aag aat ctc tcc att ttt gac ttc tcc	1455
Ile Ala Thr Ser Cys Ser Asp Lys Asn Leu Ser Ile Phe Asp Phe Ser	
445 450 455	
tca ggc gag tgc gtg gcc acc atg ttt ggc cac tca gag att gtc act	1503
Ser Gly Glu Cys Val Ala Thr Met Phe Gly His Ser Glu Ile Val Thr	
460 465 470	
ggc atg aaa ttt agt aat gat tgt aaa cat ctc atc tct gtg tct ggg	1551
Gly Met Lys Phe Ser Asn Asp Cys Lys His Leu Ile Ser Val Ser Gly	
475 480 485	
gac agc tgc ata ttt gtg tgg cgc ctg agc tct gag atg acc atc agc	1599
Asp Ser Cys Ile Phe Val Trp Arg Leu Ser Ser Glu Met Thr Ile Ser	
490 495 500	
atg agg cag cgt ctg gcc gag ttg cgc cag cgt cag cgg ggc ggc aag	1647
Met Arg Gln Arg Leu Ala Glu Leu Arg Gln Arg Gln Arg Gly Gly Lys	
505 510 515 520	

cag caa gga cca tcc tct ccc caa agg gct tct gga ccc aac cgg cac	1695
Gln Gln Gly Pro Ser Ser Pro Gln Arg Ala Ser Gly Pro Asn Arg His	
525 530 535	
cag gcc cca tca atg ctg tct cct gga ccg gct ctc tca tca gac agt	1743
Gln Ala Pro Ser Met Leu Ser Pro Gly Pro Ala Leu Ser Ser Asp Ser	
540 545 550	
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Asp Lys Glu Gly Glu Asp Glu Gly Thr Glu Glu Glu Leu Pro Ala Leu	
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ccc gtc ctt gcc aag agt acc aag aag gca ctg gcc tcg gtc ccc agc	1839
Pro Val Leu Ala Lys Ser Thr Lys Lys Ala Leu Ala Ser Val Pro Ser	
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cca gct ttg ccc cga agc ctg tcc cac tgg gag atg agt cgg gca cag	1887
Pro Ala Leu Pro Arg Ser Leu Ser His Trp Glu Met Ser Arg Ala Gln	
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gag tcc gtg ggg ttc ctg gac cca gct cct gca gcc aac cca gga ccc	1935
Glu Ser Val Gly Phe Leu Asp Pro Ala Pro Ala Ala Asn Pro Gly Pro	
605 610 615	
aga aga aga ggg cgc tgg gtt cag cca ggt gtg gaa ctg agc gtt aga	1983
Arg Arg Arg Gly Arg Trp Val Gln Pro Gly Val Glu Leu Ser Val Arg	
620 625 630	
tcc atg ctg gat ctg ccg cag ctg gaa aca ctg gcc cca agc ctg cag	2031
Ser Met Leu Asp Leu Arg Gln Leu Glu Thr Leu Ala Pro Ser Leu Gln	
635 640 645	
gac cct agc cag gac tcg ctg gcc atc atc cca tct ggt ccc agg aag	2079
Asp Pro Ser Gln Asp Ser Leu Ala Ile Ile Pro Ser Gly Pro Arg Lys	
650 655 660	
cat ggg cag gag gcc ctt gag act tca ctc act agc cag aat gaa aag	2127
His Gly Gln Glu Ala Leu Glu Thr Ser Leu Thr Ser Gln Asn Glu Lys	
665 670 675 680	
ccc cct cgg cct cag gct tcc caa cct tgt tcc tat ccc cat att atc	2175
Pro Pro Arg Pro Gln Ala Ser Gln Pro Cys Ser Tyr Pro His Ile Ile	
685 690 695	
cga tta ttg tca caa gag gaa ggg gtc ttt gcc caa gat ctg gaa cct	2223
Arg Leu Leu Ser Gln Glu Glu Gly Val Phe Ala Gln Asp Leu Glu Pro	
700 705 710	
gca ccc att gaa gat ggt att gtc tac ccg gag ccg agt gac aac ccc	2271
Ala Pro Ile Glu Asp Gly Ile Val Tyr Pro Glu Pro Ser Asp Asn Pro	
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acc atg gat acc agt gag ttc caa gtg cag gct cca gcc cgg gga act	2319
Thr Met Asp Thr Ser Glu Phe Gln Val Gln Ala Pro Ala Arg Gly Thr	
730 735 740	
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Leu Gly Arg Val Tyr Pro Gly Ser Arg Ser Ser Glu Lys His Ser Pro	
745 750 755 760	
gac agt gcc tgc tct gtg gat tac agc agc agc tgc ctt tcc agc ccg	2415
Asp Ser Ala Cys Ser Val Asp Tyr Ser Ser Ser Cys Leu Ser Ser Pro	
765 770 775	

gag cac ccc act gaa gac tct gag agc acg gag ccc ctc agt gtg gat Glu His Pro Thr Glu Asp Ser Glu Ser Thr Glu Pro Leu Ser Val Asp 780 785 790	2463
ggc atc tcc tca gac ctt gaa gag cca gct gag ggt gat gaa gaa gag Gly Ile Ser Ser Asp Leu Glu Glu Pro Ala Glu Gly Asp Glu Glu Glu 795 800 805	2511
gaa gaa gag gag gga ggc atg ggc ccc tat ggg cta cag gag ggc agc Glu Glu Glu Glu Gly Gly Met Gly Pro Tyr Gly Leu Gln Glu Gly Ser 810 815 820	2559
ccc cag act cca gac cag gag cag ttt cta aaa cag cac ttt gag act Pro Gln Thr Pro Asp Gln Glu Gln Phe Leu Lys Gln His Phe Glu Thr 825 830 835 840	2607
ctg gcc agt gga gct gct cca ggg gcc cca gtg cag gtc cca gag agg Leu Ala Ser Gly Ala Ala Pro Gly Ala Pro Val Gln Val Pro Glu Arg 845 850 855	2655
tca gag tct cgg agt atc tct tca cga ttc ctg ttg caa gta cag acc Ser Glu Ser Arg Ser Ile Ser Ser Arg Phe Leu Leu Gln Val Gln Thr 860 865 870	2703
cgc cca ctc agg gaa cca tcc cca tcc tcc tca agc ctg gca ctg atg Arg Pro Leu Arg Glu Pro Ser Pro Ser Ser Ser Ser Leu Ala Leu Met 875 880 885	2751
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aat ggt gcc aat ccc cct gga gca ccc ccg gag gtg gaa ccg tcc tct Asn Gly Ala Asn Pro Pro Gly Ala Pro Pro Glu Val Glu Pro Ser Ser 905 910 915 920	2847
ggc aac ccc agc ccc cag cag gca gcc tct gtg ctg ttg cca cga tgc Gly Asn Pro Ser Pro Gln Gln Ala Ala Ser Val Leu Leu Pro Arg Cys 925 930 935	2895
cgt ctc aac cct gac agc agc tgg gct ccc aag aga gtg gcc aca gcc Arg Leu Asn Pro Asp Ser Ser Trp Ala Pro Lys Arg Val Ala Thr Ala 940 945 950	2943
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ctg ctg tct cgg gag atc gaa gct cag gat ggt ctg ggc tcc ctg ccc Leu Leu Ser Arg Glu Ile Glu Ala Gln Asp Gly Leu Gly Ser Leu Pro 985 990 995 1000	3087
cca gct gat ggc cct ccg tct cgg cct cac tcc tat cag aac ccc acc Pro Ala Asp Gly Pro Pro Ser Arg Pro His Ser Tyr Gln Asn Pro Thr 1005 1010 1015	3135
acc agt tcc atg gcc aag ata tcc cgc agt atc tct gtt ggg gag aac Thr Ser Ser Met Ala Lys Ile Ser Arg Ser Ile Ser Val Gly Glu Asn 1020 1025 1030	3183

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cca ctc agc aag ctg gcc ctg ccc agc cgg gct cac ctg gtc ctg gac Pro Leu Ser Lys Leu Ala Leu Pro Ser Arg Ala His Leu Val Leu Asp 1050 1055 1060	3279
atc ccc aaa cca ctg cct gac cgt cct acc ctg gct gca ttc tct cct Ile Pro Lys Pro Leu Pro Asp Arg Pro Thr Leu Ala Ala Phe Ser Pro 1065 1070 1075 1080	3327
gtc acc aaa ggc cgg gcc cct ggc gag gca gaa aag cct ggc ttc ccg Val Thr Lys Gly Arg Ala Pro Gly Glu Ala Glu Lys Pro Gly Phe Pro 1085 1090 1095	3375
gtg ggc cta gga aaa gct cac agt aca act gag aga tgg gcc tgt ttg Val Gly Leu Gly Lys Ala His Ser Thr Thr Glu Arg Trp Ala Cys Leu 1100 1105 1110	3423
ggg gag ggc acc act ccc aag cct agg aca gag tgc cag gct cat cct Gly Glu Gly Thr Thr Pro Lys Pro Arg Thr Glu Cys Gln Ala His Pro 1115 1120 1125	3471
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caa ggc cct gaa aac ttg cag ccc cca ccc cct gag aag act ccc aac Gln Gly Pro Glu Asn Leu Gln Pro Pro Pro Pro Glu Lys Thr Pro Asn 1145 1150 1155 1160	3567
ccc atg gaa tgc acc aag cca ggg gca gcc ctg agc cag gac tca gag Pro Met Glu Cys Thr Lys Pro Gly Ala Ala Leu Ser Gln Asp Ser Glu 1165 1170 1175	3615
cca gcg gtg agc ctg gag cag tgt gag cag ctg gtg gca gag ctc cgc Pro Ala Val Ser Leu Glu Gln Cys Glu Gln Leu Val Ala Glu Leu Arg 1180 1185 1190	3663
ggc agc gtg cgc cag gca gtg cgg ctc tac cac tcg gtg gct ggc tgc Gly Ser Val Arg Gln Ala Val Arg Leu Tyr His Ser Val Ala Gly Cys 1195 1200 1205	3711
aag atg ccc tca gca gag caa agt cgg att gcc cag ctc ctc aga gac Lys Met Pro Ser Ala Glu Gln Ser Arg Ile Ala Gln Leu Leu Arg Asp 1210 1215 1220	3759
acc ttc tct tca gtg cga cag gag ctg gaa gct gtg gct ggg gca gtg Thr Phe Ser Ser Val Arg Gln Glu Leu Glu Ala Val Ala Gly Ala Val 1225 1230 1235 1240	3807
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cag gcc ctg ctg gag caa tac tca gaa ctg ttg ctt cga gcc gtg gaa Gln Ala Leu Leu Glu Gln Tyr Ser Glu Leu Leu Leu Arg Ala Val Glu 1260 1265 1270	3903
cgg cgt atg gaa cgc aaa ctc tga gttctggaag cctgtcccaa gtgaatgaat Arg Arg Met Glu Arg Lys Leu * 1275 1280	3957

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<210> 648
 <211> 1436
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (166)..(837)

<220>
 <221> misc_feature
 <222> (1)...(1436)
 <223> n = a,t,c or g

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 tcatccaaga tcatctcacc tcccatgaag ggaacggtct tctaa atg cag ttt 174
 Met Gln Phe
 1
 tcc ttc cag cag ggt gga tgg gga gca tcg ctg gct gac agg ctg gtc 222
 Ser Phe Gln Gln Gly Gly Trp Gly Ala Ser Leu Ala Asp Arg Leu Val
 5 10 15
 aga aaa tgt gat gtt ctg aat cgt gga ttt tca ggt tac aat acc agg 270
 Arg Lys Cys Asp Val Leu Asn Arg Gly Phe Ser Gly Tyr Asn Thr Arg
 20 25 30 35
 tgg gcc aaa att atc ctt cca aga tta atc agg aaa gga aac agt ttg 318
 Trp Ala Lys Ile Ile Leu Pro Arg Leu Ile Arg Lys Gly Asn Ser Leu
 40 45 50
 gac atc cca gta gca gtt aca att ttc ttt ggg gcc aat gac agt gca 366
 Asp Ile Pro Val Ala Val Thr Ile Phe Phe Gly Ala Asn Asp Ser Ala
 55 60 65
 cta aaa gat gag aat ccc aag cag cac att ccc ctg gag gag tac gct 414
 Leu Lys Asp Glu Asn Pro Lys Gln His Ile Pro Leu Glu Glu Tyr Ala
 70 75 80
 gcg aac cta aag agc atg gtg cag tac ctg aag tcc gtg gac atc cct 462
 Ala Asn Leu Lys Ser Met Val Gln Tyr Leu Lys Ser Val Asp Ile Pro
 85 90 95
 gag aat cga gtc att ctc atc acg ccg acc cca ctt tgt gaa aca gcc 510
 Glu Asn Arg Val Ile Leu Ile Thr Pro Thr Pro Leu Cys Glu Thr Ala
 100 105 110 115
 tgg gaa gaa cag tgc atc ata caa ggt tgc aaa cta aat cgc ctg aac 558
 Trp Glu Glu Gln Cys Ile Ile Gln Gly Cys Lys Leu Asn Arg Leu Asn
 120 125 130
 tct gtt gtt ggt gaa tat gcc aat gcg tgt tta caa gtg gcc caa gac 606
 Ser Val Val Gly Glu Tyr Ala Asn Ala Cys Leu Gln Val Ala Gln Asp
 135 140 145
 tgt ggg act gac gta ctt gac ctg tgg acc ctg atg cag gac agc cag 654
 Cys Gly Thr Asp Val Leu Asp Leu Trp Thr Leu Met Gln Asp Ser Gln
 150 155 160

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gac ttc tca tct tat tta tca gat gga cta cat ttg tct cca aag ggg      702
Asp Phe Ser Ser Tyr Leu Ser Asp Gly Leu His Leu Ser Pro Lys Gly
    165                      170                      175

aat gaa ttt ttg ttc tcg cat ctc tgg cct ttg ata gag aaa aag gtc      750
Asn Glu Phe Leu Phe Ser His Leu Trp Pro Leu Ile Glu Lys Lys Val
    180                      185                      190                      195

tct tct cta cct ttg ctg ctt cct tac tgg cgg gat gta gca gaa gca      798
Ser Ser Leu Pro Leu Leu Leu Pro Tyr Trp Arg Asp Val Ala Glu Ala
                200                      205                      210

aaa cct gaa tta agt ctg ctg gga gat gga gac cat tag ccaatcacag      847
Lys Pro Glu Leu Ser Leu Leu Gly Asp Gly Asp His *
                215                      220

gagacccaaa tctgcttggt atctacagaa ctcaaagttg tcaatacgtg gaggtacgct      907

tttttctca ggcttaaacc ttgccactg atattaataa taaaagtatt agatgatttt      967

tcagggaagt tttatactta ggtccattgt gtttcgacag tatttattaa tgcagatatt 1027

agtgtacag ctataaaata taccctgagc agcttggttaa ttctataaat gacaaagact 1087

atgtttttta aaagtcacaa ttttataaaa atggtttttt ttacattctt ttgagaactg 1147

tttcactcat acatacaccc acacacccca ctcaaccttg tatcaaattc caaaagtgtg 1207

actaaaggta taaggattat catgactagg ttaaaaggat aggcaaatac cataagggtg 1267

caagttccaa ggtattaggt ataacaaggt atctggggta accaaatgtc cttgggaatg 1327

gggggggtgg nggggtatat ggtaggtcc cggggttggg ttaactgcc ntcaaattta 1387

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<210> 649
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 <212> DNA
 <213> Homo sapiens

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 <222> (118)..(252)

<220>
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 <223> n = a,t,c or g

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agctgaaggt aagtacattt tccactaatt cctcagcttg ctaagtgtt ttggacc      117
atg aat aga gca gct agg aac aaa tct gag aag agg tac tat tca gaa      165
Met Asn Arg Ala Ala Arg Asn Lys Ser Glu Lys Arg Tyr Tyr Ser Glu
    1                      5                      10                      15

ttc ctc caa ata gct cat ctt ttt aat tat ggg ctt tca tcc ttc cta      213
Phe Leu Gln Ile Ala His Leu Phe Asn Tyr Gly Leu Ser Ser Phe Leu

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20

25

30

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agg gag ttt att att ttt cta att aaa cta cta caa tga aggtattac 262
Arg Glu Phe Ile Ile Phe Leu Ile Lys Leu Leu Gln *
      35              40              45

ctttttgtct agctaaaaca atctttccta ttaatgaatt tattggcttc tctagtactc 322
ttcaaattgt cattgagctc tattcaagga ctacagccag ttttttccta atagaattag 382
gggtgaaaca aatcatgctt ctattatcac ttctggagtt agcccttcac ctgatcagct 442
tgtctagggt taagagtgcg ggggttttag cgccacaaag acgtgggcat gcggcagctt 502
cctgaacctc aggcattggt gtctaagcaa ctccaccatc cacacgtgtg acgttacagt 562
tctgggagat gcacgcacac tntctgtgcc tttctcaacc actagcttaa tcagcctcca 622
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gccagcctct cgtgtcgcgc c 1183

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<210> 650

<211> 1885

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1115) .. (1744)

<400> 650

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gatgactggc tgctctacct tctttttgga cttcatcttt ttctttgcgg aggccttagg 180
gtcatcactt atggggatgt attccggagc ctcaactttg actggcttct ttttacttcc 240
tttcctaggg ctgctctcca tggacctgga gggcttggag tggcctggga gggcatctcc 300
ctcctgggtg attttttttt tcttcttcac ctcccatgtg tgttctctgg ggctcttcog 360
cttcggttcc tgcccaagg ctgcctgttc ctcatccttc tccccactg agcaagtgtc 420

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cccaacatcc ctggcctccc tggcctcaca gaaccaaggg tcttggaccg agaaggctgt      480
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ttcctcctca cctgtcttag ggtctgggga ggttttcacc ccagaggcat gggacatggc      600
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cttctgagg ctgggtgact tctctgtccg tctagcaggc agcgtggtct caggttctac      720
atgctcctcg caaagggtgc tgacaccctt ctttttcttc ttctttttct tcaactagagg      780
catctcaggt gcctgcccac gggccacact cttagagggg gatgtagctc ttaaaggaga      840
aacatcagca aagtaatcat cattgtttta aactgagtat cgagtctctg gttctttgac      900
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cattccggtg ggcgaaattt ccccgctccc acgtgagagc cagctccgcc gtgaccggga      1020
agtcacttcc gagtcgccgg cccaccctct cgggttccgg cttcttccgg gtgcggcctt      1080
tccggcgaac gcggttaccg tggaaaccgc ggcc      atg gcg gca ccg cgg caa      1132
                                         Met Ala Ala Pro Arg Gln
                                         1                    5

atc ccc agc cac ata gtg cgc ctc aag ccc agc tgc tct aca gac tcg      1180
Ile Pro Ser His Ile Val Arg Leu Lys Pro Ser Cys Ser Thr Asp Ser
              10                    15                    20

tcg ttc acc cgg acg ccg gtg ccc acc gtg tct ctc gcg tcc cgc gag      1228
Ser Phe Thr Arg Thr Pro Val Pro Thr Val Ser Leu Ala Ser Arg Glu
              25                    30                    35

ctg cct gtc tcg tcg tgg cag gtc acc gag ccg tca agc aag aat ctg      1276
Leu Pro Val Ser Ser Trp Gln Val Thr Glu Pro Ser Ser Lys Asn Leu
              40                    45                    50

tgg gag cag atc tgc aag gag tat gaa gct gag cag cct ccc ttt cca      1324
Trp Glu Gln Ile Cys Lys Glu Tyr Glu Ala Glu Gln Pro Pro Phe Pro
              55                    60                    65                    70

gaa gga tat aaa gtc aaa cag gag cct gtg att acg gtt gcg cca gta      1372
Glu Gly Tyr Lys Val Lys Gln Glu Pro Val Ile Thr Val Ala Pro Val
              75                    80                    85

gag gaa atg ctt ttt cat ggc ttc agt gca gag cac tat ttt ccg gtt      1420
Glu Glu Met Leu Phe His Gly Phe Ser Ala Glu His Tyr Phe Pro Val
              90                    95                    100

tcc cat ttc acc atg atc tca cgt aca ccc tgt cct caa gat aaa tcg      1468
Ser His Phe Thr Met Ile Ser Arg Thr Pro Cys Pro Gln Asp Lys Ser
              105                    110                    115

gaa aca atc aac cca aaa aca tgt tct ccc aaa gaa tat ttg gaa act      1516
Glu Thr Ile Asn Pro Lys Thr Cys Ser Pro Lys Glu Tyr Leu Glu Thr
              120                    125                    130

ttc atc ttt cct gtt ctg ctt ccc gga atg gct agc ctg ctt cac caa      1564
Phe Ile Phe Pro Val Leu Leu Pro Gly Met Ala Ser Leu Leu His Gln
              135                    140                    145                    150

gcg aag aaa gaa aaa tgt ttt gag gtt cgc tgt gat cct gag att caa      1612

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Ala Lys Lys Glu Lys Cys Phe Glu Val Arg Cys Asp Pro Glu Ile Gln
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 gaa ctg cgt cag tgg cag aag aaa ctt cgc gag gcc aag cac att cac 1660
 Glu Leu Arg Gln Trp Gln Lys Lys Leu Arg Glu Ala Lys His Ile His
 170 175 180
 cag caa gtc aaa att ttc tgg gcc aag caa gaa caa aaa gtg aaa tgc 1708
 Gln Gln Val Lys Ile Phe Trp Ala Lys Gln Glu Gln Lys Val Lys Cys
 185 190 195
 aaa atg gag gac gat cag tac ctg cag cca aga tga aaat tccatcatct 1758
 Lys Met Glu Asp Asp Gln Tyr Leu Gln Pro Arg *
 200 205 210
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 aaaaaaa 1885

<210> 651
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 <213> Homo sapiens

<220>
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 <222> (115)..(363)

<400> 651
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 Met
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 gat tcc ttt ggg caa ccc aga cca gaa gat aat cag tca gta gtc aga 165
 Asp Ser Phe Gly Gln Pro Arg Pro Glu Asp Asn Gln Ser Val Val Arg
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 aga atg caa aag aaa tac tgg aaa act aaa cag gtc ttt atc aaa gca 213
 Arg Met Gln Lys Lys Tyr Trp Lys Thr Lys Gln Val Phe Ile Lys Ala
 20 25 30
 aca gga aaa aaa gag gat gag cac ttg gtg gcg tct gat gct gaa ctg 261
 Thr Gly Lys Lys Glu Asp Glu His Leu Val Ala Ser Asp Ala Glu Leu
 35 40 45
 gat gct aaa ctt gag gtt ttt cac tct gtt caa gag aca tgc act gaa 309
 Asp Ala Lys Leu Glu Val Phe His Ser Val Gln Glu Thr Cys Thr Glu
 50 55 60 65
 ctt ctg aag ata atc gag aaa tac cag cta aga ctc aat ggt atg aaa 357
 Leu Leu Lys Ile Ile Glu Lys Tyr Gln Leu Arg Leu Asn Gly Met Lys
 70 75 80
 tca tag ttatctatct gataattccc atttaaaata aataattagca ttttttaaaa 413
 Ser *

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 tacagctacc tgttctcaaa ggccccagta ttctctcttc tttcttcagt taatcaaadc 533
 ctctgaccca gatttatctt ttgctgatat tttttttctt tgagacaggg tctttctctg 593
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 tgggggtgtc agcaggagag cctgagggtt gaggccagc gtgaac atg gca gct 415
 Met Ala Ala
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 aat ggg gac tct ccc cca tgg tcc ccg gcc ctg gct gca gag gga cgt 463
 Asn Gly Asp Ser Pro Pro Trp Ser Pro Ala Leu Ala Ala Glu Gly Arg
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 ggc agc tca tgt gag gct tca gtg tca ttt gag gac gtg act gtg gac 511
 Gly Ser Ser Cys Glu Ala Ser Val Ser Phe Glu Asp Val Thr Val Asp
 20 25 30 35
 ttc agc aag gag gag tgg cag cac ttg gac cct gcc cag aga cgc ctg 559
 Phe Ser Lys Glu Glu Trp Gln His Leu Asp Pro Ala Gln Arg Arg Leu
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 tac tgg gat gtg aca cta gag aac tac agc cac ctg ctc tca gtg ggg 607
 Tyr Trp Asp Val Thr Leu Glu Asn Tyr Ser His Leu Leu Ser Val Gly
 55 60 65
 tac caa att ccc aag tca gag gct gcc ttc aag ttg gag caa gga gag 655
 Tyr Gln Ile Pro Lys Ser Glu Ala Ala Phe Lys Leu Glu Gln Gly Glu
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 ggg cca tgg atg ctg gag ggg gaa gcc cca cat cag agc tgt tca ggt 703
 Gly Pro Trp Met Leu Glu Gly Glu Ala Pro His Gln Ser Cys Ser Gly
 85 90 95
 gag gct att ggg aaa atg cag caa cag gga att cct gga gga att ttc 751
 Glu Ala Ile Gly Lys Met Gln Gln Gln Gly Ile Pro Gly Gly Ile Phe
 100 105 110 115

ttc cac tgt gag aga ttt gat caa ccc ata gga gaa gat tca tta tgt	799
Phe His Cys Glu Arg Phe Asp Gln Pro Ile Gly Glu Asp Ser Leu Cys	
120 125 130	
tct att tta gaa gaa ctg tgg caa gat aat gac cag cta gag caa cgt	847
Ser Ile Leu Glu Glu Leu Trp Gln Asp Asn Asp Gln Leu Glu Gln Arg	
135 140 145	
cag gaa aac cag aat aac ctt tta agt cat gtg aaa gta ttg att aag	895
Gln Glu Asn Gln Asn Asn Leu Leu Ser His Val Lys Val Leu Ile Lys	
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gag agg ggc tat gaa cat aaa aac att gaa aaa ata att cat gtg act	943
Glu Arg Gly Tyr Glu His Lys Asn Ile Glu Lys Ile Ile His Val Thr	
165 170 175	
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Thr Lys Leu Val Pro Ser Ile Lys Arg Leu His Asn Cys Asp Thr Ile	
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Leu Lys His Thr Leu Asn Ser His Asn His Asn Arg Asn Ser Ala Thr	
200 205 210	
aag aac ctt ggc aag att ttt gga aat ggt aac aat ttc ccc cat agc	1087
Lys Asn Leu Gly Lys Ile Phe Gly Asn Gly Asn Asn Phe Pro His Ser	
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cct tcc tct act aag aat gag aat gct aaa aca gga gca aat tcc tgt	1135
Pro Ser Ser Thr Lys Asn Glu Asn Ala Lys Thr Gly Ala Asn Ser Cys	
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gaa cat gac cac tat gaa aaa cat ctc agc cac aaa caa gct ccc acc	1183
Glu His Asp His Tyr Glu Lys His Leu Ser His Lys Gln Ala Pro Thr	
245 250 255	
cac cat cag aaa att cat cct gag gag aag ctt tat gtg tgt act gaa	1231
His His Gln Lys Ile His Pro Glu Glu Lys Leu Tyr Val Cys Thr Glu	
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Cys Val Met Gly Phe Thr Gln Lys Ser His Leu Phe Glu His Gln Arg	
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Ile His Ala Gly Glu Lys Ser Arg Glu Cys Asp Lys Ser Asn Lys Val	
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Phe Pro Gln Lys Pro Gln Val Asp Val His Pro Ser Val Tyr Thr Gly	
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Glu Lys Pro Tyr Leu Cys Thr Gln Cys Gly Lys Val Phe Thr Leu Lys	
325 330 335	
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Ser Asn Leu Ile Thr His Gln Lys Ile His Thr Gly Gln Lys Pro Tyr	
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Lys Cys Ser Glu Cys Gly Lys Ala Phe Phe Gln Arg Ser Asp Leu Phe	
360 365 370	

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Arg His Leu Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Ser Glu	
375 380 385	
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Cys Gly Lys Gly Phe Ser Gln Asn Ser Asp Leu Ser Ile His Gln Lys	
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Thr His Thr Gly Glu Lys His Tyr Glu Cys Asn Glu Cys Gly Lys Ala	
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Phe Thr Arg Lys Ser Ala Leu Arg Met His Gln Arg Ile His Thr Gly	
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Glu Lys Pro Tyr Val Cys Ala Asp Cys Gly Lys Ala Phe Ile Gln Lys	
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Ser His Phe Asn Thr His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr	
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Val His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Ile Cys Thr Glu	
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Cys Gly Lys Val Phe Thr His Arg Thr Asn Leu Thr Thr His Gln Lys	
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act cat act ggg gaa aaa ccc tat atg tgt gct gaa tgt gga aag gct	1999
Thr His Thr Gly Glu Lys Pro Tyr Met Cys Ala Glu Cys Gly Lys Ala	
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Phe Thr Asp Gln Ser Asn Leu Ile Lys His Gln Lys Thr His Thr Gly	
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Glu Lys Pro Tyr Lys Cys Asn Gly Cys Gly Lys Ala Phe Ile Trp Lys	
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Ser Arg Leu Lys Ile His Gln Lys Ser His Ile Gly Glu Arg His Tyr	
565 570 575	
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Glu Cys Lys Asp Cys Gly Lys Ala Phe Ile Gln Lys Ser Thr Leu Ser	
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Val His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Val Cys Pro Glu	
600 605 610	
tgc ggg aag gcc ttt atc cag aaa tcg cac ttc att gcg cat cat aga	2287
Cys Gly Lys Ala Phe Ile Gln Lys Ser His Phe Ile Ala His His Arg	
615 620 625	

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atc cat act gga gag aag cct tat gaa tgc agc gac tgt ggg aaa tgc      2335
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Phe Thr Lys Lys Ser Gln Leu Arg Val His Gln Lys Ile His Thr Gly
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gag aag ccc aat ata tgt gct gaa tgt gga aag gcc ttc act gac cga      2431
Glu Lys Pro Asn Ile Cys Ala Glu Cys Gly Lys Ala Phe Thr Asp Arg
      660                      665                      670                      675

tca aat ctc ata aca cat cag aaa atc cac act agg gag aaa ccc tat      2479
Ser Asn Leu Ile Thr His Gln Lys Ile His Thr Arg Glu Lys Pro Tyr
      680                      685                      690

gaa tgt ggt gac tgc ggg aaa acc ttc acc tgg aag tca cgc ctc aat      2527
Glu Cys Gly Asp Cys Gly Lys Thr Phe Thr Trp Lys Ser Arg Leu Asn
      695                      700                      705

ata cat cag aag tct cat act gga gaa aga cac tat gaa tgt agt aaa      2575
Ile His Gln Lys Ser His Thr Gly Glu Arg His Tyr Glu Cys Ser Lys
      710                      715                      720

tgt ggg aaa gct ttc atc cag aaa gcc aca cta agt atg cat cag ata      2623
Cys Gly Lys Ala Phe Ile Gln Lys Ala Thr Leu Ser Met His Gln Ile
      725                      730                      735

att cat aca gga aag aaa cct tat gct tgt aca gaa tgt cag aag gcc      2671
Ile His Thr Gly Lys Lys Pro Tyr Ala Cys Thr Glu Cys Gln Lys Ala
      740                      745                      750                      755

ttt act gac aga tcg aat ctc att aaa cac cag aaa atg cat agt gga      2719
Phe Thr Asp Arg Ser Asn Leu Ile Lys His Gln Lys Met His Ser Gly
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gaa aaa cgc tat aaa gcc agt gac tga gaaag tcttcacctg gaaatcacia      2771
Glu Lys Arg Tyr Lys Ala Ser Asp *
      775                      780

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ctgctgagta ggcgctgtga tttcaga      atg tct ggg cga ggt aaa ggt ggc      171
Met Ser Gly Arg Gly Lys Gly Gly

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aag ggg ctg ggt aag gga ggc gcc aag cgc cac cgg aag gtg ctg cgg 219
 Lys Gly Leu Gly Lys Gly Gly Ala Lys Arg His Arg Lys Val Leu Arg
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 gac aat atc caa ggc att aca aag ccg gcg att cgc cgt ctc gcc cga 267
 Asp Asn Ile Gln Gly Ile Thr Lys Pro Ala Ile Arg Arg Leu Ala Arg
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 cgt ggg ggc gtc aag cgc att tct ggt ctc atc tac gag gag acc cgg 315
 Arg Gly Gly Val Lys Arg Ile Ser Gly Leu Ile Tyr Glu Glu Thr Arg
 45 50 55
 gga gtc ctc aaa gtc ttc ctg gag aac gtg atc cgt gac gcg gtg act 363
 Gly Val Leu Lys Val Phe Leu Glu Asn Val Ile Arg Asp Ala Val Thr
 60 65 70
 tac acg gag cac gcc aag cgc aag acc gtc acg gcc atg gat gtg gtg 411
 Tyr Thr Glu His Ala Lys Arg Lys Thr Val Thr Ala Met Asp Val Val
 75 80 85
 tac gcg ctg aaa cgc cag ggt cgc acc ctt tat ggt ttc ggc ggt tga 459
 Tyr Ala Leu Lys Arg Gln Gly Arg Thr Leu Tyr Gly Phe Gly Gly *
 90 95 100
 gctgtcccca cagcttctct acagactcca aaaggccctt ttcagggccc ccaaactgtc 519
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 Glu Ala Lys Leu Met Gly Phe Thr Gln Gly Cys Val Thr Phe Glu Asp
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 gtg gcc att tac ttc tcc cag gaa gaa tgg ggg ctc ctt gat gag gct 144
 Val Ala Ile Tyr Phe Ser Gln Glu Glu Trp Gly Leu Leu Asp Glu Ala
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 cag agg ctc ctg tac cgc gat gtg atg ctg gag aac ttt gca ctt ata 192

Gln	Arg	Leu	Leu	Tyr	Arg	Asp	Val	Met	Leu	Glu	Asn	Phe	Ala	Leu	Ile	
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Thr	Ala	Leu	Val	Cys	Trp	His	Gly	Met	Glu	Asp	Glu	Glu	Thr	Pro	Glu	
65					70					75					80	
caa	agt	gtt	tct	gta	gaa	gga	gta	cct	cag	gtc	agg	act	cca	gag	gcc	288
Gln	Ser	Val	Ser	Val	Glu	Gly	Val	Pro	Gln	Val	Arg	Thr	Pro	Glu	Ala	
				85				90						95		
agt	cca	tcc	acc	cag	aag	att	caa	tcc	tgt	gac	atg	tgt	gtc	cca	ttc	336
Ser	Pro	Ser	Thr	Gln	Lys	Ile	Gln	Ser	Cys	Asp	Met	Cys	Val	Pro	Phe	
			100					105					110			
ctg	acc	gac	att	ttg	cac	ctg	acc	gat	ttg	cct	ggg	cag	gaa	cta	tac	384
Leu	Thr	Asp	Ile	Leu	His	Leu	Thr	Asp	Leu	Pro	Gly	Gln	Glu	Leu	Tyr	
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Leu	Thr	Gly	Ala	Cys	Ala	Val	Phe	His	Gln	Asp	Gln	Lys	His	His	Ser	
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gca	gag	aaa	ccc	ttg	gaa	agt	gac	atg	gac	aag	gcc	tca	ttt	gtg	cag	480
Ala	Glu	Lys	Pro	Leu	Glu	Ser	Asp	Met	Asp	Lys	Ala	Ser	Phe	Val	Gln	
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tgc	tgc	ctg	ttc	cat	gag	tca	gga	atg	cct	ttc	acc	agc	agt	gag	gtt	528
Cys	Cys	Leu	Phe	His	Glu	Ser	Gly	Met	Pro	Phe	Thr	Ser	Ser	Glu	Val	
				165					170					175		
ggg	aag	gac	ttc	cta	gcc	cca	ttg	ggc	att	ctt	cag	ccg	caa	gct	att	576
Gly	Lys	Asp	Phe	Leu	Ala	Pro	Leu	Gly	Ile	Leu	Gln	Pro	Gln	Ala	Ile	
			180					185					190			
gct	aac	tat	gag	aag	cca	aac	aaa	atc	agc	aaa	tgt	gag	gag	gcc	ttt	624
Ala	Asn	Tyr	Glu	Lys	Pro	Asn	Lys	Ile	Ser	Lys	Cys	Glu	Glu	Ala	Phe	
		195					200					205				
cat	gtt	gga	ata	agt	cat	tac	aag	tgg	agt	caa	tgc	agg	aga	gag	tcc	672
His	Val	Gly	Ile	Ser	His	Tyr	Lys	Trp	Ser	Gln	Cys	Arg	Arg	Glu	Ser	
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Ser	His	Lys	His	Thr	Phe	Phe	His	Pro	Arg	Val	Cys	Thr	Gly	Lys	Arg	
225					230					235					240	
ctt	tat	gaa	tct	agc	aaa	tgt	ggg	aaa	gcc	tgc	tgc	tgt	gag	tgc	tcc	768
Leu	Tyr	Glu	Ser	Ser	Lys	Cys	Gly	Lys	Ala	Cys	Cys	Cys	Glu	Cys	Ser	
				245					250					255		
ctt	gtt	cag	ctg	caa	aga	gtc	cac	cct	gga	gaa	agg	cct	tat	gag	tgc	816
Leu	Val	Gln	Leu	Gln	Arg	Val	His	Pro	Gly	Glu	Arg	Pro	Tyr	Glu	Cys	
			260					265					270			
agt	gaa	tgt	ggg	aaa	tct	ttt	agc	caa	acc	tct	cat	ctg	aat	gat	cat	864
Ser	Glu	Cys	Gly	Lys	Ser	Phe	Ser	Gln	Thr	Ser	His	Leu	Asn	Asp	His	
		275					280					285				
cgg	aga	atc	cac	act	gga	gaa	agg	cct	tat	gtg	tgt	ggg	cag	tgt	ggg	912
Arg	Arg	Ile	His	Thr	Gly	Glu	Arg	Pro	Tyr	Val	Cys	Gly	Gln	Cys	Gly	
	290					295					300					
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Lys Ser Phe Ser Gln Arg Ala Thr Leu Ile Lys His His Arg Val His	
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act gga gaa agg cct tac gag tgt ggt gaa tgt ggg aaa tct ttt agc	1008
Thr Gly Glu Arg Pro Tyr Glu Cys Gly Glu Cys Gly Lys Ser Phe Ser	
325 330 335	
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Gln Ser Ser Asn Leu Ile Glu His Cys Arg Ile His Thr Gly Glu Arg	
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cct tat gag tgt gat gaa tgt gga aaa gcc ttt ggg tcc aaa tcc act	1104
Pro Tyr Glu Cys Asp Glu Cys Gly Lys Ala Phe Gly Ser Lys Ser Thr	
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ctt gtt cga cac cag aga act cac aca gga gaa aag cca tat gag tgt	1152
Leu Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys	
370 375 380	
ggt gaa tgt ggg aaa tta ttc aga caa agc ttc agc ctt gtt gta cac	1200
Gly Glu Cys Gly Lys Leu Phe Arg Gln Ser Phe Ser Leu Val Val His	
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Gln Arg Ile His Thr Thr Ala Arg Pro Tyr Glu Cys Gly Gln Cys Gly	
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aaa tca ttt agc cta aag tgt ggc ctc att cag cac cag tta att cac	1296
Lys Ser Phe Ser Leu Lys Cys Gly Leu Ile Gln His Gln Leu Ile His	
420 425 430	
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Ser Gly Ala Arg Pro Phe Glu Cys Asp Glu Cys Gly Lys Ser Phe Ser	
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Gln Arg Thr Thr Leu Asn Lys His His Lys Val His Thr Ala Glu Arg	
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cct tat gta tgt ggg gaa tgt ggg aaa gct ttt atg ttc aaa tct aaa	1440
Pro Tyr Val Cys Gly Glu Cys Gly Lys Ala Phe Met Phe Lys Ser Lys	
465 470 475 480	
ctt gtt agg cac cag aga act cac act gga gaa agg cct ttt gag tgc	1488
Leu Val Arg His Gln Arg Thr His Thr Gly Glu Arg Pro Phe Glu Cys	
485 490 495	
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Ser Glu Cys Gly Lys Phe Phe Arg Gln Ser Tyr Thr Leu Val Glu His	
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Gln Lys Ile His Thr Gly Leu Arg Pro Tyr Asp Cys Gly Gln Cys Gly	
515 520 525	
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Lys Ser Phe Ile Gln Lys Ser Ser Leu Ile Gln His Gln Val Val His	
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aca gga gaa agg cca tat gag tgt ggc aaa tgt ggg aag tcc ttt aca	1680
Thr Gly Glu Arg Pro Tyr Glu Cys Gly Lys Cys Gly Lys Ser Phe Thr	
545 550 555 560	
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Gln His Ser Gly Leu Ile Leu His Arg Lys Ser His Thr Val Glu Arg
565 570 575

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Pro Arg Asp Ser Ser Lys Cys Gly Lys Pro Tyr Ser Pro Arg Ser Asn
580 585 590

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595

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Met Ala Gly
1

ccg ggc cca ggc ccg ggg gac ccg gac gag cag tac gat ttc ctg ttc 222
Pro Gly Pro Gly Pro Gly Asp Pro Asp Glu Gln Tyr Asp Phe Leu Phe
5 10 15

aag ctg gtg ctg gtg ggc gac gca agc gtg ggc aag acg tgc gtg gtg 270
Lys Leu Val Leu Val Gly Asp Ala Ser Val Gly Lys Thr Cys Val Val
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cag cgc ttc aag acc ggc gcc ttc tcg gag cgc cag gga agc acc atc 318
Gln Arg Phe Lys Thr Gly Ala Phe Ser Glu Arg Gln Gly Ser Thr Ile
40 45 50

ggc gtc gac ttc acc atg aag acg ctg gag atc cag ggc aag cgg gtc 366
Gly Val Asp Phe Thr Met Lys Thr Leu Glu Ile Gln Gly Lys Arg Val
55 60 65

aag ctg cag atc tgg gac acg gcc ggc cag gag cgg ttc cgc acc atc 414
Lys Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile
70 75 80

acc cag agc tac tac cgc agt gcc aat ggg gcc atc ctt gcc tac gac 462
Thr Gln Ser Tyr Tyr Arg Ser Ala Asn Gly Ala Ile Leu Ala Tyr Asp
85 90 95

atc acc aag agg agc tcc ttc ctg tcg gtg cct cac tgg att gag gat 510
Ile Thr Lys Arg Ser Ser Phe Leu Ser Val Pro His Trp Ile Glu Asp
100 105 110 115

gtg agg aag tat gcg ggc tcc aac att gtg cag ctg ctg atc ggg aac 558
Val Arg Lys Tyr Ala Gly Ser Asn Ile Val Gln Leu Leu Ile Gly Asn

	120	125	130	
aag tca gac ctc agc gag ctt cgg gag gtc tcc ttg gct gag gca cag				606
Lys Ser Asp Leu Ser Glu Leu Arg Glu Val Ser Leu Ala Glu Ala Gln				
	135	140	145	
agc ctg gct gag cac tat gac atc ctg tgt gcc att gag acg tct gcc				654
Ser Leu Ala Glu His Tyr Asp Ile Leu Cys Ala Ile Glu Thr Ser Ala				
	150	155	160	
aag gac tcg agc aac gtg gag gag gcc ttc ctg agg gtg gcc acg gag				702
Lys Asp Ser Ser Asn Val Glu Glu Ala Phe Leu Arg Val Ala Thr Glu				
	165	170	175	
ctc atc atg cgg cac ggg ggc ccc ttg ttc agc gag aag agc ccc gac				750
Leu Ile Met Arg His Gly Gly Pro Leu Phe Ser Glu Lys Ser Pro Asp				
	180	185	190	195
cac atc cag ctg aac agc aag gac atc gga gaa ggc tgg ggc tgc ggg				798
His Ile Gln Leu Asn Ser Lys Asp Ile Gly Glu Gly Trp Gly Cys Gly				
	200	205	210	
tgc tga ccaggggccc ggccggcaga ctgggggttc cccacctcct tgctctcccc				854
Cys *				
agcctgccaa gccagccct ccagagccag cctcctggg taccggcaac tacagcagcc				914
gggtgaagct ctggagctct gcatcctgtg gcttggtgc gggatggagg ctctccttga				974
ggaaggggaa gcaggatacc ctggcgggcc accctgccag ccagcagctg gccctccacc				1034
atcttcacat tccaagactg gcctgaaccc gccggtgtgg gccacagtgg gaggggccag				1094
cagtcctccc tgtcccatg				1113

<210> 656
 <211> 1406
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (907)..(1029)

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aactacctgg ggagggtgag acaacaaaat ccctttaaac tgggaggcaa aaaattcaat	120
gaaccgggat tttggttctg cctcccacc cgggggcaaa aggaggctcc ctccaaaaaa	180
aaaaaaaaaa aaaaattcaa ctaatacttt agtcattgtg actttaagaa agagacttgg	240
tcacctttac tgtaacactc agacatcatt tacttcagtt gatggagatt tcaaaattcc	300
ttttcaaaag agctaacaat acaaacacca tgaaaaagtc acctaggcct tgcaaaacgg	360
aaacttagaa aacgtgagaa aatacagcac tatcagtcct tgaaattgcg aagatgtcaa	420
ctggctagag ttttaataaca agaattgagta aactctggga attctgaaaa atcacacaca	480

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tgaacatac agtctagtta tcatttctag acttcctgct cattaataaa taatggtaac 540
ctgaagatgt cacactgctt ctctacagat ttgactgggt tctgggttct gcctaaaagg 600
accctgttgg caacaaccta agttcacttg tactgatcac attttccaag tactctagtc 660
ggttaattta cactttattt ttttaaaaag ttgatttaaa aaagaaacaa cacaagttta 720
gaatccataa aatgtcagca atgctgatgt gcactggact gaaacatctt gatcatcttc 780
tgatagaagt aatattccat acaaaaagat tcttagatc cattttttgc ttcattattg 840
tttgtggctt gctttctttg agcaataaag gggtaacatac acttgtccgc tcctaggaac 900
cgatac atg cac aca act gct tca aat ggt agg atg ctc ttc atg aag 948
      Met His Thr Thr Ala Ser Asn Gly Arg Met Leu Phe Met Lys
        1             5             10

gtc acg atg tac atg agg cgg gga gtg cag atc atg ggc tgg tca gtg 996
Val Thr Met Tyr Met Arg Arg Gly Val Gln Ile Met Gly Trp Ser Val
  15             20             25             30

agg atg gcc ttc atg gcc tgc ttc aca cag taa tcaggctt cagaggtggc 1047
Arg Met Ala Phe Met Ala Cys Phe Thr Gln *
        35             40

agaaaaggct caatttcttt cctgaaagtt atttattcaa aaacaaaatg aaaaattaac 1107
tcaatagaaa agactggaaa tacatatcaa aacattaaca gtgatgttat ctgagtgatg 1167
ggattttggg tacattttgt tttcttcata gtgcttttct gtattttcca aattttcctg 1227
ctatgaacac attttatttg cacagtctgg agaacaagtt gggaaaaaaa agcaaaattg 1287
gtctgctttt ccataagatg aaaaagtcac gtttttaaga tgccttaaaa gtattttcaa 1347
ttattttcct atgaaagctt caatgaaaag gagaagggtg ttggccggac gcgtgggtc 1406

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<210> 657
 <211> 1537
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (375) .. (1127)

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<400> 657
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aacgtctggg ccctcacctg gccgggggag tcgtccctt ccaggactcc ctggtttaac 120
gcgttcccc ccatgtecta gctgccctcc ctgtggcggtg agccttcggc ctggtgcgcc 180
ccgctgccct tcctggctgt gactctgggtg gggttccgaa ggccccctta tgcccggcag 240
acccctaccg acggcggcac tacattctgg ggccacgagg aggcactcat cgtttcgttc 300
caaccgccgc caacggccct ggccctcgcg agctctggaa ctacagaggt cgcacgccgc 360

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ggcagtgagt gtgg	atg gct tgg cag gtg agc ctg ctg gag ctg gag gac	410
	Met Ala Trp Gln Val Ser Leu Leu Glu Leu Glu Asp	
	1 5 10	
egg ctt cag tgt ccc atc tgc ctg gag gtc ttc aag gag tcc cta atg	458	
Arg Leu Gln Cys Pro Ile Cys Leu Glu Val Phe Lys Glu Ser Leu Met		
	15 20 25	
cta cag tgc ggc cac tcc tac tgc aag ggc tgc ctg gtt tcc ctg tcc	506	
Leu Gln Cys Gly His Ser Tyr Cys Lys Gly Cys Leu Val Ser Leu Ser		
	30 35 40	
tac cac ctg gac acc aag gtg cgc tgc ccc atg tgc tgg cag gtg gtg	554	
Tyr His Leu Asp Thr Lys Val Arg Cys Pro Met Cys Trp Gln Val Val		
	45 50 55 60	
gac ggc agc agc tcc ttg ccc aac gtc tcc ctg gcc tgg gtg atc gaa	602	
Asp Gly Ser Ser Ser Leu Pro Asn Val Ser Leu Ala Trp Val Ile Glu		
	65 70 75	
gcc ctg agg ctc cct ggg gac ccg gag ccc aag gtc tgc gtg cac cac	650	
Ala Leu Arg Leu Pro Gly Asp Pro Glu Pro Lys Val Cys Val His His		
	80 85 90	
egg aac ccg ctc agc ctt ttc tgc gag aag gac cag gag ctc atc tgt	698	
Arg Asn Pro Leu Ser Leu Phe Cys Glu Lys Asp Gln Glu Leu Ile Cys		
	95 100 105	
ggc ctc tgc ggt ctg ctg ggc tcc cac caa cac cac ccg gtc acg ccc	746	
Gly Leu Cys Gly Leu Leu Gly Ser His Gln His His Pro Val Thr Pro		
	110 115 120	
gtc tcc acc gtc tgc agc cgc atg aag gag gag ctc gca gcc ctc ttc	794	
Val Ser Thr Val Cys Ser Arg Met Lys Glu Glu Leu Ala Ala Leu Phe		
	125 130 135 140	
tct gag ctg aag cag gag cag aag aag gtg gat gag ctc atc gcc aaa	842	
Ser Glu Leu Lys Gln Glu Gln Lys Lys Val Asp Glu Leu Ile Ala Lys		
	145 150 155	
ctg gtg aaa aac cgg acc cga atc gtc aat gag tcg gat gtc ttc agc	890	
Leu Val Lys Asn Arg Thr Arg Ile Val Asn Glu Ser Asp Val Phe Ser		
	160 165 170	
tgg gtg atc cgc cgc gag ttc cag gag ctg cgc cac ccg gtg gac gag	938	
Trp Val Ile Arg Arg Glu Phe Gln Glu Leu Arg His Pro Val Asp Glu		
	175 180 185	
gag cag gcc cgc tgc ctg gag ggg ata ggg ggt cac acc cgt ggc ctg	986	
Glu Gln Ala Arg Cys Leu Glu Gly Ile Gly Gly His Thr Arg Gly Leu		
	190 195 200	
gtg gcc tcc ctg gac atg cag ctg gag cag gcc cag gga acc cgg gag	1034	
Val Ala Ser Leu Asp Met Gln Leu Glu Gln Ala Gln Gly Thr Arg Glu		
	205 210 215 220	
cgg ctg gcc caa gcc gag tgt gtg ctg gaa cag ttc ggc aat gag gac	1082	
Arg Leu Ala Gln Ala Glu Cys Val Leu Glu Gln Phe Gly Asn Glu Asp		
	225 230 235	
cac cat gag ttc atc tgg aag ttc cac tcc atg gcc tcc agg taa taa	1130	
His His Glu Phe Ile Trp Lys Phe His Ser Met Ala Ser Arg *		
	240 245 250	

ccttgagag agctcagcca gggctctggtg gctgcgggca cgggcatctc agctccactg 1190
gttcctccat tcagcttaac cagcgccctcc caagcagctg cctatagctg gctctataac 1250
tgagcctggg gaagatagag gaaagtcacg tccctgcctt caagggctctc gcagacaggt 1310
ggggaggcag atggtgaact gtgggtacct agaacagcag aagttcactc aagctacaga 1370
aatactagag gaggggtggct catgcctgca atcccagtac tttgggaggc caaggcagga 1430
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tacaaaaaat acaaaaataa aaaaattagt tgggaaaaaa aaaaaaa 1537

<210> 658
<211> 2214
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (71)..(988)

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tattcttaaa atg gcg ccg cta gac ctg gac aag tat gtg gaa ata gcg 109
Met Ala Pro Leu Asp Leu Asp Lys Tyr Val Glu Ile Ala
1 5 10
cgg ctg tgc aag tac ctg cca gag aac gac ctg aag cgg cta tgt gac 157
Arg Leu Cys Lys Tyr Leu Pro Glu Asn Asp Leu Lys Arg Leu Cys Asp
15 20 25
tac gtt tgt gac ctc ctc tta gaa gag tca aat gtt cag cca gta tca 205
Tyr Val Cys Asp Leu Leu Leu Glu Glu Ser Asn Val Gln Pro Val Ser
30 35 40 45
aca cca gta aca gtg tgt gga gat atc cat gga cag ttt tat gac ctt 253
Thr Pro Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu
50 55 60
tgt gaa ctg ttc aga act gga ggt cag gtt cct gac aca aac tac ata 301
Cys Glu Leu Phe Arg Thr Gly Gly Gln Val Pro Asp Thr Asn Tyr Ile
65 70 75
ttt atg ggt gat ttt gta gac aga ggt tac tat agt ttg gag acc ttc 349
Phe Met Gly Asp Phe Val Asp Arg Gly Tyr Tyr Ser Leu Glu Thr Phe
80 85 90
act tac ctt ctt gca tta aag gct aaa tgg cct gat cgt att aca ctt 397
Thr Tyr Leu Leu Ala Leu Lys Ala Lys Trp Pro Asp Arg Ile Thr Leu
95 100 105
ttg cga gga aat cat gag agt aga cag ata aca cag gtc tat gga ttt 445
Leu Arg Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe
110 115 120 125
tat gat gag tgc caa acc aaa tat gga aat gct aat gcc tgg aga tac 493
Tyr Asp Glu Cys Gln Thr Lys Tyr Gly Asn Ala Asn Ala Trp Arg Tyr
130 135 140

tgt acc aaa gtt ttt gac atg ctc aca gta gca gct tta ata gat gag	541
Cys Thr Lys Val Phe Asp Met Leu Thr Val Ala Ala Leu Ile Asp Glu	
145 150 155	
cag att ttg tgt gtc cat ggt ggt tta tct cct gat atc aaa aca ctg	589
Gln Ile Leu Cys Val His Gly Gly Leu Ser Pro Asp Ile Lys Thr Leu	
160 165 170	
gat caa att cga acc atc gaa cgg aat cag gaa att cct cat aaa gga	637
Asp Gln Ile Arg Thr Ile Glu Arg Asn Gln Glu Ile Pro His Lys Gly	
175 180 185	
gca ttt tgt gat ctg gtt tgg tca gat cct gaa gat gtg gat acc tgg	685
Ala Phe Cys Asp Leu Val Trp Ser Asp Pro Glu Asp Val Asp Thr Trp	
190 195 200 205	
gct atc agt ccc cga gga gca ggt tgg ctt ttt gga gca aag gtc aca	733
Ala Ile Ser Pro Arg Gly Ala Gly Trp Leu Phe Gly Ala Lys Val Thr	
210 215 220	
aat gag ttt gtt cat atc aac aac tta aaa ctc atc tgc aga gca cat	781
Asn Glu Phe Val His Ile Asn Asn Leu Lys Leu Ile Cys Arg Ala His	
225 230 235	
caa cta gtg cac gaa ggc tat aaa ttt atg ttt gat gag aag ctg gtg	829
Gln Leu Val His Glu Gly Tyr Lys Phe Met Phe Asp Glu Lys Leu Val	
240 245 250	
aca gta tgg tct gct cct aat tac tgc tat cgt tgt gga aat att gct	877
Thr Val Trp Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Ile Ala	
255 260 265	
tcg atc atg gtc ttc aaa gat gta aat aca aga gaa cca aag tta ttc	925
Ser Ile Met Val Phe Lys Asp Val Asn Thr Arg Glu Pro Lys Leu Phe	
270 275 280 285	
cgg gca gtt cca gat tca gaa cgt gtt att cct ccc aga acg aca acg	973
Arg Ala Val Pro Asp Ser Glu Arg Val Ile Pro Pro Arg Thr Thr Thr	
290 295 300	
cca tat ttc ctt tga ggccttcgcc catcctgctg acccattttt ctgccctctt	1028
Pro Tyr Phe Leu *	
305	
cttaccoccaa ttttcttgta ttaccctcta caatatactt tttattgagc actttgctgc	1088
tgaaatgctg cctcttgcc tttttttttt aaattttaaa ttatctaaat ttattgtttg	1148
ttgtggtgtc tatagcaaag tttttctatc aattttcccc catcccatcc ccaccctgga	1208
ctcatttgag aagacttgag aaatgtctta atactcacac tgctgcatgt agctcttgct	1268
tatttactgg tctgggaaac aggatgtgtt tcctttttttt aaaagccaat tgacagatta	1328
cacctaaata ctccctcttt tgtatcattc agccttttgt tttagtttgg taagttttaa	1388
gaaatttcag cagcaaagtt gttattcagt gggcacgatg gactccaaat gcctcaagtt	1448
atgtatacct gtcccagatg taaacttcat tgtcctttgt tggatgatat tttaaatgga	1508
tataaaataa attggtctaa agggctgccc tccttgttgt gtttttaaat tttagttaaa	1568
aactgctaca gcttatgact ttgtacttta agataattgt attgatcttt tttcagattc	1628

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cttgtatttt ttaataaagt aatcttaaat aaaactcaga taggttaagt gttagaaatt 1688
ttaaacagct tacattgtta gcgtaaagtt atcttttctt ttttccta atcagagttctt 1748
gacccttttg ttattgagtt taaaacttca attgaaattc aatagtattt attttttaaa 1808
aaaatcacta aactgtgcct aaagaacata actgccatat taatgttttg gtttatatcc 1868
tctatagtaa tagaaaaaca ttttaatactt gtaatgctga tgtgttaatt tgataccagt 1928
tgagtagaat gtgatcaatc cagtttacaa tctatcatga gtattattaa ctaaaatcta 1988
tgtgcttttc aataggaatc attcttctct tgcgtgaaca cttgacctta acttttagaa 2048
agtgttcatt tttaaactgc aactggaaag gttgaaaagt taggactctt gtatttgtga 2108
actgtaatct gaagcagatt atttaaagtg tagaaaaaga aacaagttct tttttgcaaa 2168
gggtctgtgat accatatttc agctttgtgt aagtaatttg aatatc 2214

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<210> 659
 <211> 2624
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (193) .. (1776)

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taaagcttgg atgggggttg acctctgcag ggcagcgccc agctatagga gttcccctgc 180
tgagcagaga ag      atg act gca gaa ttg aga gaa gcc atg gcc cta gcc 228
                  Met Thr Ala Glu Leu Arg Glu Ala Met Ala Leu Ala
                   1             5             10

cca tgg ggc cca gtg aag gtg aaa aag gag gag gaa gaa gaa gaa aac 276
Pro Trp Gly Pro Val Lys Val Lys Lys Glu Glu Glu Glu Glu Glu Asn
                   15             20             25

ttc cca ggt cag gca tcc agc caa caa gtg cac tcc gag aac atc aaa 324
Phe Pro Gly Gln Ala Ser Ser Gln Gln Val His Ser Glu Asn Ile Lys
                   30             35             40

gtc tgg gcc cca gtg cag ggt ctt cag aca ggc ctt gat gga tca gaa 372
Val Trp Ala Pro Val Gln Gly Leu Gln Thr Gly Leu Asp Gly Ser Glu
                   45             50             55             60

gag gaa gaa aag ggt cag aac ata tcc tgg gat atg gcg gta gtc ctg 420
Glu Glu Glu Lys Gly Gln Asn Ile Ser Trp Asp Met Ala Val Val Leu
                   65             70             75

aaa gca act cag gag gca cct gct gct tca acc ctt ggc agc tac tca 468
Lys Ala Thr Gln Glu Ala Pro Ala Ala Ser Thr Leu Gly Ser Tyr Ser
                   80             85             90

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tta cca ggg act ctg gcc aag agt gag ata ctg gag act cat ggg acc	516
Leu Pro Gly Thr Leu Ala Lys Ser Glu Ile Leu Glu Thr His Gly Thr	
95 100 105	
atg aac ttt cta ggt gct gaa acc aag aac cta cag tta ctg gtt cca	564
Met Asn Phe Leu Gly Ala Glu Thr Lys Asn Leu Gln Leu Leu Val Pro	
110 115 120	
aaa act gag ata tgt gag gaa gct gaa aaa ccc ctc atc ata tca gaa	612
Lys Thr Glu Ile Cys Glu Glu Ala Glu Lys Pro Leu Ile Ile Ser Glu	
125 130 135 140	
aga atc cag aaa gct gat cct caa gga cct gag tta gga gaa gct tgt	660
Arg Ile Gln Lys Ala Asp Pro Gln Gly Pro Glu Leu Gly Glu Ala Cys	
145 150 155	
gaa aag gga aac atg tta aag agg cag aga ata aag aga gaa aag aaa	708
Glu Lys Gly Asn Met Leu Lys Arg Gln Arg Ile Lys Arg Glu Lys Lys	
160 165 170	
gat ttc aga caa gtg ata gtg aat gac tgt cac tta cct gaa agc ttc	756
Asp Phe Arg Gln Val Ile Val Asn Asp Cys His Leu Pro Glu Ser Phe	
175 180 185	
aaa gaa gag gaa aac cag aaa tgt aag aaa tct gga gga aaa tat agc	804
Lys Glu Glu Glu Asn Gln Lys Cys Lys Lys Ser Gly Gly Lys Tyr Ser	
190 195 200	
ctt aat tct ggc gct gtt aaa aat cca aaa acc cag ctt gga caa aag	852
Leu Asn Ser Gly Ala Val Lys Asn Pro Lys Thr Gln Leu Gly Gln Lys	
205 210 215 220	
cct ttt acg tgt agc gtg tgt ggg aaa gga ttt agt cag agt gca aac	900
Pro Phe Thr Cys Ser Val Cys Gly Lys Gly Phe Ser Gln Ser Ala Asn	
225 230 235	
ctc gtt gtg cat cag cga atc cac act gga gag aaa ccc ttt gaa tgt	948
Leu Val Val His Gln Arg Ile His Thr Gly Glu Lys Pro Phe Glu Cys	
240 245 250	
cat gag tgt ggg aag gcc ttc att cag agt gca aac ctc gtt gtg cat	996
His Glu Cys Gly Lys Ala Phe Ile Gln Ser Ala Asn Leu Val Val His	
255 260 265	
cag aga atc cac act gga cag aaa cct tat gtt tgc tca aaa tgt ggg	1044
Gln Arg Ile His Thr Gly Gln Lys Pro Tyr Val Cys Ser Lys Cys Gly	
270 275 280	
aaa gcc ttc act cag agt tca aat ctg act gta cat caa aaa atc cac	1092
Lys Ala Phe Thr Gln Ser Ser Asn Leu Thr Val His Gln Lys Ile His	
285 290 295 300	
tcc tta gaa aaa act ttt aag tgc aat gaa tgt gag aaa gcc ttt agt	1140
Ser Leu Glu Lys Thr Phe Lys Cys Asn Glu Cys Glu Lys Ala Phe Ser	
305 310 315	
tac agc tca caa ctt gct cgg cac cag aaa gtc cac att acg gaa aaa	1188
Tyr Ser Ser Gln Leu Ala Arg His Gln Lys Val His Ile Thr Glu Lys	
320 325 330	
tgc tat gaa tgt aat gaa tgt ggg aaa aca ttt act agg agc tca aac	1236
Cys Tyr Glu Cys Asn Glu Cys Gly Lys Thr Phe Thr Arg Ser Ser Asn	
335 340 345	

ctc att gtc cac cag agg atc cac act ggg gag aag ccc ttt gcc tgt	1284
Leu Ile Val His Gln Arg Ile His Thr Gly Glu Lys Pro Phe Ala Cys	
350 355 360	
aac gac tgt ggc aaa gcc ttt acc cag agt gca aat ctt att gta cat	1332
Asn Asp Cys Gly Lys Ala Phe Thr Gln Ser Ala Asn Leu Ile Val His	
365 370 375 380	
cag cga agc cat act ggt gag aag cca tat gag tgt aaa gag tgt ggg	1380
Gln Arg Ser His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly	
385 390 395	
aaa gcc ttt agt tgt ttt tca cac ctt att gtg cac cag aga att cac	1428
Lys Ala Phe Ser Cys Phe Ser His Leu Ile Val His Gln Arg Ile His	
400 405 410	
act gca gag aaa cct tac gac tgc agc gaa tgt ggg aaa gcc ttc agt	1476
Thr Ala Glu Lys Pro Tyr Asp Cys Ser Glu Cys Gly Lys Ala Phe Ser	
415 420 425	
cag ctc tct tgc ctt att gtc cac cag aga att cac agt gga gat ctt	1524
Gln Leu Ser Cys Leu Ile Val His Gln Arg Ile His Ser Gly Asp Leu	
430 435 440	
cct tac gtg tgt aat gaa tgt ggg aag gcc ttc aca tgt agc tca tac	1572
Pro Tyr Val Cys Asn Glu Cys Gly Lys Ala Phe Thr Cys Ser Ser Tyr	
445 450 455 460	
cta ctt att cat cag aga att cat aat gga gaa aaa cct tac aca tgt	1620
Leu Leu Ile His Gln Arg Ile His Asn Gly Glu Lys Pro Tyr Thr Cys	
465 470 475	
aat gag tgt ggg aag gcc ttc aga cag agg tcg agc ctc acc gtg cac	1668
Asn Glu Cys Gly Lys Ala Phe Arg Gln Arg Ser Ser Leu Thr Val His	
480 485 490	
cag aga acc cac act ggg gag aag ccc tat gaa tgt gag aag tgt ggt	1716
Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Glu Lys Cys Gly	
495 500 505	
gca gct ttc att tcc aac tca cac ctc atg cga cac cat aga acc cat	1764
Ala Ala Phe Ile Ser Asn Ser His Leu Met Arg His His Arg Thr His	
510 515 520	
ctt gtt gaa taa caa gtaaggaaga ggaagacctc cagcattggt cataaccttc	1819
Leu Val Glu *	
525	
tgccctcccta atgagacacc tctttgtgtg tttcttcctc ctctataaaa gtgagggctg	1879
tgctccttaaa agttatagtt ttcaggaatg cagcagaaga cacaagaaaa gcatttcaga	1939
ggctaattta aaacaaaaag taagcaccta aaggggaagga ctttgtttta actgtacctt	1999
aagcgggcat gttctctgaa gtggaatgtg gctttcctag gaatgggtcg tacaaagcta	2059
agtggtaatg atgctatttg gggaaaggtc ttttttgctt aattttgttt tttaaaactc	2119
tgatgattgc ttgagcaaca ggcagggttat ctgcctgggt gaattctggt tgaaccgtgt	2179
attctaatat ttctgggttaa gtgggtgactg ggtaaggaaa ccacttgggg tagcagttca	2239
acaattcact tacgaatggt tataagcttt ccatttccta ggtaattttt taaaagccag	2299

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tcaaaacaaa aactttactg aaaatggaca gaaataggaa atggactttt tccttactgt 2359
ctatacctcc tgaaccttgg tattgtaaag atctggggac ctctgggtct gttctgacca 2419
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catttgccaa gatcaacagc tcctttctcca aacaactcaa gcccacaatt cccatcgcat 2539
tccatttggg tgagatgcaa ctaacagccc ctctctggat gaaggagtca aagaataaag 2599
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<210> 660
<211> 2215
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (293) .. (2215)

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His Tyr Val Asp Leu Lys Asp Arg Pro Phe Phe Ala Gly Leu Val Lys		
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Tyr Met His Ser Gly Pro Val Val Ala Met Val Trp Glu Gly Leu Asn		
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Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg		
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Asn Ile Ile His Gly Ser Asp Ser Val Glu Ser Ala Glu Lys Glu Ile		
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 Ala Glu Glu Lys Gly Thr Gln Ala Gly Glu Ile His Asp Leu Lys Asp
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 Met Leu Asp Val Lys Glu Arg Lys Val Asn Val Leu Gln Lys Lys Ile
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 Glu Asn Leu Gln Glu Gln Leu Arg Asp Lys Glu Lys Gln Met Ser Ser
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 Ile Glu Arg Leu Lys Glu Gln Arg Asp Arg Asp Glu Arg Glu Lys Gln
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 Glu Glu Ile Asp Asn Tyr Lys Lys Asp Leu Lys Asp Leu Lys Glu Lys
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 Val Ser Leu Leu Gln Gly Asp Leu Ser Glu Lys Glu Ala Ser Leu Leu
 125 130 135 140
 gat ctg aaa gag cat gct tct tct ctg gca tcc tca gga ctg aaa aag 603

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Asp Ser Arg Leu Lys Thr Leu Glu Ile Ala Leu Glu Gln Lys Lys Glu	160	165	170	
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Glu Cys Leu Lys Met Glu Ser Gln Leu Lys Lys Ala His Glu Ala Ala	175	180	185	
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Leu Pro Trp Leu Val Ser Gln Leu Asp Leu Gly Gln Leu Glu Gly Val
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Ala Trp Val Asn Lys Ser Arg Thr Arg Phe Arg Ile Pro Trp Lys His
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tgg gcc gag gcc act ggt gca tat gtt ccc ggg agg gat aag cca gac 423
Trp Ala Glu Ala Thr Gly Ala Tyr Val Pro Gly Arg Asp Lys Pro Asp
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Leu Pro Thr Trp Lys Arg Asn Phe Arg Ser Ala Leu Asn Arg Lys Glu
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Pro Asp Pro Gly Pro Pro Ser Leu Ala Val Ala Pro Glu Pro Cys Pro	
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cag ccc ctg cgg agc ccc agc ttg gac aat ccc act ccc ttc cca aac	759
Gln Pro Leu Arg Ser Pro Ser Leu Asp Asn Pro Thr Pro Phe Pro Asn	
170 175 180	
ctg ggg ccc tct gag aac cca ctg aag cgg ctg ttg gtg ccg ggg gaa	807
Leu Gly Pro Ser Glu Asn Pro Leu Lys Arg Leu Leu Val Pro Gly Glu	
185 190 195 200	
gag tgg gag ttc gag gtg aca gcc ttc tac cgg ggc cgc caa gtc ttc	855
Glu Trp Glu Phe Glu Val Thr Ala Phe Tyr Arg Gly Arg Gln Val Phe	
205 210 215	
cag cag acc atc tcc tgc ccg gag ggc ctg cgg ctg gtg ggg tcc gaa	903
Gln Gln Thr Ile Ser Cys Pro Glu Gly Leu Arg Leu Val Gly Ser Glu	
220 225 230	
gtg gga gac agg acg ctg cct gga tgg cca gtc aca ctg cca gac cct	951
Val Gly Asp Arg Thr Leu Pro Gly Trp Pro Val Thr Leu Pro Asp Pro	
235 240 245	
ggc atg tcc ctg aca gac agg gga gtg atg agc tac gtg agg cat gtg	999
Gly Met Ser Leu Thr Asp Arg Gly Val Met Ser Tyr Val Arg His Val	
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ctg agc tgc ctg ggt ggg gga ctg gct ctc tgg cgg gcc ggg cag tgg	1047
Leu Ser Cys Leu Gly Gly Gly Leu Ala Leu Trp Arg Ala Gly Gln Trp	
265 270 275 280	
ctc tgg gcc cag cgg ctg ggg cac tgc cac aca tac tgg gca gtg agc	1095
Leu Trp Ala Gln Arg Leu Gly His Cys His Thr Tyr Trp Ala Val Ser	
285 290 295	
gag gag ctg ctc ccc aac agc ggg cat ggg cct gat ggc gag gtc ccc	1143
Glu Glu Leu Leu Pro Asn Ser Gly His Gly Pro Asp Gly Glu Val Pro	
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Lys Asp Lys Glu Gly Gly Val Phe Asp Leu Gly Pro Phe Ile Val Asp	
315 320 325	
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Leu Ile Thr Phe Thr Glu Gly Ser Gly Arg Ser Pro Arg Tyr Ala Leu	
330 335 340	
tgg ttc tgt gtg ggg gag tca tgg ccc cag gac cag ccg tgg acc aag	1287
Trp Phe Cys Val Gly Glu Ser Trp Pro Gln Asp Gln Pro Trp Thr Lys	
345 350 355 360	


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agg ctc gtg atg gtc aag gtt gtg ccc acg tgc ctc agg gcc ttg gta      1335
Arg Leu Val Met Val Lys Val Val Pro Thr Cys Leu Arg Ala Leu Val
          365          370          375

gaa atg gcc cgg gta ggg ggt gcc tcc tcc ctg gag aat act gtg gac      1383
Glu Met Ala Arg Val Gly Gly Ala Ser Ser Leu Glu Asn Thr Val Asp
          380          385          390

ctg cac att tcc aac agc cac cca ctc tcc ctc acc tcc gac cag tac      1431
Leu His Ile Ser Asn Ser His Pro Leu Ser Leu Thr Ser Asp Gln Tyr
          395          400          405

aag gcc tac ctg cag gac ttg gtg gag ggc atg gat ttc cag ggc cct      1479
Lys Ala Tyr Leu Gln Asp Leu Val Glu Gly Met Asp Phe Gln Gly Pro
          410          415          420

ggg gag agc tga gcc ctgctcctc atggtgtgcc tccaaccccc ctgttccccca      1534
Gly Glu Ser *
425

ccacctcaac caataaactg gttcctgcta tgaaaaaaa aaaa      1578

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Lys Ala Ala Ala Ala Asn Ala Val Gly Leu Phe Ser Arg Leu Gln Ala
          10          15          20

ccc att cca aca gta aga gct tct tcc aca tca cag ccc ttg gat caa      149
Pro Ile Pro Thr Val Arg Ala Ser Ser Thr Ser Gln Pro Leu Asp Gln
          25          30          35

gtg aca ggt tct gtg tgg aac ctg ggt cga ctc aac cat gta gcc ata      197
Val Thr Gly Ser Val Trp Asn Leu Gly Arg Leu Asn His Val Ala Ile
          40          45          50

gca gtg cca gat ttg gaa aag gct gca gca ttt tat aag aat att ctg      245
Ala Val Pro Asp Leu Glu Lys Ala Ala Ala Phe Tyr Lys Asn Ile Leu
          55          60          65

ggg gcc cag gta agt gaa gcg gtc cct ctt cct gaa cat gga gta tct      293
Gly Ala Gln Val Ser Glu Ala Val Pro Leu Pro Glu His Gly Val Ser
          70          75          80          85

gtt gtt ttt gtc aac ctg gga aat acc aag atg gaa ctg ctt cat cca      341
Val Val Phe Val Asn Leu Gly Asn Thr Lys Met Glu Leu Leu His Pro
          90          95          100

ttg gga cgt gac agt cca att gca ggt ttt ctg cag aaa aac aag gct      389

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Leu Gly Arg Asp Ser Pro Ile Ala Gly Phe Leu Gln Lys Asn Lys Ala
 105 110 115
 gga gga atg cat cac atc tgc atc gag gtg gat aat att aat gca gct 437
 Gly Gly Met His His Ile Cys Ile Glu Val Asp Asn Ile Asn Ala Ala
 120 125 130
 gtg atg gat ttg aaa aaa aag aag atc cgc agt cta agt gaa gag gtc 485
 Val Met Asp Leu Lys Lys Lys Lys Ile Arg Ser Leu Ser Glu Glu Val
 135 140 145
 aaa ata gga gca cat gga aaa cca gtg att ttt ctc cat cct aaa gac 533
 Lys Ile Gly Ala His Gly Lys Pro Val Ile Phe Leu His Pro Lys Asp
 150 155 160 165
 tgt ggt gga gtc ctt gtg gaa ctg gag caa gct tga ttta tatttgcaag 583
 Cys Gly Gly Val Leu Val Glu Leu Glu Gln Ala *
 170 175
 caactaaatt aattgacctg aaaaagccta tcaaatacta tcaaaatgta ctatgacatt 643
 gagtccttca ctgcttccat catgtaaaag ttcacagtta aagactgaat tacagaaaga 703
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 Ser Asn Leu Val Leu Gln Ala Asp Arg Ser Leu Ile Asp Arg Thr Arg
 20 25 30
 cgg gat gaa ccc aca gga gag gtg ctg tcc ctt gtt ggg aag ctg gag 144
 Arg Asp Glu Pro Thr Gly Glu Val Leu Ser Leu Val Gly Lys Leu Glu
 35 40 45
 ggc acc cgt atg gga gac aag gct caa cgg acc aaa ccg cag atg cag 192
 Gly Thr Arg Met Gly Asp Lys Ala Gln Arg Thr Lys Pro Gln Met Gln
 50 55 60
 gag gaa aga aga gcc aag cga aga aag cgt gat gag gac cgg cat gac 240
 Glu Glu Arg Arg Ala Lys Arg Arg Lys Arg Asp Glu Asp Arg His Asp
 65 70 75 80
 atc aac aag atg aag ggt tat act ctg ctg tcg gag ggc att gat gag 288
 Ile Asn Lys Met Lys Gly Tyr Thr Leu Leu Ser Glu Gly Ile Asp Glu

85										90										95									
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Met	Val	Gly	Ile	Ile	Tyr	Lys	Pro	Lys	Thr	Lys	Glu	Thr	Arg	Glu	Thr														
			100																										
tat	gag	gtg	cta	ctc	agc	ttc	atc	cag	gct	gct	ctt	ggg	gac	cag	cca														
Tyr	Glu	Val	Leu	Leu	Ser	Phe	Ile	Gln	Ala	Ala	Leu	Gly	Asp	Gln	Pro														
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cgt	gat	atc	ctt	tgt	ggg	gca	gct	gat	gaa	gtt	cta	gct	gtt	cta	aag														
Arg	Asp	Ile	Leu	Cys	Gly	Ala	Ala	Asp	Glu	Val	Leu	Ala	Val	Leu	Lys														
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aat	gaa	aag	ctg	cgg	gac	aag	gaa	agg	cga	aag	gag	att	gac	ctg	ctg														
Asn	Glu	Lys	Leu	Arg	Asp	Lys	Glu	Arg	Arg	Lys	Glu	Ile	Asp	Leu	Leu														
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ctg	ggt	caa	aca	gat	gat	acc	aga	tac	cat	gtg	cta	gtg	aac	ctg	ggc														
Leu	Gly	Gln	Thr	Asp	Asp	Thr	Arg	Tyr	His	Val	Leu	Val	Asn	Leu	Gly														
aaa	aag	atc	aca	gac	tat	ggt	gga	gat	aag	gaa	atc	caa	aat	atg	gat														
Lys	Lys	Ile	Thr	Asp	Tyr	Gly	Gly	Asp	Lys	Glu	Ile	Gln	Asn	Met	Asp														
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gac	aac	att	gat	gag	aca	tac	ggt	gtg	aat	gtg	cag	ttt	gag	tct	gat														
Asp	Asn	Ile	Asp	Glu	Thr	Tyr	Gly	Val	Asn	Val	Gln	Phe	Glu	Ser	Asp														
			195																										
gag	gag	gaa	ggt	gat	gaa	gac	gta	tac	ggg	gag	gtt	cga	gaa	gag	gca														
Glu	Glu	Glu	Gly	Asp	Glu	Asp	Val	Tyr	Gly	Glu	Val	Arg	Glu	Glu	Ala														
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tct	gat	gat	gac	atg	gaa	ggg	gac	gag	gct	gtc	gtg	cgc	tgc	acc	ctc														
Ser	Asp	Asp	Asp	Met	Glu	Gly	Asp	Glu	Ala	Val	Val	Arg	Cys	Thr	Leu														
tcg	gct	aat	atg	tat	gtt	gat	gaa	atc	tta	gtc	tgg	tgt	gct	tct	gaa														
Ser	Ala	Asn	Met	Tyr	Val	Asp	Glu	Ile	Leu	Val	Trp	Cys	Ala	Ser	Glu														
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Leu	Asn	Ile	Pro	Glu	Phe	Phe	Pro	Leu	Glu	Ser	Pro	His	Lys	Lys	Val														
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Gly	Tyr	Gly	Leu	Ser	Ser	Arg	Thr	Trp	Leu	Gln	Gly	Gly	Gly	Lys	Val														
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Ile	Glu	Ala	Gly	Arg	Asp	Leu	Leu	Val	Ala	Ser	Gly	Glu	Leu	Met	Ser														
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tcc	aag	aag	aag	gat	ttg	cac	cct	cgg	gat	att	gat	gca	ttt	tgg	ctg														
Ser	Lys	Lys	Lys	Asp	Leu	His	Pro	Arg	Asp	Ile	Asp	Ala	Phe	Trp	Leu														
cag	cgg	cag	ctc	agt	cgt	ttc	tat	gat	gat	gcc	atc	gtg	tcg	cag	aag														
Gln	Arg	Gln	Leu	Ser	Arg	Phe	Tyr	Asp	Asp	Ala	Ile	Val	Ser	Gln	Lys														
aag	gca	gat	gaa	gta	ttg	gag	att	ttg	aag	acg	gcc	agt	gat	gat	cgg														
Lys	Ala	Asp	Glu	Val	Leu	Glu	Ile	Leu	Lys	Thr	Ala	Ser	Asp	Asp	Arg														

340	345	350	
gaa tgt gaa aat cag ctg gtt ctg ctg ctt ggt ttc aac acc ttt gat			1104
Glu Cys Glu Asn Gln Leu Val Leu Leu Leu Gly Phe Asn Thr Phe Asp			
355	360	365	
ttc att aaa gtg ttg cgg cag cac agg atg atg att tta tac tgt acc			1152
Phe Ile Lys Val Leu Arg Gln His Arg Met Met Ile Leu Tyr Cys Thr			
370	375	380	
ttg ctg gcc agt gca caa agt gaa gct gaa aag gaa agg att atg gga			1200
Leu Leu Ala Ser Ala Gln Ser Glu Ala Glu Lys Glu Arg Ile Met Gly			
385	390	395	400
aag atg gaa gct gac cca gag cta tcc aag ttc ctc tac cag ctt cat			1248
Lys Met Glu Ala Asp Pro Glu Leu Ser Lys Phe Leu Tyr Gln Leu His			
405	410	415	
gaa acc gag aag gag gat ctg atc cga gag gaa agg tcc cgg aga gag			1296
Glu Thr Glu Lys Glu Asp Leu Ile Arg Glu Glu Arg Ser Arg Arg Glu			
420	425	430	
cga gtg cgt cag tct cga atg gac aca gat ctg gaa acc atg gat ctc			1344
Arg Val Arg Gln Ser Arg Met Asp Thr Asp Leu Glu Thr Met Asp Leu			
435	440	445	
gac cag ggt gga gag gca ctg gct cca cgg cag gtt ctg gac ttg gag			1392
Asp Gln Gly Gly Glu Ala Leu Ala Pro Arg Gln Val Leu Asp Leu Glu			
450	455	460	
gac ctg gtt ttt acc caa ggg agc cac ttt atg gcc aat aaa cgc tgt			1440
Asp Leu Val Phe Thr Gln Gly Ser His Phe Met Ala Asn Lys Arg Cys			
465	470	475	480
cag ctt cct gat gga tcc ttc cgt cgc cag cgt aag ggc tat gaa gag			1488
Gln Leu Pro Asp Gly Ser Phe Arg Arg Gln Arg Lys Gly Tyr Glu Glu			
485	490	495	
gtg cat gtg cct gct ctg aag ccc aag ccc ttt ggc tca gaa gaa caa			1536
Val His Val Pro Ala Leu Lys Pro Lys Pro Phe Gly Ser Glu Glu Gln			
500	505	510	
ctg ctt cca gtg gaa aag ctg cca aag tat gcc cag gct ggg ttt gag			1584
Leu Leu Pro Val Glu Lys Leu Pro Lys Tyr Ala Gln Ala Gly Phe Glu			
515	520	525	
ggc ttc aaa aca ctg aat cgg atc cag agt aag ctc tac cgt gct gcc			1632
Gly Phe Lys Thr Leu Asn Arg Ile Gln Ser Lys Leu Tyr Arg Ala Ala			
530	535	540	
ctt gag acg gat gag aat ctg ctg ctg tgt gct cct act ggt gct ggg			1680
Leu Glu Thr Asp Glu Asn Leu Leu Leu Cys Ala Pro Thr Gly Ala Gly			
545	550	555	560
aag acc aac gtg gcc ctg atg tgc atg ctc cga gag att ggg aaa cac			1728
Lys Thr Asn Val Ala Leu Met Cys Met Leu Arg Glu Ile Gly Lys His			
565	570	575	
ata aac atg gac ggc acc atc aat gtg gat gac ttc aag att atc tac			1776
Ile Asn Met Asp Gly Thr Ile Asn Val Asp Asp Phe Lys Ile Ile Tyr			
580	585	590	
att gcc ccc atg cgc tcc ttg gtg cag gag atg gtg ggc agc ttt gga			1824
Ile Ala Pro Met Arg Ser Leu Val Gln Glu Met Val Gly Ser Phe Gly			

595					600					605							
aag	cgc	ctg	gcc	act	tat	ggc	atc	act	gtt	gct	gaa	ctg	act	ggg	gac	1872	
Lys	Arg	Leu	Ala	Thr	Tyr	Gly	Ile	Thr	Val	Ala	Glu	Leu	Thr	Gly	Asp		
610					615					620							
cac	cag	ctg	tgc	aaa	gaa	gag	atc	agt	gcc	act	cag	atc	atc	gtc	tgc	1920	
His	Gln	Leu	Cys	Lys	Glu	Glu	Ile	Ser	Ala	Thr	Gln	Ile	Ile	Val	Cys		
625					630					635					640		
acc	ccc	gag	aag	tgg	gac	atc	atc	acc	cgc	aag	ggt	ggt	gag	cgc	acc	1968	
Thr	Pro	Glu	Lys	Trp	Asp	Ile	Ile	Thr	Arg	Lys	Gly	Gly	Glu	Arg	Thr		
645					650					655							
tac	acc	cag	ctg	gtg	cgg	ctc	atc	att	ctg	gat	gag	att	cat	ctt	ctc	2016	
Tyr	Thr	Gln	Leu	Val	Arg	Leu	Ile	Ile	Leu	Asp	Glu	Ile	His	Leu	Leu		
660					665					670							
cac	gat	gac	aga	ggg	cct	gtc	tta	gaa	gct	tta	gtg	gcc	agg	gcc	atc	2064	
His	Asp	Asp	Arg	Gly	Pro	Val	Leu	Glu	Ala	Leu	Val	Ala	Arg	Ala	Ile		
675					680					685							
cga	aac	att	gag	atg	acc	caa	gag	gat	gtc	cga	ctc	att	ggg	ctc	agt	2112	
Arg	Asn	Ile	Glu	Met	Thr	Gln	Glu	Asp	Val	Arg	Leu	Ile	Gly	Leu	Ser		
690					695					700							
gcc	acc	cta	ccc	aac	tat	gaa	gat	gta	gcc	acc	ttt	cta	cgt	gtt	gac	2160	
Ala	Thr	Leu	Pro	Asn	Tyr	Glu	Asp	Val	Ala	Thr	Phe	Leu	Arg	Val	Asp		
705					710					715					720		
cct	gcc	aag	ggg	ctc	ttt	tac	ttt	gac	aac	agc	ttc	cgt	cca	gtg	cct	2208	
Pro	Ala	Lys	Gly	Leu	Phe	Tyr	Phe	Asp	Asn	Ser	Phe	Arg	Pro	Val	Pro		
725					730					735							
ctg	gaa	cag	aca	tat	gtg	ggg	atc	aca	gag	aaa	aaa	gct	atc	aag	cgt	2256	
Leu	Glu	Gln	Thr	Tyr	Val	Gly	Ile	Thr	Glu	Lys	Lys	Ala	Ile	Lys	Arg		
740					745					750							
ttc	cag	atc	atg	aat	gaa	ata	gtc	tat	gaa	aaa	atc	atg	gaa	cat	gct	2304	
Phe	Gln	Ile	Met	Asn	Glu	Ile	Val	Tyr	Glu	Lys	Ile	Met	Glu	His	Ala		
755					760					765							
gga	aaa	aat	cag	gtg	ctc	gtg	ttt	gtc	cat	tct	cgc	aaa	gaa	act	ggg	2352	
Gly	Lys	Asn	Gln	Val	Leu	Val	Phe	Val	His	Ser	Arg	Lys	Glu	Thr	Gly		
770					775					780							
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Lys	Thr	Ala	Arg	Ala	Ile	Arg	Asp	Met	Cys	Leu	Glu	Lys	Asp	Thr	Leu		
785					790					795					800		
ggt	ctg	ttt	ctt	cgc	gag	ggg	tct	gcc	tcc	act	gaa	gtc	ctt	cgt	aca	2448	
Gly	Leu	Phe	Leu	Arg	Glu	Gly	Ser	Ala	Ser	Thr	Glu	Val	Leu	Arg	Thr		
805					810					815							
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Glu	Ala	Glu	Gln	Cys	Lys	Asn	Leu	Glu	Leu	Lys	Asp	Leu	Leu	Pro	Tyr		
820					825					830							
ggc	ttt	gct	att	cat	cat	gca	ggc	atg	act	aga	gtt	gac	cga	aca	ctt	2544	
Gly	Phe	Ala	Ile	His	His	Ala	Gly	Met	Thr	Arg	Val	Asp	Arg	Thr	Leu		
835					840					845							
gta	gaa	gat	ctt	ttt	ggg	gac	aag	cat	att	cag	gtt	tta	gtt	tcc	acc	2592	
Val	Glu	Asp	Leu	Phe	Gly	Asp	Lys	His	Ile	Gln	Val	Leu	Val	Ser	Thr		

850	855	860	
gca act ctg gcg tgg ggt gta aat ctt cct gca cat aca gtc atc att			2640
Ala Thr Leu Ala Trp Gly Val Asn Leu Pro Ala His Thr Val Ile Ile			
865	870	875	880
aaa ggt acc caa gtg tac agt cca gag aag ggg cgt tgg aca gag ctg			2688
Lys Gly Thr Gln Val Tyr Ser Pro Glu Lys Gly Arg Trp Thr Glu Leu			
	885	890	895
gga gca ctg gat atc ctg cag atg ctg ggc cgt gct gga cgg ccg cag			2736
Gly Ala Leu Asp Ile Leu Gln Met Leu Gly Arg Ala Gly Arg Pro Gln			
	900	905	910
tat gac acc aag ggt gaa ggc atc ctc atc aca tcc cat ggg gag ctc			2784
Tyr Asp Thr Lys Gly Glu Gly Ile Leu Ile Thr Ser His Gly Glu Leu			
	915	920	925
cag tac tac ctc tcc ctc ctc aac cag cag ctg cct atc gag agc cag			2832
Gln Tyr Tyr Leu Ser Leu Leu Asn Gln Gln Leu Pro Ile Glu Ser Gln			
	930	935	940
atg gtc tcc aag ctg cct gac atg ctc aat gcg gaa att gtt ctg ggc			2880
Met Val Ser Lys Leu Pro Asp Met Leu Asn Ala Glu Ile Val Leu Gly			
	945	950	955
aat gtc cag aat gca aag gat gca gtg aac tgg ctg ggc tat gcc tac			2928
Asn Val Gln Asn Ala Lys Asp Ala Val Asn Trp Leu Gly Tyr Ala Tyr			
	965	970	975
cta tac atc cga atg ctc cgg tcc cct acc ctc tat ggc att tct cat			2976
Leu Tyr Ile Arg Met Leu Arg Ser Pro Thr Leu Tyr Gly Ile Ser His			
	980	985	990
gat gac ctc aag gga gat ccc ttg ctg gac cag cgc cga ctc gat ctt			3024
Asp Asp Leu Lys Gly Asp Pro Leu Leu Asp Gln Arg Arg Leu Asp Leu			
	995	1000	1005
gtt cac act gct gcc ttg atg ctg gac aag aac aat ctg gtc aag tac			3072
Val His Thr Ala Ala Leu Met Leu Asp Lys Asn Asn Leu Val Lys Tyr			
	1010	1015	1020
gac aag aag aca ggc aac ttc cag gtg aca gaa ctt ggc cgg ata gca			3120
Asp Lys Lys Thr Gly Asn Phe Gln Val Thr Glu Leu Gly Arg Ile Ala			
1025	1030	1035	1040
agt cac tac tat atc acc aat gat act gtg cag acc tac aac cag ctg			3168
Ser His Tyr Tyr Ile Thr Asn Asp Thr Val Gln Thr Tyr Asn Gln Leu			
	1045	1050	1055
ctg aag cct act ctg agt gag att gag ctt ttc cga gtg ttc tcc ttg			3216
Leu Lys Pro Thr Leu Ser Glu Ile Glu Leu Phe Arg Val Phe Ser Leu			
	1060	1065	1070
tcc tca gag ttc aag aac atc act gta aga gag gag gag aag ctg gag			3264
Ser Ser Glu Phe Lys Asn Ile Thr Val Arg Glu Glu Glu Lys Leu Glu			
	1075	1080	1085
ctg cag aag ttg ctg gag aga gtg ccc atc cct gta aag gag agc att			3312
Leu Gln Lys Leu Leu Glu Arg Val Pro Ile Pro Val Lys Glu Ser Ile			
	1090	1095	1100
gag gaa ccc agc gct aag atc aac gtg ctt ctc caa gcc ttc atc tca			3360
Glu Glu Pro Ser Ala Lys Ile Asn Val Leu Leu Gln Ala Phe Ile Ser			

1105	1110	1115	1120	
cag ctg aaa ctc gaa ggc ttt gcg ctg atg gct gac atg gtg tat gtg				3408
Gln Leu Lys Leu Glu Gly Phe Ala Leu Met Ala Asp Met Val Tyr Val				
1125		1130	1135	
acc cag tcg gct ggc cgg ttg atg cgt gca atc ttc gaa att gtc ctg				3456
Thr Gln Ser Ala Gly Arg Leu Met Arg Ala Ile Phe Glu Ile Val Leu				
1140	1145		1150	
aac cga ggt tgg gca cag ctt aca gat aag acc ctg aat ctc tgc aag				3504
Asn Arg Gly Trp Ala Gln Leu Thr Asp Lys Thr Leu Asn Leu Cys Lys				
1155	1160		1165	
atg att gac aag cgc atg tgg cag tcc atg tgt cct ctt cgc cag ttc				3552
Met Ile Asp Lys Arg Met Trp Gln Ser Met Cys Pro Leu Arg Gln Phe				
1170	1175		1180	
cga aaa ctt cct gag gaa gta gtg aag aag att gag aag aaa aac ttc				3600
Arg Lys Leu Pro Glu Glu Val Val Lys Lys Ile Glu Lys Lys Asn Phe				
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ccc ttt gag cgg ctg tat gac ttg aat cat aat gag ata ggt gaa ctt				3648
Pro Phe Glu Arg Leu Tyr Asp Leu Asn His Asn Glu Ile Gly Glu Leu				
1205		1210	1215	
att cga atg ccg aag atg ggg aag acc atc cac aag tat gtc cat ctt				3696
Ile Arg Met Pro Lys Met Gly Lys Thr Ile His Lys Tyr Val His Leu				
1220	1225		1230	
ttc ccc aag ttg gag ttg tca gtg cac ctg cag cct att aca cgc tct				3744
Phe Pro Lys Leu Glu Leu Ser Val His Leu Gln Pro Ile Thr Arg Ser				
1235	1240		1245	
acg ctg aaa gta gag ctg act atc aca cca gat ttc cag tgg gat gaa				3792
Thr Leu Lys Val Glu Leu Thr Ile Thr Pro Asp Phe Gln Trp Asp Glu				
1250	1255		1260	
aag gtc cat ggt tcg tca gag gca ttt tgg att ctg gtg gag gat gtg				3840
Lys Val His Gly Ser Ser Glu Ala Phe Trp Ile Leu Val Glu Asp Val				
1265	1270	1275	1280	
gac agc gag gtg att ctg cac cat gaa tat ttt ctg ctg aag gcc aag				3888
Asp Ser Glu Val Ile Leu His His Glu Tyr Phe Leu Leu Lys Ala Lys				
1285		1290	1295	
tat gcc cag gat gag cac ctc atc aca ttc ttt gtt cca gtc ttt gaa				3936
Tyr Ala Gln Asp Glu His Leu Ile Thr Phe Phe Val Pro Val Phe Glu				
1300	1305		1310	
cca cta cct cct cag tac ttc att cga gta gtg tct gat cgc tgg ctc				3984
Pro Leu Pro Pro Gln Tyr Phe Ile Arg Val Val Ser Asp Arg Trp Leu				
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tct tgt gag acg cag cta cct gtc tcc ttc cgg cat ctg atc cta cca				4032
Ser Cys Glu Thr Gln Leu Pro Val Ser Phe Arg His Leu Ile Leu Pro				
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Glu Lys Tyr Pro Pro Pro Thr Glu Leu Leu Asp Leu Gln Pro Leu Pro				
1345	1350	1355	1360	
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Val Ser Ala Leu Arg Asn Ser Ala Phe Glu Ser Leu Tyr Gln Asp Lys				

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Phe Pro Phe Phe Asn Pro Ile Gln Thr Gln Val Phe Asn Thr Val Tyr			
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Asn Ser Asp Asp Asn Val Phe Val Gly Ala Pro Thr Gly Ser Gly Lys			
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Thr Ile Cys Ala Glu Phe Ala Ile Leu Arg Met Leu Leu Gln Asn Ser			
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Glu Gly Arg Cys Val Tyr Ile Thr Pro Met Arg Leu Trp Gln Glu Gln			
1425	1430	1435	1440
gta tac atg gac tgg tat gag aag ttt cag gac agg ctc aac aag aag			4368
Val Tyr Met Asp Trp Tyr Glu Lys Phe Gln Asp Arg Leu Asn Lys Lys			
1445	1450	1455	
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Val Val Leu Leu Thr Gly Glu Thr Ser Thr Asp Leu Lys Leu Leu Gly			
1460	1465	1470	
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Lys Gly Asn Ile Ile Ile Ser Thr Pro Glu Lys Trp Asp Ile Leu Ser			
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Arg Arg Trp Lys Gln Arg Lys Asn Val Gln Asn Ile Asn Leu Phe Val			
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Val Asp Glu Val His Leu Ile Gly Gly Glu Asn Gly Pro Val Leu Glu			
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Val Ile Cys Ser Arg Met Arg Tyr Ile Ser Ser Gln Ile Glu Arg Pro			
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Ile Arg Ile Val Ala Leu Ser Ser Ser Leu Ser Asn Ala Lys Asp Val			
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gct cac tgg ctg ggc tgc agt gcc acc tcc acc ttc aac ttc cat cct			4704
Ala His Trp Leu Gly Cys Ser Ala Thr Ser Thr Phe Asn Phe His Pro			
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Asn Val Arg Pro Val Pro Leu Glu Leu His Ile Gln Gly Phe Asn Ile			
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Ser His Thr Gln Thr Arg Leu Leu Ser Met Ala Lys Pro Val Phe His			
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Ala Ile Thr Lys His Ser Pro Lys Lys Pro Val Ile Val Phe Val Pro			
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Ser Arg Lys Gln Thr Arg Leu Thr Ala Ile Asp Ile Leu Thr Thr Cys			

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tac tat tac ata aac tac acc acc att gag ctc ttc agc atg tct ctg Tyr Tyr Tyr Ile Asn Tyr Thr Thr Ile Glu Leu Phe Ser Met Ser Leu			5664

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Arg Gln Leu Ala Gln Lys Val Pro His Lys Leu Asn Asn Pro Lys Phe			
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Ser Lys Ala Ile Arg Leu Ile Gln Ala Cys Val Asp Val Leu Ser Ser			
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Ser Val Phe Asp Ile Met Glu Met Glu Asp Glu Glu Arg Asn Ala Leu			
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Leu Gln Leu Thr Asp Ser Gln Ile Ala Asp Val Ala Arg Phe Cys Asn			
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Arg Tyr Pro Asn Ile Glu Leu Ser Tyr Glu Val Val Asp Lys Asp Ser			
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Ile Arg Ser Gly Gly Pro Val Val Val Leu Val Gln Leu Glu Arg Glu			
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Glu Glu Gly Trp Trp Val Val Ile Gly Asp Ala Lys Ser Asn Ser Leu			
2115	2120	2125	
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Ile Ser Ile Lys Arg Leu Thr Leu Gln Gln Lys Ala Lys Val Lys Leu			

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Ser Asn Leu Val Leu Gln Ala Asp Arg Ser Leu Ile Asp Arg Thr Arg	
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Arg Asp Glu Pro Thr Gly Glu Val Leu Ser Leu Val Gly Lys Leu Glu	
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Gly Thr Arg Met Gly Asp Lys Ala Gln Arg Thr Lys Pro Gln Met Gln	
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Glu Glu Arg Arg Ala Lys Arg Arg Lys Arg Asp Glu Asp Arg His Asp	
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Ile Asn Lys Met Lys Gly Tyr Thr Leu Leu Ser Glu Gly Ile Asp Glu	
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Met Val Gly Ile Ile Tyr Lys Pro Lys Thr Lys Glu Thr Arg Glu Thr	
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Tyr Glu Val Leu Leu Ser Phe Ile Gln Ala Ala Leu Gly Asp Gln Pro	
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Arg Asp Ile Leu Cys Gly Ala Ala Asp Glu Val Leu Ala Val Leu Lys	
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Glu Glu Glu Gly Asp Glu Asp Val Tyr Gly Glu Val Arg Glu Glu Ala	
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Val His Val Pro Ala Leu Lys Pro Lys Pro Phe Gly Ser Glu Glu Gln	
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Lys Arg Leu Ala Thr Tyr Gly Ile Thr Val Ala Glu Leu Thr Gly Asp	
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1855

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 His Val Ser Lys Leu Leu Ser Gln Cys Lys Phe Asp Leu Leu Glu Glu
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cgg gat att aag tgt tct aac att ttg ctg aat aac agt ggg caa atc Arg Asp Ile Lys Cys Ser Asn Ile Leu Leu Asn Asn Ser Gly Gln Ile 860 865 870	2762
aaa cta gca gat ttt gga ctt gct cgg ctc tat aac tct gaa gag agt Lys Leu Ala Asp Phe Gly Leu Ala Arg Leu Tyr Asn Ser Glu Glu Ser 875 880 885	2810

cgc cct tac aca aac aaa gtc att act ttg tgg tac cga cct cca gaa	2858
Arg Pro Tyr Thr Asn Lys Val Ile Thr Leu Trp Tyr Arg Pro Pro Glu	
890 895 900 905	
cta ctg cta gga gag gaa cgt tac aca cca gcc ata gat gtt tgg agc	2906
Leu Leu Leu Gly Glu Glu Arg Tyr Thr Pro Ala Ile Asp Val Trp Ser	
910 915 920	
tgt gga tgt att ctt ggg gaa cta ttc aca aag aag cct att ttt caa	2954
Cys Gly Cys Ile Leu Gly Glu Leu Phe Thr Lys Lys Pro Ile Phe Gln	
925 930 935	
gcc aat ctg gaa ctg gct cag cta gaa ctg atc agc cga ctt tgt ggt	3002
Ala Asn Leu Glu Leu Ala Gln Leu Glu Leu Ile Ser Arg Leu Cys Gly	
940 945 950	
agc cct tgt cca gct gtg tgg cct gat gtt atc aaa ctg ccc tac ttc	3050
Ser Pro Cys Pro Ala Val Trp Pro Asp Val Ile Lys Leu Pro Tyr Phe	
955 960 965	
aac acc atg aaa ccg aag aag caa tat cga agg cgt cta cga gaa gaa	3098
Asn Thr Met Lys Pro Lys Lys Gln Tyr Arg Arg Arg Leu Arg Glu Glu	
970 975 980 985	
ttc tct ttc att cct tct gca gca ctt gat tta ttg gac cac atg ctg	3146
Phe Ser Phe Ile Pro Ser Ala Ala Leu Asp Leu Leu Asp His Met Leu	
990 995 1000	
aca cta gat cct agt aag cgg tgc aca gct gaa cag acc cta cag agc	3194
Thr Leu Asp Pro Ser Lys Arg Cys Thr Ala Glu Gln Thr Leu Gln Ser	
1005 1010 1015	
gac ttc ctt aaa gat gtc gaa ctc agc aaa atg gct cct cca gac ctc	3242
Asp Phe Leu Lys Asp Val Glu Leu Ser Lys Met Ala Pro Pro Asp Leu	
1020 1025 1030	
ccc cac tgg cag gat tgc cat gag ttg tgg agt aag aaa cgg cga cgt	3290
Pro His Trp Gln Asp Cys His Glu Leu Trp Ser Lys Lys Arg Arg Arg	
1035 1040 1045	
cag cga caa agt ggt gtt gta gtc gaa gag cca cct cca tcc aaa act	3338
Gln Arg Gln Ser Gly Val Val Glu Glu Pro Pro Pro Ser Lys Thr	
1050 1055 1060 1065	
tct cga aaa gaa act acc tca ggg aca agt act gag cct gtg aag aac	3386
Ser Arg Lys Glu Thr Thr Ser Gly Thr Ser Thr Glu Pro Val Lys Asn	
1070 1075 1080	
agc agc cca gca cca cct cag cct gct cct ggc aag gtg gag tct ggg	3434
Ser Ser Pro Ala Pro Pro Gln Pro Ala Pro Gly Lys Val Glu Ser Gly	
1085 1090 1095	
gct ggg gat gca ata ggc ctt gct gac atc aca caa cag ctg aat caa	3482
Ala Gly Asp Ala Ile Gly Leu Ala Asp Ile Thr Gln Gln Leu Asn Gln	
1100 1105 1110	
agt gaa ttg gca gtg tta tta aac ctg ctg cag agc caa acc gac ctg	3530
Ser Glu Leu Ala Val Leu Leu Asn Leu Leu Gln Ser Gln Thr Asp Leu	
1115 1120 1125	
agc atc cct caa atg gca cag ctg ctt aac atc cac tcc aac cca gag	3578
Ser Ile Pro Gln Met Ala Gln Leu Leu Asn Ile His Ser Asn Pro Glu	
1130 1135 1140 1145	

atg cag cag cag ctg gaa gcc ctg aac caa tcc atc agt gcc ctg acg Met Gln Gln Gln Leu Glu Ala Leu Asn Gln Ser Ile Ser Ala Leu Thr 1150 1155 1160	3626
gaa gct act tcc cag cag cag gac tca gag acc atg gcc cca gag gag Glu Ala Thr Ser Gln Gln Gln Asp Ser Glu Thr Met Ala Pro Glu Glu 1165 1170 1175	3674
tct ttg aag gaa gca ccc tct gcc cca gtg atc ctg cct tca gca gaa Ser Leu Lys Glu Ala Pro Ser Ala Pro Val Ile Leu Pro Ser Ala Glu 1180 1185 1190	3722
cag atg acc ctt gaa gct tca agc aca cca gct gac atg cag aat ata Gln Met Thr Leu Glu Ala Ser Ser Thr Pro Ala Asp Met Gln Asn Ile 1195 1200 1205	3770
ttg gca gtt ctc ttg agt cag ctg atg aaa acc caa gag cca gca ggc Leu Ala Val Leu Leu Ser Gln Leu Met Lys Thr Gln Glu Pro Ala Gly 1210 1215 1220 1225	3818
agt ctg gag gaa aac aac agt gac aag aac agt ggg cca cag ggg ccc Ser Leu Glu Glu Asn Asn Ser Asp Lys Asn Ser Gly Pro Gln Gly Pro 1230 1235 1240	3866
cga aga act ccc aca atg cca cag gag gag gca gca gca tgt cct cct Arg Arg Thr Pro Thr Met Pro Gln Glu Glu Ala Ala Ala Cys Pro Pro 1245 1250 1255	3914
cac att ctt cca cca gag aag agg ccc cct gag ccc ccc gga cct cca His Ile Leu Pro Pro Glu Lys Arg Pro Pro Glu Pro Pro Gly Pro Pro 1260 1265 1270	3962
ccg ccg cca cct cca ccc cct ctg gtt gaa ggc gat ctt tcc agc gcc Pro Pro Pro Pro Pro Pro Pro Leu Val Glu Gly Asp Leu Ser Ser Ala 1275 1280 1285	4010
ccc cag gag ttg aac cca gcc gtg aca gcc gcc ttg ctg caa ctt tta Pro Gln Glu Leu Asn Pro Ala Val Thr Ala Ala Leu Leu Gln Leu Leu 1290 1295 1300 1305	4058
tcc cag cct gaa gca gag cct cct ggc cac ctg cca cat gag cac cag Ser Gln Pro Glu Ala Glu Pro Pro Gly His Leu Pro His Glu His Gln 1310 1315 1320	4106
gcc ttg aga cca atg gag tac tcc acc cga ccc cgt cca aac agg act Ala Leu Arg Pro Met Glu Tyr Ser Thr Arg Pro Arg Pro Asn Arg Thr 1325 1330 1335	4154
tat gga aac act gat ggg cct gaa aca ggg ttc agt gcc att gac act Tyr Gly Asn Thr Asp Gly Pro Glu Thr Gly Phe Ser Ala Ile Asp Thr 1340 1345 1350	4202
gat gaa cga aac tct ggt cca gcc ttg aca gaa tcc ttg gtc cag acc Asp Glu Arg Asn Ser Gly Pro Ala Leu Thr Glu Ser Leu Val Gln Thr 1355 1360 1365	4250
ctg gtg aag aac agg acc ttc tca ggc tct ctg agc cac ctt ggg gag Leu Val Lys Asn Arg Thr Phe Ser Gly Ser Leu Ser His Leu Gly Glu 1370 1375 1380 1385	4298
tcc agc agt tac cag ggc aca ggg tag gagca acggtgggaa tgccctctga Ser Ser Ser Tyr Gln Gly Thr Gly *	4350
1390	

ggaatgcagt gatgtccatc agtcacctct caccagagc ctggcaaatt cagtctcttt 4410
 cacagaacct aaagccaagc caggttcagt gggaaatccc acctgtccaa acactgtgtg 4470
 agacaccaga attagaggcc tgcaagcctg cttccttcat cccaatgcc cagatgggac 4530
 aggtcaccag cctcctgtgc tacccccacc tttcttgctt gctg 4574

<210> 670
 <211> 426
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (121)..(426)

<400> 670
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 ggttctgcct accccgagac tgetgctgtt cggagacctg caggtgaatg ccccatcacc 120
 atg tct gac ctg gag gca aaa ctt tca act gag cat ttg ggg gat aag 168
 Met Ser Asp Leu Glu Ala Lys Leu Ser Thr Glu His Leu Gly Asp Lys
 1 5 10 15
 ata aaa gat gaa gat att aaa ctc agg gtt att gga cag gat agc agt 216
 Ile Lys Asp Glu Asp Ile Lys Leu Arg Val Ile Gly Gln Asp Ser Ser
 20 25 30
 gag att cat ttc aaa gtg aaa atg aca aca cct ctc aag aaa ctc aag 264
 Glu Ile His Phe Lys Val Lys Met Thr Thr Pro Leu Lys Lys Leu Lys
 35 40 45
 aaa tcg tac tgt cag aga cag ggc gtt cca gtg aat tcc ctc agg ttt 312
 Lys Ser Tyr Cys Gln Arg Gln Gly Val Pro Val Asn Ser Leu Arg Phe
 50 55 60
 ctc ttt gaa ggt cag aga att gct gat aat cat act cca gaa gaa ctg 360
 Leu Phe Glu Gly Gln Arg Ile Ala Asp Asn His Thr Pro Glu Glu Leu
 65 70 75 80
 gga atg gag gaa gaa gat gtg att gag gtt tat cag gaa caa atc gga 408
 Gly Met Glu Glu Glu Asp Val Ile Glu Val Tyr Gln Glu Gln Ile Gly
 85 90 95
 ggt cat tca aca gtt tag 426
 Gly His Ser Thr Val *
 100

<210> 671
 <211> 1830
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (59) .. (1546)

<400> 671

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Met Pro His Gln Arg Pro Arg Thr Cys Ala Met Asn Pro Glu Leu Thr
   1             5             10             15

atg gaa agt ctg ggc act ttg cac ggc gcg cgc ggc ggc ggc agt ggc      154
Met Glu Ser Leu Gly Thr Leu His Gly Ala Arg Gly Gly Gly Ser Gly
           20             25             30

ggg ggc ggc ggc ggg ggc ggc ggg ggc ggc ggc ggg ggc ccg ggc cat      202
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro Gly His
       35             40             45

gag cag gag ctg ctg gcc agc ccc agc ccc cac cac gcg cgc cgc ggc      250
Glu Gln Glu Leu Leu Ala Ser Pro Ser Pro His His Ala Arg Arg Gly
   50             55             60

ccg cgt ggc tcg ctg cgg ggc cct ccg ccg cct cca acc gcg cac cag      298
Pro Arg Gly Ser Leu Arg Gly Pro Pro Pro Pro Thr Ala His Gln
   65             70             75             80

gag ctg ggc acg gcg gca gcg gcg gca gcg gcg gcg tcg cgc tcg gcc      346
Glu Leu Gly Thr Ala Ala Ala Ala Ala Ala Ala Ala Ser Arg Ser Ala
           85             90             95

atg gtc acc agc atg gcc tcg atc ctg gac ggc ggc gac tac cgg ccc      394
Met Val Thr Ser Met Ala Ser Ile Leu Asp Gly Gly Asp Tyr Arg Pro
       100             105             110

gag ctc tcc atc ccg ctg cac cac gcc atg agc atg tcc tgc gac tcg      442
Glu Leu Ser Ile Pro Leu His His Ala Met Ser Met Ser Cys Asp Ser
       115             120             125

tct ccg cct ggc atg ggc atg agc aac acc tac acc acg ctg aca ccg      490
Ser Pro Pro Gly Met Gly Met Ser Asn Thr Tyr Thr Thr Leu Thr Pro
       130             135             140

ctc cag ccg ctg cca ccc atc tcc acc gtg tct gac aag ttc cac cac      538
Leu Gln Pro Leu Pro Pro Ile Ser Thr Val Ser Asp Lys Phe His His
       145             150             155             160

cct cac ccg cac cac cat ccg cac cac cac cac cac cac cac cac cag      586
Pro His Pro His His His Pro His His His His His His His His Gln
           165             170             175

cgc ctg tcc ggc aac gtc agc ggc agc ttc acc ctc atg cgc gac gag      634
Arg Leu Ser Gly Asn Val Ser Gly Ser Phe Thr Leu Met Arg Asp Glu
       180             185             190

cgc ggg ctc ccg gcc atg aac aac ctc tac agt ccc tac aag gag atg      682
Arg Gly Leu Pro Ala Met Asn Asn Leu Tyr Ser Pro Tyr Lys Glu Met
       195             200             205

ccc ggc atg agc cag agc ctg tcc ccg ctg gcc gcc acg ccg ctg ggc      730
Pro Gly Met Ser Gln Ser Leu Ser Pro Leu Ala Ala Thr Pro Leu Gly
       210             215             220

aac ggg cta ggc ggc ctc cac aac gcg cag cag agt ctg ccc aac tac      778
Asn Gly Leu Gly Gly Leu His Asn Ala Gln Gln Ser Leu Pro Asn Tyr
       225             230             235             240

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ggt ccg ccg ggc cac gac aaa atg ctc agc ccc aac ttc gac gcg cac Gly Pro Pro Gly His Asp Lys Met Leu Ser Pro Asn Phe Asp Ala His 245 250 255	826
cac act gcc atg ctg acc cgc ggt gag caa cac ctg tcc cgc ggc ctg His Thr Ala Met Leu Thr Arg Gly Glu Gln His Leu Ser Arg Gly Leu 260 265 270	874
ggc acc cca cct gcg gcc atg atg tcg cac ctg aac ggc ctg cac cac Gly Thr Pro Pro Ala Ala Met Met Ser His Leu Asn Gly Leu His His 275 280 285	922
ccg ggc cac act cag tct cac ggg ccg gtg ctg gca ccc agt cgc gag Pro Gly His Thr Gln Ser His Gly Pro Val Leu Ala Pro Ser Arg Glu 290 295 300	970
cgg cca ccc tcg tcc tca tcg ggc tcg cag gtg gcc acg tcg ggc cag Arg Pro Pro Ser Ser Ser Ser Gly Ser Gln Val Ala Thr Ser Gly Gln 305 310 315 320	1018
ctg gaa gaa atc aac acc aaa gag gtg gcc cag cgc atc aca gcg gag Leu Glu Glu Ile Asn Thr Lys Glu Val Ala Gln Arg Ile Thr Ala Glu 325 330 335	1066
ctg aag cgc tac agt atc ccc cag gcg atc ttt gcg cag agg gtg ctg Leu Lys Arg Tyr Ser Ile Pro Gln Ala Ile Phe Ala Gln Arg Val Leu 340 345 350	1114
tgc cgg tct cag ggg act ctc tcc gac ctg ctc cgg aat cca aaa ccg Cys Arg Ser Gln Gly Thr Leu Ser Asp Leu Leu Arg Asn Pro Lys Pro 355 360 365	1162
tgg agt aaa ctc aaa tct ggc agg gag acc ttc cgc agg atg tgg aag Trp Ser Lys Leu Lys Ser Gly Arg Glu Thr Phe Arg Arg Met Trp Lys 370 375 380	1210
tgg ctt cag gag ccc gag ttc cag cgc atg tcc gcc tta cgc ctg gca Trp Leu Gln Glu Pro Glu Phe Gln Arg Met Ser Ala Leu Arg Leu Ala 385 390 395 400	1258
gcg tgc aaa cgc aaa gag caa gaa cca aac aaa gac agg aac aat tcc Ala Cys Lys Arg Lys Glu Gln Glu Pro Asn Lys Asp Arg Asn Asn Ser 405 410 415	1306
cag aag aag tcc cgc ctg gtg ttc act gac ctc caa cgc cga aca ctc Gln Lys Lys Ser Arg Leu Val Phe Thr Asp Leu Gln Arg Arg Thr Leu 420 425 430	1354
ttc gcc atc ttc aag gag aac aaa cgc ccg tca aag gag atg cag atc Phe Ala Ile Phe Lys Glu Asn Lys Arg Pro Ser Lys Glu Met Gln Ile 435 440 445	1402
acc att tcc cag cag ctg ggc ctg gag ctc aca acc gtc agc aac ttc Thr Ile Ser Gln Gln Leu Gly Leu Glu Leu Thr Thr Val Ser Asn Phe 450 455 460	1450
ttc atg aac gcc cgg cgc cgc agc ctg gag aag tgg caa gac gat ctg Phe Met Asn Ala Arg Arg Ser Leu Glu Lys Trp Gln Asp Asp Leu 465 470 475 480	1498
agc aca ggg ggc tcc tcg tcc acc tcc agc acg tgt acc aaa gca tga Ser Thr Gly Gly Ser Ser Ser Thr Ser Ser Thr Cys Thr Lys Ala * 485 490 495	1546

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tggaaggact ctcaacttggg cacaagtcac ctccaaatga ggacaacaga taccaaaaga 1606
aaacaaagga aaaagacacc ggattcctag ctggggccct tcaactgggtga tttgaaagca 1666
caattctctt gcaaagaaac ttatattcta gctgtaatca taggccaggt gttcttcttt 1726
tgtttttaat ggctatggag tccaagtgc aagctgaaaaa ttaattctctt agaaccagac 1786
actgttctct gagcatgcta agcatcagaa acccaaattgg ggcc 1830

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<210> 672
<211> 3239
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (281)..(2407)

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<220>
<221> misc_feature
<222> (1)...(3239)
<223> n = a,t,c or g

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gcgaaaagct gaggcggcaa cgtcggggac ggctgcgcgg gacggctctg taggaaggaa 120
cttggttccc cctccctcag cttccgcccc aaaagcagaa gtagaaagta atgaaaagga 180
caacagacct gaggaagaag agcaagtaat acatgaagat gatgaaagac cttctgagaa 240
aatgaattt tctagacgaa aacgttctaa atcagaagac atg gac aat gta cag 295
Met Asp Asn Val Gln
1 5

tct aaa cgt cgt cga tat atg gaa gaa gaa tat gag gca gaa ttt caa 343
Ser Lys Arg Arg Tyr Met Glu Glu Glu Tyr Glu Ala Glu Phe Gln
10 15 20

gta aag att aca gcc aaa gga gac att aac cag aaa ctt caa aag gtt 391
Val Lys Ile Thr Ala Lys Gly Asp Ile Asn Gln Lys Leu Gln Lys Val
25 30 35

ata cag tgg ttg ctg gaa gaa aaa ttg tgt gcg ctg cag tgt gct gta 439
Ile Gln Trp Leu Leu Glu Glu Lys Leu Cys Ala Leu Gln Cys Ala Val
40 45 50

ttt gat aag act ttg gca gaa ttg aaa aca cga gtg gaa aag att gaa 487
Phe Asp Lys Thr Leu Ala Glu Leu Lys Thr Arg Val Glu Lys Ile Glu
55 60 65

tgt aac aag agg cat aaa aca gtt ctc act gaa cta cag gcc aag ata 535
Cys Asn Lys Arg His Lys Thr Val Leu Thr Glu Leu Gln Ala Lys Ile
70 75 80 85

gcc agg tta acc aaa cgc ttt gaa gca gcc aaa gaa gat ctt aag aaa 583
Ala Arg Leu Thr Lys Arg Phe Glu Ala Ala Lys Glu Asp Leu Lys Lys
90 95 100

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aga cat gaa cat cca ccc aac cca cca gta tca cca gga aaa act gta	631
Arg His Glu His Pro Pro Asn Pro Pro Val Ser Pro Gly Lys Thr Val	
105 110 115	
aat gat gtc aac agc aat aat aac atg tct tac aga aat gca ggc aca	679
Asn Asp Val Asn Ser Asn Asn Asn Met Ser Tyr Arg Asn Ala Gly Thr	
120 125 130	
gtg aga cag atg ctg gag tcc aaa aga aat gta agc gag agt gca cca	727
Val Arg Gln Met Leu Glu Ser Lys Arg Asn Val Ser Glu Ser Ala Pro	
135 140 145	
cca tcc ttt caa act cct gtg aat aca gta tct tca acc aat ctt gtc	775
Pro Ser Phe Gln Thr Pro Val Asn Thr Val Ser Ser Thr Asn Leu Val	
150 155 160 165	
act cct cca gca gtt gtc agt agt caa cct aaa ttg cag act cca gtg	823
Thr Pro Pro Ala Val Val Ser Ser Gln Pro Lys Leu Gln Thr Pro Val	
170 175 180	
act tcg ggt tcc ctc aca gca acg tca gtt ctt cct gca ccc aat aca	871
Thr Ser Gly Ser Leu Thr Ala Thr Ser Val Leu Pro Ala Pro Asn Thr	
185 190 195	
gct act gta gtt gct act act cag gtg cct agt gga aat ccc cag cct	919
Ala Thr Val Val Ala Thr Thr Gln Val Pro Ser Gly Asn Pro Gln Pro	
200 205 210	
aca atc tct tta cag cct ttg cca gtg att ttg cat gta cct gtt gca	967
Thr Ile Ser Leu Gln Pro Leu Pro Val Ile Leu His Val Pro Val Ala	
215 220 225	
gta tcc tcc cag cct cag ctt cta cag agc cat cca ggg act ttg gtg	1015
Val Ser Ser Gln Pro Gln Leu Leu Gln Ser His Pro Gly Thr Leu Val	
230 235 240 245	
act aat caa cca tct ggc aat gtt gaa ttc att tct gtg caa agc cca	1063
Thr Asn Gln Pro Ser Gly Asn Val Glu Phe Ile Ser Val Gln Ser Pro	
250 255 260	
cct aca gtg agt ggt ctt acc aaa aat cca gta tcc ttg cca tcc ttg	1111
Pro Thr Val Ser Gly Leu Thr Lys Asn Pro Val Ser Leu Pro Ser Leu	
265 270 275	
cca aat ccc act aaa cca aac aac gtt cct tct gtg ccc agt cct agt	1159
Pro Asn Pro Thr Lys Pro Asn Asn Val Pro Ser Val Pro Ser Pro Ser	
280 285 290	
att caa agg aac cct act gcc agt gct gca cca ttg gga aca aca ctt	1207
Ile Gln Arg Asn Pro Thr Ala Ser Ala Ala Pro Leu Gly Thr Thr Leu	
295 300 305	
gct gtg cag gct gtt cca aca gca cac tct att gta caa gcc aca agg	1255
Ala Val Gln Ala Val Pro Thr Ala His Ser Ile Val Gln Ala Thr Arg	
310 315 320 325	
act tct tta ccc aca gtg ggc cca tca gga ctc tat agt cca tca act	1303
Thr Ser Leu Pro Thr Val Gly Pro Ser Gly Leu Tyr Ser Pro Ser Thr	
330 335 340	
aat cga ggt cct ata cag atg aaa att cca att tct gca ttt agt act	1351
Asn Arg Gly Pro Ile Gln Met Lys Ile Pro Ile Ser Ala Phe Ser Thr	
345 350 355	

tcg tct gct gca gaa cag aac agc aat acc acc cca aga att gaa aac Ser Ser Ala Ala Glu Gln Asn Ser Asn Thr Thr Pro Arg Ile Glu Asn 360 365 370	1399
cag aca aac aaa aca ata gat gct tct gtc agt aag aaa gca gct gat Gln Thr Asn Lys Thr Ile Asp Ala Ser Val Ser Lys Lys Ala Ala Asp 375 380 385	1447
agc aca tca cag tgt gga aaa gcc act ggc agt gat tca agt ggt gtc Ser Thr Ser Gln Cys Gly Lys Ala Thr Gly Ser Asp Ser Ser Gly Val 390 395 400 405	1495
att gat ctc aca atg gat gat gaa gag agt gga gct tca caa gac ccc Ile Asp Leu Thr Met Asp Asp Glu Glu Ser Gly Ala Ser Gln Asp Pro 410 415 420	1543
aaa aaa cta aat cac act cct gta tca acc atg agt tct tct cag cct Lys Lys Leu Asn His Thr Pro Val Ser Thr Met Ser Ser Ser Gln Pro 425 430 435	1591
gtg tca cga cca ttg caa ccc ata caa cca gca ccg cct ctt caa cca Val Ser Arg Pro Leu Gln Pro Ile Gln Pro Ala Pro Pro Leu Gln Pro 440 445 450	1639
tct ggg gtg cca aca agt gga cca tct cag acc acc ata cac tta cta Ser Gly Val Pro Thr Ser Gly Pro Ser Gln Thr Thr Ile His Leu Leu 455 460 465	1687
cct aca gct cca act acc gtg aat gta aca cat cgt cca gta act cag Pro Thr Ala Pro Thr Thr Val Asn Val Thr His Arg Pro Val Thr Gln 470 475 480 485	1735
gtg acc aca aga ctc cct gta cca aga gct cct gca aac cac cag gtg Val Thr Thr Arg Leu Pro Val Pro Arg Ala Pro Ala Asn His Gln Val 490 495 500	1783
gtt tat aca act ctt cct gca cca cca gct cag gct ccc ttg cga gga Val Tyr Thr Thr Leu Pro Ala Pro Pro Ala Gln Ala Pro Leu Arg Gly 505 510 515	1831
act gtt atg cag gct cct gct gtt cgg cag gtc aat ccc caa aat agt Thr Val Met Gln Ala Pro Ala Val Arg Gln Val Asn Pro Gln Asn Ser 520 525 530	1879
gtt aca gtt cga gtg cct caa aca acc aca tat gtt gta aac aat gga Val Thr Val Arg Val Pro Gln Thr Thr Thr Tyr Val Val Asn Asn Gly 535 540 545	1927
cta acc ctg gga tca aca gga cct cag ctc aca gtg cat cac cga cca Leu Thr Leu Gly Ser Thr Gly Pro Gln Leu Thr Val His His Arg Pro 550 555 560 565	1975
cca caa gtg cat act gag ccc cca cgc ccc gtg cac cca gca ccc tta Pro Gln Val His Thr Glu Pro Pro Arg Pro Val His Pro Ala Pro Leu 570 575 580	2023
cca gaa gct cca caa cca cag cgt ctg ccc cca gaa gct gcc agc aca Pro Glu Ala Pro Gln Pro Gln Arg Leu Pro Pro Glu Ala Ala Ser Thr 585 590 595	2071
tct ctg cct cag aag cca cac ttg aag tta gca cgc gtt cag agt caa Ser Leu Pro Gln Lys Pro His Leu Lys Leu Ala Arg Val Gln Ser Gln 600 605 610	2119


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aat ggc ata gta ctg tca tgg agt gtc ctg gag gtg gat cga agc tgt      2167
Asn Gly Ile Val Leu Ser Trp Ser Val Leu Glu Val Asp Arg Ser Cys
    615                      620                      625

gcc act gtt gat agc tac cat ctc tat gct tac cat gag gaa ccc agt      2215
Ala Thr Val Asp Ser Tyr His Leu Tyr Ala Tyr His Glu Glu Pro Ser
    630                      635                      640                      645

gcc act gtg ccc tca caa tgg aaa aag att ggg gaa gtc aag gca ctt      2263
Ala Thr Val Pro Ser Gln Trp Lys Lys Ile Gly Glu Val Lys Ala Leu
                      650                      655                      660

ccc ttg ccc atg gca tgt act ctc acc cag ttt gta tct ggt agc aaa      2311
Pro Leu Pro Met Ala Cys Thr Leu Thr Gln Phe Val Ser Gly Ser Lys
                      665                      670                      675

tac tac ttt gca gta cga gcc aag gat att tat gga cgt ttt ggg cct      2359
Tyr Tyr Phe Ala Val Arg Ala Lys Asp Ile Tyr Gly Arg Phe Gly Pro
                      680                      685                      690

ttc tgt gat cct cag tca aca gat gtg atc tct tct acc cag agc agt      2407
Phe Cys Asp Pro Gln Ser Thr Asp Val Ile Ser Ser Thr Gln Ser Ser
    695                      700                      705

taaaccttgg agcctttata ttttcctctt ttaaaatttc caccttttgg tcttgttttt      2467

aatcttgtgc atgatacccc atgtaaaatc caccttgtgc aagatttctt ggacagatgt      2527

gtgtatacac tacatttggt tataaccaga agcaaaataa actcagccca caaagctaga      2587

atcttttctt ggacagttta ggctttgggg tttggaaatg taaatgtgta ccttgcttta      2647

gttttgaggc tggggaatat gtgtgggtgt ttatgtgtgt ttttccttat gtaggtgtta      2707

ttgcattgga gtctcccatt ttcattctca aatttacctc ttaaagtacg aagtaagtag      2767

atcaaaggat ttgagatgtg taactggcat gattctgctt ttgaaggatc tatagtatca      2827

ttttagttaa gtgggtcaaa cagaatcaaa acaaaaccca aagaaaaaaa aaacaaaatg      2887

gctaaatagt ttaaaatagg ttaattcgaa cacaggaaag gatctatttg ttgtttcttt      2947

tgtctggtct cctgagttgt taattaggtg aaaaaagatc tgcaatggcc cctcccttt      3007

cctaactctgg cttttacatt tattttgtgc cttaaagatt aactacaaag ataaacatgg      3067

ccaaaaataa ataaataaat atggccatat gtccgntggt gcttagtctt cccttgacgc      3127

cttttaccct tgatttctcc ttcattctta ccaaatatag cacaactcct caagtaattt      3187

tttttttttg aaatggagtt ttgctcttgt tgcccaggct ggaaaggcgg gg      3239

```

<210> 673

<211> 1144

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (314)..(1144)

<400> 673

cggtccggaa ttcccgggtc gacccacgcg tcggagagaa gcagcttcgg ctgcagcaaa 60

ccacgcaggt ccttcttgat catctagaac tgaccgctcc gccttgccag gagtctgcag 120

aaccacgtgg ctagcctgcc tgaagttctc acctctccag gaaggcgggg ggtttctaat 180

ggctgcagct gcgctggggg ctgggggctc ccgctggggac tccacttcgg tggatgtcta 240

agcttcacct ttcttgcgcc cgcaggggca tgactcaggt gaaagggagc cattttctca 300

gaccctggc ctc atg cag ccc ttc agc atc ccc gtg caa atc aca ctt 349
Met Gln Pro Phe Ser Ile Pro Val Gln Ile Thr Leu
1 5 10

cag ggc agc cgg agg cgc cag ggg agg aca gcc ttt cct gcc tca ggg 397
Gln Gly Ser Arg Arg Arg Gln Gly Arg Thr Ala Phe Pro Ala Ser Gly
15 20 25

aag aag aga gag aca gac tac agt gat gga gac cca cta gat gtg cac 445
Lys Lys Arg Glu Thr Asp Tyr Ser Asp Gly Asp Pro Leu Asp Val His
30 35 40

aag agg ctg cca tcc agt act gga gag gac cga gcc gtg atg ctg ggg 493
Lys Arg Leu Pro Ser Ser Thr Gly Glu Asp Arg Ala Val Met Leu Gly
45 50 55 60

ttt gcc atg atg ggc ttc tca gtc cta atg ttc ttc ttg ctc gga aca 541
Phe Ala Met Met Gly Phe Ser Val Leu Met Phe Phe Leu Leu Gly Thr
65 70 75

acc att cta aag cct ttt atg ctc agc att cag aga gaa gaa tcg acc 589
Thr Ile Leu Lys Pro Phe Met Leu Ser Ile Gln Arg Glu Glu Ser Thr
80 85 90

tgc act gcc atc cac aca gat atc atg gac gac tgg ctg gac tgt gcc 637
Cys Thr Ala Ile His Thr Asp Ile Met Asp Asp Trp Leu Asp Cys Ala
95 100 105

ttc acc tgt ggt gtg cac tgc cac ggt cag ggg aag tac cca tgt ctt 685
Phe Thr Cys Gly Val His Cys His Gly Gln Gly Lys Tyr Pro Cys Leu
110 115 120

cag gtg ttt gtg aac ctc agc cat cca ggt cag aaa gct ctc cta cat 733
Gln Val Phe Val Asn Leu Ser His Pro Gly Gln Lys Ala Leu Leu His
125 130 135 140

tat aat gaa gag gct gtc cag ata aat ccc aag tgc ttt tac aca cct 781
Tyr Asn Glu Glu Ala Val Gln Ile Asn Pro Lys Cys Phe Tyr Thr Pro
145 150 155

aag tgc cac caa gat aga aat gat ttg ctc aac agt gct ctg gac ata 829
Lys Cys His Gln Asp Arg Asn Asp Leu Leu Asn Ser Ala Leu Asp Ile
160 165 170

aaa gaa ttc ttc gat cac aaa aat gga act ccc ttt tca tgc ttc tac 877
Lys Glu Phe Phe Asp His Lys Asn Gly Thr Pro Phe Ser Cys Phe Tyr
175 180 185

agt cca gcc agc caa tct gaa gat gtc att ctt ata aaa aag tat gac 925
Ser Pro Ala Ser Gln Ser Glu Asp Val Ile Leu Ile Lys Lys Tyr Asp
190 195 200

```

caa atg gct atc ttc cac tgt tta ttt tgg cct tca ctg act ctg cta      973
Gln Met Ala Ile Phe His Cys Leu Phe Trp Pro Ser Leu Thr Leu Leu
205                      210                      215                      220

ggg ggt gcc ctg att gtt ggc atg gtg aga tta aca caa cac ctg tcc      1021
Gly Gly Ala Leu Ile Val Gly Met Val Arg Leu Thr Gln His Leu Ser
                      225                      230                      235

tta ctg tgt gaa aaa tat agc act gta gtc aga gat gag gta ggt gga      1069
Leu Leu Cys Glu Lys Tyr Ser Thr Val Val Arg Asp Glu Val Gly Gly
                      240                      245                      250

aaa gta cct tat ata gaa cag cat cag ttc aaa ctg tgc att atg agg      1117
Lys Val Pro Tyr Ile Glu Gln His Gln Phe Lys Leu Cys Ile Met Arg
                      255                      260                      265

agg agc aaa gga aga gca gag aaa tct                                1144
Arg Ser Lys Gly Arg Ala Glu Lys Ser
270                      275

```

```

<210> 674
<211> 1310
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (99)..(974)

```

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<400> 674
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actagtccag tgtggtggaa ttgcgcctga gcgtctcc      atg gcc tgc ctg agc      113
Met Ala Cys Leu Ser
                      1                      5

ccc tcg cag ctc cag aag ttc caa cag gat gga ttc ctg gtg ctg gaa      161
Pro Ser Gln Leu Gln Lys Phe Gln Gln Asp Gly Phe Leu Val Leu Glu
                      10                      15                      20

gga ttc ttg tct gcg gaa gag tgt gtg gcc atg caa caa agg att ggc      209
Gly Phe Leu Ser Ala Glu Glu Cys Val Ala Met Gln Gln Arg Ile Gly
                      25                      30                      35

gag ata gtg gct gaa atg gat gtt cct ctc cac tgc cgc aca gaa ttc      257
Glu Ile Val Ala Glu Met Asp Val Pro Leu His Cys Arg Thr Glu Phe
                      40                      45                      50

tcc acc cag gaa gag gag cag ctt cga gcc cag ggc agc aca gac tat      305
Ser Thr Gln Glu Glu Glu Gln Leu Arg Ala Gln Gly Ser Thr Asp Tyr
                      55                      60                      65

ttc ttg agc agt ggt gac aag att cga ttc ttc ttt gag aaa ggc gtt      353
Phe Leu Ser Ser Gly Asp Lys Ile Arg Phe Phe Phe Glu Lys Gly Val
                      70                      75                      80                      85

ttt gat gag aaa gga aat ttc ctg gtc cct ccg gag aaa tcc atc aac      401
Phe Asp Glu Lys Gly Asn Phe Leu Val Pro Pro Glu Lys Ser Ile Asn
                      90                      95                      100

```

aaa att ggc cac gct ctg cac gcc cac gac ccc gtc ttc aag agc atc 449
 Lys Ile Gly His Ala Leu His Ala His Asp Pro Val Phe Lys Ser Ile
 105 110 115

aca cac tcc ttc aag gtg cag acc ttg gcc aga agt ctg ggc ctc cag 497
 Thr His Ser Phe Lys Val Gln Thr Leu Ala Arg Ser Leu Gly Leu Gln
 120 125 130

atg ccc gtg gtg gtg cag agc atg tac atc ttt aag caa cct cac ttt 545
 Met Pro Val Val Val Gln Ser Met Tyr Ile Phe Lys Gln Pro His Phe
 135 140 145

ggc ggt gaa gtc tcc cct cat cag gac gcc tcc ttc ctg tac acg gag 593
 Gly Gly Glu Val Ser Pro His Gln Asp Ala Ser Phe Leu Tyr Thr Glu
 150 155 160 165

ccc ctg ggc cgg gtg ctg ggc gtg tgg atc gca gtg gag gat gcc acg 641
 Pro Leu Gly Arg Val Leu Gly Val Trp Ile Ala Val Glu Asp Ala Thr
 170 175 180

ctg gag aac ggc tgt ctc tgg ttc atc cct ggc tcc cac acc agt ggt 689
 Leu Glu Asn Gly Cys Leu Trp Phe Ile Pro Gly Ser His Thr Ser Gly
 185 190 195

gtg tca aga agg atg gtc cgg gcc cct gtt ggc tca gcg cct ggt acc 737
 Val Ser Arg Arg Met Val Arg Ala Pro Val Gly Ser Ala Pro Gly Thr
 200 205 210

agc ttc ctt ggg tca gag cca gcc cgg gat aac agc ctc ttt gtg ccc 785
 Ser Phe Leu Gly Ser Glu Pro Ala Arg Asp Asn Ser Leu Phe Val Pro
 215 220 225

acc cca gtg cag aga ggg gcc ctg gtc ctc atc cat gga gaa gtg gta 833
 Thr Pro Val Gln Arg Gly Ala Leu Val Leu Ile His Gly Glu Val Val
 230 235 240 245

cac aag agc aag cag aac ctc tct gac cgc tcg cgc cag gcc tac act 881
 His Lys Ser Lys Gln Asn Leu Ser Asp Arg Ser Arg Gln Ala Tyr Thr
 250 255 260

ttc cac ctc atg gag gcc tct ggc acc acc tgg agc ccg gag aac tgg 929
 Phe His Leu Met Glu Ala Ser Gly Thr Thr Trp Ser Pro Glu Asn Trp
 265 270 275

ctc cag cca aca gct gaa ctg ccc ttt ccc caa ctg tac acc taa agg 977
 Leu Gln Pro Thr Ala Glu Leu Pro Phe Pro Gln Leu Tyr Thr *
 280 285 290

ctctcgcagg gcaggagccc tcgcccctcc cgggtgaagc tgtgggctgt aaacaccagt 1037
 gccttgctca gcctcctggt tgcaacaggg aggtcttgtc tcccctcctg ggctttcctc 1097
 ctgccctgtg ggcagcagcc taggctgggt caggggcttc cctaagatct tcacctctct 1157
 gcctccctac tgccccaaca tagccttgag gaggtctctc agccaccaaa gggttcttggc 1217
 cccttctcac tctcctctcc tctcagatgg aactctgggtt attatggtgt tagttatoga 1277
 ataaaaacga cttcagaatg caaaaaaaaaaaa aaa 1310

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<211> 707
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (164) .. (364)
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<400> 675	
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gcagcattct gggatatttc ttccttcaag gagtcacagt gcttcacatg ggtcaaggca	120
aagacaggtc tctgccaag gcacccaaga tgaaatcttg aaa atg aga aac aca	175
	Met Arg Asn Thr
	1
ttt gct gaa ctg aag aat tca tta gag gct ctc agc agt aga atg gac	223
Phe Ala Glu Leu Lys Asn Ser Leu Glu Ala Leu Ser Ser Arg Met Asp	
5 10 15 20	
cag gca gag gaa aga att ggg acc cag gct gga gtg cag tgg cgt gat	271
Gln Ala Glu Glu Arg Ile Gly Thr Gln Ala Gly Val Gln Trp Arg Asp	
25 30 35	
cat ggc tca ctg cag cct caa cct cct gaa ttc aag caa tgc ttc cac	319
His Gly Ser Leu Gln Pro Gln Pro Pro Glu Phe Lys Gln Cys Phe His	
40 45 50	
ctc agt ctc cca agt agc tgg gac tac agg gcg tgc ctt tct tag agc	367
Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Ala Cys Leu Ser *	
55 60 65	
aatcctgggtg ccactaaaag ctgcattttc aatatgagat aaaaatgtat ttacaaaaa	427
gtgcaaggtc ttcatgtctg ctggcattgc tgcaacagtg gcttgtgtga gagatcactt	487
tttacggcaa tacccaattt attggagaga caaactgctc aagcaaggat gattagcatt	547
ctatggcatt ttaaaaaggat acttgcaatg cttgacctta ccacaatagc aacaggagggt	607
agctacaaaa ttattacaat agtagagtat ggtaccacag ttaattttat gtagctataa	667
tttaatactg catctttaat gttgttcaca tttctctgga	707

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<210> 676
<211> 929
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (78) .. (779)
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<220>
<221> misc_feature
<222> (1) ... (929)
<223> n = a, t, c or g
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<400> 676
ctgaattccc gggtcgaccc acgcgtccgc gcgtcgggca gcgggcgcg cgccccgcg 60

cagccatgga ctggctc atg ggg aag tcc aaa gcc aag ccc aat ggc aag 110
 Met Gly Lys Ser Lys Ala Lys Pro Asn Gly Lys
 1 5 10

aag ccc gct gcg gag gag agg aag gcc tac ctg gag cct gag cac acc 158
 Lys Pro Ala Ala Glu Glu Arg Lys Ala Tyr Leu Glu Pro Glu His Thr
 15 20 25

aag gcc agg atc acc gac ttc cag ttc aag gag ctg gtg gtg ctg ccc 206
 Lys Ala Arg Ile Thr Asp Phe Gln Phe Lys Glu Leu Val Val Leu Pro
 30 35 40

cgc gag att gac ctt aac gag tgg ctg gcc agc aac acc acg acg ttt 254
 Arg Glu Ile Asp Leu Asn Glu Trp Leu Ala Ser Asn Thr Thr Thr Phe
 45 50 55

ttc cac cac atc aac ctg cag tat agc acc atc tcg gag ttc tgc aca 302
 Phe His His Ile Asn Leu Gln Tyr Ser Thr Ile Ser Glu Phe Cys Thr
 60 65 70 75

gga gag acg tgt cag acg atg gcc gtg tgc aac aca cag tac tac tgg 350
 Gly Glu Thr Cys Gln Thr Met Ala Val Cys Asn Thr Gln Tyr Tyr Trp
 80 85 90

tat gac gag cgg ggg aag aag gtc aag tgc acg gcc cca cag tac gtt 398
 Tyr Asp Glu Arg Gly Lys Lys Val Lys Cys Thr Ala Pro Gln Tyr Val
 95 100 105

gac ttc gtc atg agc tcc gtg cag aag ctg gtg acg gat gag gac gtg 446
 Asp Phe Val Met Ser Ser Val Gln Lys Leu Val Thr Asp Glu Asp Val
 110 115 120

ttc ccc aca aaa tac ggc aga gaa ttc ccc agc tcc ttt gag tcc ctg 494
 Phe Pro Thr Lys Tyr Gly Arg Glu Phe Pro Ser Ser Phe Glu Ser Leu
 125 130 135

gtg agg aag atc tgc aga cac ctg ttc cac gtg ctg gca cac atc tac 542
 Val Arg Lys Ile Cys Arg His Leu Phe His Val Leu Ala His Ile Tyr
 140 145 150 155

tgg gcc cac ttc aag gag acg ctg gcc ctg gag ctg cac gga cac ttg 590
 Trp Ala His Phe Lys Glu Thr Leu Ala Leu Glu Leu His Gly His Leu
 160 165 170

aac acg ctc tac gtc cac ttc atc ctc ttt gct cgg gag ttc aac ctg 638
 Asn Thr Leu Tyr Val His Phe Ile Leu Phe Ala Arg Glu Phe Asn Leu
 175 180 185

ctg gac ccc aaa gag acc gcc atc atg gac gac ctc acc gag gtg cta 686
 Leu Asp Pro Lys Glu Thr Ala Ile Met Asp Asp Leu Thr Glu Val Leu
 190 195 200

tgc agc ggg gcc ggc ggg gtc cac agt ggg ggc agt ggg gat ggg gcc 734
 Cys Ser Gly Ala Gly Gly Val His Ser Gly Gly Ser Gly Asp Gly Ala
 205 210 215

ggc agc ggg ggc ccg gga gca cag aac cac gtg aag gag aga tga gcc 782
 Gly Ser Gly Gly Pro Gly Ala Gln Asn His Val Lys Glu Arg *
 220 225 230

ccccgggccg gacaggggca cacgtgtgca aagagacggt ggtgtgtgtt ctctcctgca 842

tctgcgtgtn cacacatgtg ctgggcacgc gtgtggcgag gacttcaggg gccccggact 902

gacctggtgt gtggetgcat aatcacg

929

<210> 677
 <211> 2663
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (894)..(1724)

<400> 677
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 tttctgcctg ggcttggtcg gccgcgcttc agcaccgcgc gagccggaca gcgcctgctg 120
 catggagctg cccgcgcggg ccggggacgc agtccggagt cccgcgcgcg ccgcgcctt 180
 catcttcccc gggggctccg gggagctaga actggcggtta gaggaggagc tggcgctgct 240
 ggcgcccggg ggagcggccg tccgaccccg gggaacaccc tcaggccgag cctgggtctc 300
 tggccgaggg gcccggaacc cagccgccgc cctcccagga ccccgagctg ctgtcgggtga 360
 tccgacagaa ggagaaggat ctggtgttgg cggcccggct gggtaaggcg ctgctcgaga 420
 ggaaccagga catgagccgg cagtacgagc agatgcataa ggagctgaca gacaagctcg 480
 agcacttaga gcaagagaaa catgaattga gaagacgatt tgagaaccga gaaggggagt 540
 gggaaggccg agtgtcagag ctggagagtg atgtgaagca gctacaggat gagttggaga 600
 ggcagcagat tcctctgcgg gaagcagatc gagaaaaatc acgggctgtc caggaactgt 660
 cggaacagaa ccaaaggcta ttggatcagc tcagcaggaa aattaagact tggatttact 720
 attctacctc agcccttctt gtatattgaa aataaaacta ccaactcttc agttaccgga 780
 ggaaaaagaa cttctctgat atcatccctc agcactgatg ttctcatggg agcagtgccg 840
 tgtctgcatg gtctcctctg tttcaggcat cagaagttga gagacaactc tcc atg 896
 Met
 1
 cag gtc cac gcc ctc aga gaa gac ttt cgg gag aaa aac tca tca acc 944
 Gln Val His Ala Leu Arg Glu Asp Phe Arg Glu Lys Asn Ser Ser Thr
 5 10 15
 aac cag cac att atc cgg ctg gag agc ctt cag gcc gag atc aag atg 992
 Asn Gln His Ile Ile Arg Leu Glu Ser Leu Gln Ala Glu Ile Lys Met
 20 25 30
 ctg tca gat cgg aaa cgg gag ctg gag cat cgt ctc agc gct act tta 1040
 Leu Ser Asp Arg Lys Arg Glu Leu Glu His Arg Leu Ser Ala Thr Leu
 35 40 45
 gag gaa aat gac ctg ctc caa ggg acc gtg gag gag cta cag gac cgg 1088
 Glu Glu Asn Asp Leu Leu Gln Gly Thr Val Glu Glu Leu Gln Asp Arg
 50 55 60 65

gtg cta atc ctg gag agg cag ggc cat gac aag gac cta cag ctg cac	1136
Val Leu Ile Leu Glu Arg Gln Gly His Asp Lys Asp Leu Gln Leu His	
70 75 80	
caa agc cag ctg gag ctt cag gag gtg cgt ctc tcc tgc cga cag ctg	1184
Gln Ser Gln Leu Glu Leu Gln Glu Val Arg Leu Ser Cys Arg Gln Leu	
85 90 95	
cag gtg aag gtg gaa gaa ctc act gag gag agg agt ctg cag agc tct	1232
Gln Val Lys Val Glu Glu Leu Thr Glu Glu Arg Ser Leu Gln Ser Ser	
100 105 110	
gcc gcc acc agc aca tcc ctc ctg tca gag atc gag cag agc atg gag	1280
Ala Ala Thr Ser Thr Ser Leu Leu Ser Glu Ile Glu Gln Ser Met Glu	
115 120 125	
gct gag gag ctg gag cag gag cga gag cag gtg aca ctg ctg agt gtg	1328
Ala Glu Glu Leu Glu Gln Glu Arg Glu Gln Val Thr Leu Leu Ser Val	
130 135 140 145	
gag atg act gcc cta aaa gag gag aga gac cga ctc aga gtc act tct	1376
Glu Met Thr Ala Leu Lys Glu Glu Arg Asp Arg Leu Arg Val Thr Ser	
150 155 160	
gag gac aag gag cca aag gag cag ctt cag aag gcc atc agg gac cgc	1424
Glu Asp Lys Glu Pro Lys Glu Gln Leu Gln Lys Ala Ile Arg Asp Arg	
165 170 175	
gac gag gcc att gca aag aag aat gct gtg gag ctg gaa ctt gcc aag	1472
Asp Glu Ala Ile Ala Lys Lys Asn Ala Val Glu Leu Glu Leu Ala Lys	
180 185 190	
tgc agg atg gat atg atg tct ctg aac agc cag ttg ctg gat gcc att	1520
Cys Arg Met Asp Met Met Ser Leu Asn Ser Gln Leu Leu Asp Ala Ile	
195 200 205	
cag cag aaa ctg aac ctc tcg cag cag ctg gaa gct tgg cag gat gac	1568
Gln Gln Lys Leu Asn Leu Ser Gln Gln Leu Glu Ala Trp Gln Asp Asp	
210 215 220 225	
atg cac agg gtc att gac cgg cag ctg atg gac acg cac ctg aaa gaa	1616
Met His Arg Val Ile Asp Arg Gln Leu Met Asp Thr His Leu Lys Glu	
230 235 240	
cgg agc cag ccg gct gct gcc ctc tgc agg ggc cac agc gct ggg cgg	1664
Arg Ser Gln Pro Ala Ala Ala Leu Cys Arg Gly His Ser Ala Gly Arg	
245 250 255	
ggg gat gag ccc agc atc gct gaa ggc aaa cga ctc ttc tca ttc ttc	1712
Gly Asp Glu Pro Ser Ile Ala Glu Gly Lys Arg Leu Phe Ser Phe Phe	
260 265 270	
agg aaa att taa gtt gggaggagtc aggccaccaa agatgggtgg actggaggca	1767
Arg Lys Ile *	
275	
gctggaaagg cggtgcaggc aaggcctccc ctgcagcttg cacctcagca gctgcctgc	1827
ccctcatgct agggcccccatt gggtcggga gggcctgctc cctttcgctg gtggggatgg	1887
agacctagag gtgggggcct gccttgacca ctgaaggctt cccttgggcc accgcctgga	1947
gaagcccagg cgtgggcttc tccaggacca cgtgcttgag cagggttagg ccacctccca	2007

gaggggcccc ttggtgttgg gctttgcagc tcacacccaa cagatcgcag cccaccccca 2067
 ggcaactgctg cctccttgat tttagcaaat ggggaacaga aggaatggag gcccttctct 2127
 gcatgcctca ggaggcctga gcccagggg cctagacctg tgggggcagc gggccaggcc 2187
 tgagcctcca ttccttcccc agccctggc ccagggtcaa aggagagatg gcagcccctc 2247
 ccccgcatgc atgcacctca gctggcagga ggccaagcct ctggccgcag ggtctaagag 2307
 ccggggctta cccaagctca gctgaggcca cccgagcccc agggaggaag aaggccctgt 2367
 cccctgtcg ccaactgctc cctcccagc cttcagtctc tgccccttag cagggcctgg 2427
 ccaggcagag tgttatcacc agtcatctgc aggttttagc catccagccc tttcccctgc 2487
 tcagggtctg ggttgacgg ggtctcctcc tcccacagcg cccacctcca cccctcacat 2547
 acatacataa tttcttggcc tagcaaaca gtccaggcca ctgaatggca ccagaggggt 2607
 ctgtgggtcag ccaccccacc ttgagggcag cacaggcacc acggggtgga ggagag 2663

<210> 678
 <211> 6792
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (6792)

<400> 678
 atg gca gtg tgg cag ctg tac tac tgg agg ggt ggg gtc act gtc agt 48
 Met Ala Val Trp Gln Leu Tyr Tyr Trp Arg Gly Gly Val Thr Val Ser
 1 5 10 15
 gtt ggt ggc agc aga cct ggg cag aca ctt aga gga agt gtc caa aat 96
 Val Gly Gly Ser Arg Pro Gly Gln Thr Leu Arg Gly Ser Val Gln Asn
 20 25 30
 aaa ctg aat ccc cga cct gga aag gta gtg ata tat agt gaa ccc gac 144
 Lys Leu Asn Pro Arg Pro Gly Lys Val Val Ile Tyr Ser Glu Pro Asp
 35 40 45
 gtc tct gag aag tgc att gaa gtt ttc agt gac att cag gat tgc agt 192
 Val Ser Glu Lys Cys Ile Glu Val Phe Ser Asp Ile Gln Asp Cys Ser
 50 55 60
 tct tgg agc ctg tct cca gtg ata ctg ata aaa gtt gtt aga gga tgt 240
 Ser Trp Ser Leu Ser Pro Val Ile Leu Ile Lys Val Val Arg Gly Cys
 65 70 75 80
 tgg att ttg tat gag caa cca aat ttt gaa ggg cac tcc atc ccc tta 288
 Trp Ile Leu Tyr Glu Gln Pro Asn Phe Glu Gly His Ser Ile Pro Leu
 85 90 95
 gaa gaa gga gaa ttg gaa ctg tct ggt ctg tgg ggt ata gaa gac att 336
 Glu Glu Gly Glu Leu Glu Leu Ser Gly Leu Trp Gly Ile Glu Asp Ile
 100 105 110
 gtg gaa agg cac gaa gaa gca gag tct gat aag cca gtg gtg att ggt 384

Val	Glu	Arg	His	Glu	Glu	Ala	Glu	Ser	Asp	Lys	Pro	Val	Val	Ile	Gly		
		115					120					125					
tcc	atc	aga	cat	gtg	gtt	cag	gat	tac	aga	gtt	agt	cac	att	gac	tta	432	
Ser	Ile	Arg	His	Val	Val	Gln	Asp	Tyr	Arg	Val	Ser	His	Ile	Asp	Leu		
		130				135					140						
ttt	act	gaa	cca	gaa	ggg	tta	gga	atc	cta	agt	tcc	tac	ttt	gat	gat	480	
Phe	Thr	Glu	Pro	Glu	Gly	Leu	Gly	Ile	Leu	Ser	Ser	Tyr	Phe	Asp	Asp		
		145			150					155					160		
act	gaa	gaa	atg	cag	gga	ttt	ggg	gta	atg	cag	aag	act	tgt	tcc	atg	528	
Thr	Glu	Glu	Met	Gln	Gly	Phe	Gly	Val	Met	Gln	Lys	Thr	Cys	Ser	Met		
			165						170						175		
aaa	gta	cat	tgg	ggc	acg	tgg	ctg	att	tat	gaa	gaa	cct	gga	ttt	cag	576	
Lys	Val	His	Trp	Gly	Thr	Trp	Leu	Ile	Tyr	Glu	Glu	Pro	Gly	Phe	Gln		
		180					185						190				
ggg	gtt	cct	ttc	atc	ctg	gaa	cct	ggg	gaa	tac	cct	gac	ttg	tcc	ttc	624	
Gly	Val	Pro	Phe	Ile	Leu	Glu	Pro	Gly	Glu	Tyr	Pro	Asp	Leu	Ser	Phe		
		195				200						205					
tgg	gat	aca	gaa	gca	gcg	tac	att	gga	tcc	atg	cgg	cct	ctg	aaa	atg	672	
Trp	Asp	Thr	Glu	Ala	Ala	Tyr	Ile	Gly	Ser	Met	Arg	Pro	Leu	Lys	Met		
		210				215					220						
ggg	ggc	cgt	aaa	gtt	gaa	ttc	cct	aca	gat	cca	aag	tcc	aga	gca	caa	720	
Gly	Gly	Arg	Lys	Val	Glu	Phe	Pro	Thr	Asp	Pro	Lys	Ser	Arg	Ala	Gln		
		225			230					235					240		
cct	cca	gaa	gac	aac	aga	agg	aag	cca	gtt	ttg	ggg	aaa	ctt	ggc	act	768	
Pro	Pro	Glu	Asp	Asn	Arg	Arg	Lys	Pro	Val	Leu	Gly	Lys	Leu	Gly	Thr		
			245						250						255		
cta	ttc	act	gca	gga	agg	aga	aga	aac	agt	aga	aac	ggg	tta	gag	agt	816	
Leu	Phe	Thr	Ala	Gly	Arg	Arg	Arg	Asn	Ser	Arg	Asn	Gly	Leu	Glu	Ser		
			260					265							270		
ccc	acc	aga	tca	aat	gcc	aaa	cca	ctc	tct	ccc	aaa	gat	gtg	gta	gcc	864	
Pro	Thr	Arg	Ser	Asn	Ala	Lys	Pro	Leu	Ser	Pro	Lys	Asp	Val	Val	Ala		
		275					280					285					
tct	cct	aag	ctc	cca	gag	aga	gag	agt	gag	agg	agc	aga	tct	cag	agc	912	
Ser	Pro	Lys	Leu	Pro	Glu	Arg	Glu	Ser	Glu	Arg	Ser	Arg	Ser	Gln	Ser		
		290				295					300						
agc	caa	ctg	aag	caa	acg	gac	aca	agc	gag	gag	ggc	tcc	ccg	cgg	gag	960	
Ser	Gln	Leu	Lys	Gln	Thr	Asp	Thr	Ser	Glu	Glu	Gly	Ser	Pro	Arg	Glu		
		305			310				315						320		
aat	ccc	cga	gag	gca	gag	ggc	gag	ctc	ccc	gag	agc	ggg	ggc	ccc	gca	1008	
Asn	Pro	Arg	Glu	Ala	Glu	Gly	Glu	Leu	Pro	Glu	Ser	Gly	Gly	Pro	Ala		
			325						330					335			
gcc	ccc	cct	gac	gcc	gag	ctg	tca	cct	cgc	tgg	agc	agc	agt	gca	gcg	1056	
Ala	Pro	Pro	Asp	Ala	Glu	Leu	Ser	Pro	Arg	Trp	Ser	Ser	Ser	Ala	Ala		
			340					345					350				
gct	gtg	gct	gtg	cag	cag	tgc	cat	gaa	aat	gat	tca	ccc	caa	tta	gaa	1104	
Ala	Val	Ala	Val	Gln	Gln	Cys	His	Glu	Asn	Asp	Ser	Pro	Gln	Leu	Glu		
		355				360						365					
cct	ctg	gag	gca	gag	gga	gag	cct	ttc	cca	gat	gcc	acc	acc	act	gcc	1152	

Pro	Leu	Glu	Ala	Glu	Gly	Glu	Pro	Phe	Pro	Asp	Ala	Thr	Thr	Thr	Ala		
370						375					380						
aag	cag	ctg	cat	tcc	tcg	ccg	gga	aat	tcc	tcc	agg	caa	gag	aac	gca	1200	
Lys	Gln	Leu	His	Ser	Ser	Pro	Gly	Asn	Ser	Ser	Arg	Gln	Glu	Asn	Ala		
385					390				395					400			
gag	acg	ccc	gcc	cgc	agt	ccg	ggg	gag	gac	gct	tca	cca	ggt	gct	ggc	1248	
Glu	Thr	Pro	Ala	Arg	Ser	Pro	Gly	Glu	Asp	Ala	Ser	Pro	Gly	Ala	Gly		
				405				410						415			
cac	gaa	cag	gag	gct	ttc	ctg	ggt	gtg	agg	ggt	gcg	cca	ggg	tcg	ccc	1296	
His	Glu	Gln	Glu	Ala	Phe	Leu	Gly	Val	Arg	Gly	Ala	Pro	Gly	Ser	Pro		
				420				425						430			
acc	cag	gag	cgg	ccc	gcg	gga	gga	cta	ggc	gag	gcc	cct	aac	gca	gcc	1344	
Thr	Gln	Glu	Arg	Pro	Ala	Gly	Gly	Leu	Gly	Glu	Ala	Pro	Asn	Ala	Ala		
				435				440						445			
ccc	agt	gtg	tgt	gcc	gaa	gaa	ggc	tcc	ctg	ggg	ccc	cgc	aac	gcc	cgc	1392	
Pro	Ser	Val	Cys	Ala	Glu	Glu	Gly	Ser	Leu	Gly	Pro	Arg	Asn	Ala	Arg		
				450				455						460			
agc	cag	ccc	ccc	aag	ggc	gcg	tct	gat	ttg	cca	ggt	gag	cct	ccg	gcc	1440	
Ser	Gln	Pro	Pro	Lys	Gly	Ala	Ser	Asp	Leu	Pro	Gly	Glu	Pro	Pro	Ala		
465					470					475					480		
gag	ggc	gca	gcg	cac	acg	gcc	agc	tcc	gcg	cag	gca	gac	tgc	aca	gcc	1488	
Glu	Gly	Ala	Ala	His	Thr	Ala	Ser	Ser	Ala	Gln	Ala	Asp	Cys	Thr	Ala		
				485					490					495			
cgc	ccc	aag	ggt	cac	gcc	cac	cct	gct	aag	gtg	cta	act	ttg	gac	atc	1536	
Arg	Pro	Lys	Gly	His	Ala	His	Pro	Ala	Lys	Val	Leu	Thr	Leu	Asp	Ile		
				500				505						510			
tac	ttg	agt	aag	act	gag	ggg	gca	caa	gtg	gac	gag	ccg	gtc	gtg	att	1584	
Tyr	Leu	Ser	Lys	Thr	Glu	Gly	Ala	Gln	Val	Asp	Glu	Pro	Val	Val	Ile		
				515				520						525			
act	ccc	aga	gcg	gaa	gat	tgc	ggt	gac	tgg	gac	gac	atg	gag	aag	agg	1632	
Thr	Pro	Arg	Ala	Glu	Asp	Cys	Gly	Asp	Trp	Asp	Asp	Met	Glu	Lys	Arg		
				530				535						540			
tcc	agc	ggc	cgt	agg	tcg	ggg	agg	cgg	agg	ggg	tcg	cag	aaa	tcc	acc	1680	
Ser	Ser	Gly	Arg	Arg	Ser	Gly	Arg	Arg	Arg	Gly	Ser	Gln	Lys	Ser	Thr		
545					550					555					560		
gac	tcc	ccc	ggc	gcg	gac	gcc	gag	ctc	cct	gag	agc	gct	gcc	agg	gac	1728	
Asp	Ser	Pro	Gly	Ala	Asp	Ala	Glu	Leu	Pro	Glu	Ser	Ala	Ala	Arg	Asp		
				565					570					575			
gac	gcg	gtg	ttc	gac	gac	gag	gtg	gcg	cca	aac	gcg	gcc	agc	gat	aac	1776	
Asp	Ala	Val	Phe	Asp	Asp	Glu	Val	Ala	Pro	Asn	Ala	Ala	Ser	Asp	Asn		
				580				585						590			
gcc	tcg	gcg	gaa	aag	aaa	gtg	aaa	tct	ccg	cgg	gca	gcc	ctc	gac	ggg	1824	
Ala	Ser	Ala	Glu	Lys	Lys	Val	Lys	Ser	Pro	Arg	Ala	Ala	Leu	Asp	Gly		
				595				600						605			
ggc	gtt	gcc	tcc	gct	gcg	agc	cca	gag	tcc	aag	ccc	agc	ccc	ggt	acc	1872	
Gly	Val	Ala	Ser	Ala	Ala	Ser	Pro	Glu	Ser	Lys	Pro	Ser	Pro	Gly	Thr		
				610				615						620			
aaa	ggg	cag	ctc	cga	ggg	gag	tcg	gac	cgg	agc	aaa	cag	cca	ccc	ccg	1920	

Lys Gly Gln Leu Arg Gly Glu Ser Asp Arg Ser Lys Gln Pro Pro Pro	
625 630 635 640	
gct tcg tcc ccc acg aag agg aag ggc agg agc cgt gcc ctc gag gcc	1968
Ala Ser Ser Pro Thr Lys Arg Lys Gly Arg Ser Arg Ala Leu Glu Ala	
645 650 655	
gtg ccc gcc ccg ccc gcc agc ggc ccc cgg gct ccc gcc aag gag tcc	2016
Val Pro Ala Pro Pro Ala Ser Gly Pro Arg Ala Pro Ala Lys Glu Ser	
660 665 670	
cca ccc aag agg gtg ccc gat ccc agc cca gtc acc aag ggc act gcg	2064
Pro Pro Lys Arg Val Pro Asp Pro Ser Pro Val Thr Lys Gly Thr Ala	
675 680 685	
gcc gag agc ggg gag gag gcg gcg cgg gcc atc ccc cgc gag ctc ccg	2112
Ala Glu Ser Gly Glu Glu Ala Ala Arg Ala Ile Pro Arg Glu Leu Pro	
690 695 700	
gtc aag agc agc tcg ctg ctg ccg gag atc aag ccc gag cac aag agg	2160
Val Lys Ser Ser Ser Leu Leu Pro Glu Ile Lys Pro Glu His Lys Arg	
705 710 715 720	
ggc ccg ctc ccc aac cac ttc aac ggc cgg gca gag gga ggt cga agc	2208
Gly Pro Leu Pro Asn His Phe Asn Gly Arg Ala Glu Gly Gly Arg Ser	
725 730 735	
aga gag ctg ggc aga gcg gcc gga gcg cct gga gct tct gac gcc gac	2256
Arg Glu Leu Gly Arg Ala Ala Gly Ala Pro Gly Ala Ser Asp Ala Asp	
740 745 750	
ggc ttg aag ccc agg aac cat ttc ggc gtg ggc agg tcg aca gtg acc	2304
Gly Leu Lys Pro Arg Asn His Phe Gly Val Gly Arg Ser Thr Val Thr	
755 760 765	
act aaa gtg acc ctc cct gcc aag ccc aaa cat gtg gaa cta aat ctt	2352
Thr Lys Val Thr Leu Pro Ala Lys Pro Lys His Val Glu Leu Asn Leu	
770 775 780	
aaa acc cct aag aat ctt gac agt ttg gga aat gag cac aat cca ttt	2400
Lys Thr Pro Lys Asn Leu Asp Ser Leu Gly Asn Glu His Asn Pro Phe	
785 790 795 800	
agc cag cca gtt cac aaa ggc aac act gcc acc aaa atc tcc tta ttt	2448
Ser Gln Pro Val His Lys Gly Asn Thr Ala Thr Lys Ile Ser Leu Phe	
805 810 815	
gaa aac aaa cgg aca aac agt agc cca aga cac act gac att cga ggc	2496
Glu Asn Lys Arg Thr Asn Ser Ser Pro Arg His Thr Asp Ile Arg Gly	
820 825 830	
caa agg aat act cct gcc tct agt aaa acg ttt gtt ggg agg gca aag	2544
Gln Arg Asn Thr Pro Ala Ser Ser Lys Thr Phe Val Gly Arg Ala Lys	
835 840 845	
ctg aat tta gcc aaa aaa gcc aaa gaa atg gag caa cct gaa aag aaa	2592
Leu Asn Leu Ala Lys Lys Ala Lys Glu Met Glu Gln Pro Glu Lys Lys	
850 855 860	
gta atg cca aac agt ccc cag aat ggt gtg ctg gtt aag gaa act gct	2640
Val Met Pro Asn Ser Pro Gln Asn Gly Val Leu Val Lys Glu Thr Ala	
865 870 875 880	
ata gaa acc aaa gtt acc gtc tcg gaa gaa gag att ctg cca gca acc	2688

Ile	Glu	Thr	Lys	Val	Thr	Val	Ser	Glu	Glu	Glu	Ile	Leu	Pro	Ala	Thr		
				885					890					895			
aga	gga	atg	aat	gga	gac	tct	tct	gag	aat	caa	gct	ctt	ggg	cct	cag	2736	
Arg	Gly	Met	Asn	Gly	Asp	Ser	Ser	Glu	Asn	Gln	Ala	Leu	Gly	Pro	Gln		
			900					905					910				
cct	aac	caa	gat	gat	aaa	gca	gat	gta	caa	aca	gat	gct	ggc	tgc	ctt	2784	
Pro	Asn	Gln	Asp	Asp	Lys	Ala	Asp	Val	Gln	Thr	Asp	Ala	Gly	Cys	Leu		
			915				920					925					
tca	gaa	cca	gtg	gct	tct	gct	ctg	att	cct	gtc	aag	gat	cat	aag	ctc	2832	
Ser	Glu	Pro	Val	Ala	Ser	Ala	Leu	Ile	Pro	Val	Lys	Asp	His	Lys	Leu		
			930				935					940					
tta	gag	aag	gag	gac	tca	gag	gct	gca	gac	agc	aaa	agc	ctt	gta	ctt	2880	
Leu	Glu	Lys	Glu	Asp	Ser	Glu	Ala	Ala	Asp	Ser	Lys	Ser	Leu	Val	Leu		
						950				955					960		
gaa	aat	gta	acc	gat	aca	gca	caa	gac	atc	ccc	acc	act	gtg	gat	acc	2928	
Glu	Asn	Val	Thr	Asp	Thr	Ala	Gln	Asp	Ile	Pro	Thr	Thr	Val	Asp	Thr		
				965					970						975		
aaa	gat	tta	cct	cca	acg	gcc	atg	cca	aag	cca	cag	cat	aca	ttt	tct	2976	
Lys	Asp	Leu	Pro	Pro	Thr	Ala	Met	Pro	Lys	Pro	Gln	His	Thr	Phe	Ser		
			980					985						990			
gac	tca	cag	tcc	cct	gct	gag	tca	tct	cct	ggg	cct	tct	ctt	tca	ctg	3024	
Asp	Ser	Gln	Ser	Pro	Ala	Glu	Ser	Ser	Pro	Gly	Pro	Ser	Leu	Ser	Leu		
			995				1000					1005					
tct	gca	ccc	gct	cct	ggg	gat	gtt	ccc	aaa	gac	aca	tgt	gtt	caa	tca	3072	
Ser	Ala	Pro	Ala	Pro	Gly	Asp	Val	Pro	Lys	Asp	Thr	Cys	Val	Gln	Ser		
			1010				1015					1020					
ccc	ata	agc	agt	ttc	cca	tgc	act	gat	cta	aaa	gtg	tca	gaa	aac	cat	3120	
Pro	Ile	Ser	Ser	Phe	Pro	Cys	Thr	Asp	Leu	Lys	Val	Ser	Glu	Asn	His		
1025					1030					1035					1040		
aaa	gga	tgt	gtt	ttg	cct	gtg	tct	cgt	cag	aac	aat	gag	aaa	atg	cca	3168	
Lys	Gly	Cys	Val	Leu	Pro	Val	Ser	Arg	Gln	Asn	Asn	Glu	Lys	Met	Pro		
				1045					1050					1055			
ctt	tta	gaa	ctt	gga	gga	gaa	aca	acc	cct	cct	ttg	tcc	aca	gag	cgt	3216	
Leu	Leu	Glu	Leu	Gly	Gly	Glu	Thr	Thr	Pro	Pro	Leu	Ser	Thr	Glu	Arg		
				1060				1065					1070				
agt	cca	gaa	gct	gtg	gga	agt	gag	tgt	cca	tcc	aga	gtc	ctc	gtc	cag	3264	
Ser	Pro	Glu	Ala	Val	Gly	Ser	Glu	Cys	Pro	Ser	Arg	Val	Leu	Val	Gln		
			1075				1080					1085					
gtc	agg	tcc	ttc	gtg	ctc	ccc	gtg	gag	agc	acc	cag	gat	gtg	agc	tcc	3312	
Val	Arg	Ser	Phe	Val	Leu	Pro	Val	Glu	Ser	Thr	Gln	Asp	Val	Ser	Ser		
			1090				1095					1100					
cag	gtc	atc	cca	gag	agc	tct	gaa	gtt	aga	gaa	gtg	cag	ttg	cca	act	3360	
Gln	Val	Ile	Pro	Glu	Ser	Ser	Glu	Val	Arg	Glu	Val	Gln	Leu	Pro	Thr		
1105						1110				1115					1120		
tgt	cac	agt	aat	gaa	cct	gaa	gtg	gtt	tcc	gtt	gca	agt	tgt	gct	ccc	3408	
Cys	His	Ser	Asn	Glu	Pro	Glu	Val	Ser	Val	Ala	Ser	Cys	Ala	Pro			
				1125					1130					1135			
cca	caa	gag	gaa	gta	ctg	ggc	aat	gaa	cac	tct	cat	tgc	aca	gca	gag	3456	

Pro Gln Glu Glu Val Leu Gly Asn Glu His Ser His Cys Thr Ala Glu	
1140	1145 1150
ctc gcg gca aaa tct ggc cca caa gtc ata ccg cca gca tca gag aaa	3504
Leu Ala Ala Lys Ser Gly Pro Gln Val Ile Pro Pro Ala Ser Glu Lys	
1155 1160 1165	
act ctg cct att cag gct caa agt cag ggc agc aga aca ccc ctg atg	3552
Thr Leu Pro Ile Gln Ala Gln Ser Gln Gly Ser Arg Thr Pro Leu Met	
1170 1175 1180	
gct gaa tcc agt ccc acc aac tct ccc agc agc gga aat cac tta gcc	3600
Ala Glu Ser Ser Pro Thr Asn Ser Pro Ser Ser Gly Asn His Leu Ala	
1185 1190 1195 1200	
act cct caa agg cca gat cag act gtt aca aat ggc cag gat agc cct	3648
Thr Pro Gln Arg Pro Asp Gln Thr Val Thr Asn Gly Gln Asp Ser Pro	
1205 1210 1215	
gcc agc ctt ttg aac att tct gct ggt agt gat gat agt gta ttt gat	3696
Ala Ser Leu Leu Asn Ile Ser Ala Gly Ser Asp Asp Ser Val Phe Asp	
1220 1225 1230	
tct tct tct gat atg gaa aaa ttc act gaa att ata aaa cag atg gat	3744
Ser Ser Ser Asp Met Glu Lys Phe Thr Glu Ile Ile Lys Gln Met Asp	
1235 1240 1245	
agc gca gtt tgt atg ccc atg aaa aga aag aag gcc agg atg cca aac	3792
Ser Ala Val Cys Met Pro Met Lys Arg Lys Lys Ala Arg Met Pro Asn	
1250 1255 1260	
tct cct gct cct cac ttt gcc atg cct cct att cac gaa gac cat tta	3840
Ser Pro Ala Pro His Phe Ala Met Pro Pro Ile His Glu Asp His Leu	
1265 1270 1275 1280	
gaa aag gtg ttt gat ccc aaa gtg ttt acc ttt ggt ttg ggg aag aag	3888
Glu Lys Val Phe Asp Pro Lys Val Phe Thr Phe Gly Leu Gly Lys Lys	
1285 1290 1295	
aag gaa agt cag cca gaa atg tca ccg gct tta cat ttg atg cag aac	3936
Lys Glu Ser Gln Pro Glu Met Ser Pro Ala Leu His Leu Met Gln Asn	
1300 1305 1310	
ctt gac aca aaa tcc aaa ctg aga ccc aaa cgt gca tct gct gaa cag	3984
Leu Asp Thr Lys Ser Lys Leu Arg Pro Lys Arg Ala Ser Ala Glu Gln	
1315 1320 1325	
agc gtc ctc ttc aag tcc ctg cac acc aac act aat ggg aac agt gag	4032
Ser Val Leu Phe Lys Ser Leu His Thr Asn Thr Asn Gly Asn Ser Glu	
1330 1335 1340	
cct ctg gtg atg ccg gaa atc aat gac aaa gag aac agg gac gtc aca	4080
Pro Leu Val Met Pro Glu Ile Asn Asp Lys Glu Asn Arg Asp Val Thr	
1345 1350 1355 1360	
aat ggt ggc att aag aga tcg aga cta gaa aaa agt gca ctt ttc tca	4128
Asn Gly Gly Ile Lys Arg Ser Arg Leu Glu Lys Ser Ala Leu Phe Ser	
1365 1370 1375	
agc ttg tta tct tct tta cca caa gac aaa atc ttt tct cct tct gtg	4176
Ser Leu Leu Ser Ser Leu Pro Gln Asp Lys Ile Phe Ser Pro Ser Val	
1380 1385 1390	
aca tca gtc aac act atg acc acg gct ttc agt act tct cag aac ggt	4224

Thr Ser Val Asn Thr Met Thr Thr Ala Phe Ser Thr Ser Gln Asn Gly	
1395 1400 1405	
tcc cta tct cag tct tca gtg tca cag ccc acg act gag ggt gcc ccg	4272
Ser Leu Ser Gln Ser Ser Val Ser Gln Pro Thr Thr Glu Gly Ala Pro	
1410 1415 1420	
ccc tgt ggt ttg aac aaa gaa cag tca aat ctt ctg ccc gac aac tcc	4320
Pro Cys Gly Leu Asn Lys Glu Gln Ser Asn Leu Leu Pro Asp Asn Ser	
1425 1430 1435 1440	
tta aag gtc ttc aat ttc aac tcg tca agt aca tca cac tcc agt ttg	4368
Leu Lys Val Phe Asn Phe Asn Ser Ser Ser Thr Ser His Ser Ser Leu	
1445 1450 1455	
aaa agt cca agc cac atg gaa aaa tac ccg caa aaa gag aaa acc aaa	4416
Lys Ser Pro Ser His Met Glu Lys Tyr Pro Gln Lys Glu Lys Thr Lys	
1460 1465 1470	
gaa gat ctg gat tca cga agc aac cta cac ttg cca gaa act aaa ttt	4464
Glu Asp Leu Asp Ser Arg Ser Asn Leu His Leu Pro Glu Thr Lys Phe	
1475 1480 1485	
tct gaa ttg tca aaa ctg aag aat gat gat atg gaa aag gct aat cat	4512
Ser Glu Leu Ser Lys Leu Lys Asn Asp Asp Met Glu Lys Ala Asn His	
1490 1495 1500	
att gaa agt gtt att aaa tca aac ttg cca aac tgt gca aac agt gac	4560
Ile Glu Ser Val Ile Lys Ser Asn Leu Pro Asn Cys Ala Asn Ser Asp	
1505 1510 1515 1520	
acc gac ttc atg ggt ctt ttc aaa tca agc ccg tat gac cca agc att	4608
Thr Asp Phe Met Gly Leu Phe Lys Ser Ser Arg Tyr Asp Pro Ser Ile	
1525 1530 1535	
tct ttt tct gga atg tca tta tca gac aca atg aca ctt aga gga agt	4656
Ser Phe Ser Gly Met Ser Leu Ser Asp Thr Met Thr Leu Arg Gly Ser	
1540 1545 1550	
gtc caa aat aaa ctc aat ccc cga cct gga aag gta gtg ata tat agt	4704
Val Gln Asn Lys Leu Asn Pro Arg Pro Gly Lys Val Val Ile Tyr Ser	
1555 1560 1565	
gaa ccc gac gtc tct gag aag tgc att gaa gtt ttc agt gac att cag	4752
Glu Pro Asp Val Ser Glu Lys Cys Ile Glu Val Phe Ser Asp Ile Gln	
1570 1575 1580	
gat tgc agt tct tgg agc ctc tct cca gtg ata ctc ata aaa gtt gtt	4800
Asp Cys Ser Ser Trp Ser Leu Ser Pro Val Ile Leu Ile Lys Val Val	
1585 1590 1595 1600	
aga gga tgt tgg att ttg tat gag caa cca aat ttt gaa ggg cac tcc	4848
Arg Gly Cys Trp Ile Leu Tyr Glu Gln Pro Asn Phe Glu Gly His Ser	
1605 1610 1615	
atc ccc tta gaa gaa gga gaa ttg gaa ctc tct ggt ctc tgg ggt ata	4896
Ile Pro Leu Glu Glu Gly Glu Leu Glu Leu Ser Gly Leu Trp Gly Ile	
1620 1625 1630	
gaa gac att ttg gaa agg cac gaa gaa gca gag tct gat aag cca gtg	4944
Glu Asp Ile Leu Glu Arg His Glu Glu Ala Glu Ser Asp Lys Pro Val	
1635 1640 1645	
gtg att ggt tcc atc aga cat gtg gtt cag gat tac aga gtt agt cac	4992

1886

Val Ala Tyr Glu Asn Pro Asp Phe Thr Gly Glu Gln Tyr Ile Leu Asp 1905 1910 1915 1920	
aaa gga ttt tat acc agt ttt gag gac tgg gga ggc aaa aat tat aag Lys Gly Phe Tyr Thr Ser Phe Glu Asp Trp Gly Gly Lys Asn Tyr Lys 1925 1930 1935	5808
atc tct tct gtt caa cct ata tgt ttg gat tct ttc act ggc cca agg Ile Ser Ser Val Gln Pro Ile Cys Leu Asp Ser Phe Thr Gly Pro Arg 1940 1945 1950	5856
aga cga aat cag att cac ttg ttt tca gaa cca cag ttt caa ggt cac Arg Arg Asn Gln Ile His Leu Phe Ser Glu Pro Gln Phe Gln Gly His 1955 1960 1965	5904
agt caa agt ttt gaa gaa aca aca agt caa att gat gat tca ttt tct Ser Gln Ser Phe Glu Glu Thr Thr Ser Gln Ile Asp Asp Ser Phe Ser 1970 1975 1980	5952
acc aag tct tgc aga gtt tca gga ggc agc tgg gtt gta tat gat gga Thr Lys Ser Cys Arg Val Ser Gly Gly Ser Trp Val Val Tyr Asp Gly 1985 1990 1995 2000	6000
gaa aat ttc act ggt aat caa tac gtg ttg gaa gaa ggc cat tat cct Glu Asn Phe Thr Gly Asn Gln Tyr Val Leu Glu Glu Gly His Tyr Pro 2005 2010 2015	6048
tgt ctg tct gca atg gga tgc ccg cct gga gca act ttc aag tct ctt Cys Leu Ser Ala Met Gly Cys Pro Pro Gly Ala Thr Phe Lys Ser Leu 2020 2025 2030	6096
cgt ttt ata gat gtt gaa ttt tct gaa cca aca att att ctc ttt gaa Arg Phe Ile Asp Val Glu Phe Ser Glu Pro Thr Ile Ile Leu Phe Glu 2035 2040 2045	6144
aga gaa gac ttc aaa gga aaa aag att gaa ctt aat gca gaa act gtc Arg Glu Asp Phe Lys Gly Lys Lys Ile Glu Leu Asn Ala Glu Thr Val 2050 2055 2060	6192
aat ctc cga tcc ctg gga ttc aac aca caa ata cgc tct gtt cag gtt Asn Leu Arg Ser Leu Gly Phe Asn Thr Gln Ile Arg Ser Val Gln Val 2065 2070 2075 2080	6240
att ggt ggc ata tgg gtt act tat gaa tat ggc agt tac aga ggg cga Ile Gly Gly Ile Trp Val Thr Tyr Glu Tyr Gly Ser Tyr Arg Gly Arg 2085 2090 2095	6288
cag ttc cta ttg tca cct gca gaa gta cct aat tgg tat gaa ttc agt Gln Phe Leu Leu Ser Pro Ala Glu Val Pro Asn Trp Tyr Glu Phe Ser 2100 2105 2110	6336
ggc tgt cgc caa ata ggt tct cta cga cct ttt gtt cag aag cga att Gly Cys Arg Gln Ile Gly Ser Leu Arg Pro Phe Val Gln Lys Arg Ile 2115 2120 2125	6384
tat ttc aga ctt cga aac aaa gca aca ggg tta ttc atg tca acc aat Tyr Phe Arg Leu Arg Asn Lys Ala Thr Gly Leu Phe Met Ser Thr Asn 2130 2135 2140	6432
gga aac tta gag gat ctg aag ctt ctg agg ata cag gtc atg gag gat Gly Asn Leu Glu Asp Leu Lys Leu Leu Arg Ile Gln Val Met Glu Asp 2145 2150 2155 2160	6480
gtc ggg gcc gat gat cag att tgg atc tat caa gaa gga tgt atc aaa	6528

Val Gly Ala Asp Gln Ile Trp Ile Tyr Gln Glu Gly Cys Ile Lys	
2165 2170 2175	
tgc agg ata gca gaa gac tgc tgc ctg acg att gtg ggc agc ctg gta	6576
Cys Arg Ile Ala Glu Asp Cys Cys Leu Thr Ile Val Gly Ser Leu Val	
2180 2185 2190	
aca tct ggc tcc aag cta ggc ctg gcc ctg gac cag aat gct gac agc	6624
Thr Ser Gly Ser Lys Leu Gly Leu Ala Leu Asp Gln Asn Ala Asp Ser	
2195 2200 2205	
cag ttc tgg agc ttg aag tcc gat ggc agg att tac agc aag ttg aag	6672
Gln Phe Trp Ser Leu Lys Ser Asp Gly Arg Ile Tyr Ser Lys Leu Lys	
2210 2215 2220	
cca aat tta gtt tta gac att aaa ggg ggc aca cag tat gat caa aat	6720
Pro Asn Leu Val Leu Asp Ile Lys Gly Gly Thr Gln Tyr Asp Gln Asn	
2225 2230 2235 2240	
cac att atc ctc aac act gtc agc aaa gag aag ttt aca caa gtg tgg	6768
His Ile Ile Leu Asn Thr Val Ser Lys Glu Lys Phe Thr Gln Val Trp	
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gaa gcc atg gtc cta tat acc tga	6792
Glu Ala Met Val Leu Tyr Thr *	
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<211> 2101
<212> DNA
<213> Homo sapiens
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<222> (185) .. (1438)
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tcaaggccc ggcgcgcat gtcctgggtg ccgcggtgcg ggcagtgaac gcgcgccggg	180
cggg atg ggc cgg cgc cgg gcg cca gag ctg tac cgg gct ccg ttc ccg	229
Met Gly Arg Arg Arg Ala Pro Glu Leu Tyr Arg Ala Pro Phe Pro	
1 5 10 15	
ttg tac gcg ctt cag gtc gac ccc agc act ggg ctg ctc atc gct gcg	277
Leu Tyr Ala Leu Gln Val Asp Pro Ser Thr Gly Leu Leu Ile Ala Ala	
20 25 30	
ggc gga gga ggc gcc gcc aag aca ggc ata aag aat ggc gtg cac ttt	325
Gly Gly Gly Gly Ala Ala Lys Thr Gly Ile Lys Asn Gly Val His Phe	
35 40 45	
ctg cag cta gag ctg att aat ggg cgc ttg agt gcc tcc ttg ctg cac	373
Leu Gln Leu Glu Leu Ile Asn Gly Arg Leu Ser Ala Ser Leu Leu His	
50 55 60	
tcc cat gac aca qaq aca cgg gcc acc atg aac ttg qca ctg gct ggt	421

Ser	His	Asp	Thr	Glu	Thr	Arg	Ala	Thr	Met	Asn	Leu	Ala	Leu	Ala	Gly		
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gac atc ctt gct gca ggg cag gat gcc cac tgt cag ctc ctg cgc ttc 469																	
Asp	Ile	Leu	Ala	Ala	Gly	Gln	Asp	Ala	His	Cys	Gln	Leu	Leu	Arg	Phe		
80					85				90					95			
cag gca cat caa cag cag ggc aac aag gca gag aag gcc ggt tcc aag 517																	
Gln	Ala	His	Gln	Gln	Gln	Gly	Asn	Lys	Ala	Glu	Lys	Ala	Gly	Ser	Lys		
			100					105					110				
gag cag ggg cct cga caa agg aag gga gca gcc cca gca gag aag aaa 565																	
Glu	Gln	Gly	Pro	Arg	Gln	Arg	Lys	Gly	Ala	Ala	Pro	Ala	Glu	Lys	Lys		
			115				120						125				
tgt gga gcg gaa acc cag cac gag ggg cta gaa ctc agg gta gag aat 613																	
Cys	Gly	Ala	Glu	Thr	Gln	His	Glu	Gly	Leu	Glu	Leu	Arg	Val	Glu	Asn		
		130					135					140					
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Leu	Gln	Ala	Val	Gln	Thr	Asp	Phe	Ser	Ser	Asp	Pro	Leu	Gln	Lys	Val		
		145					150				155						
gtg tgc ttc aac cac gat aat acc ctg ctt gcc act gga gga aca gat 709																	
Val	Cys	Phe	Asn	His	Asp	Asn	Thr	Leu	Leu	Ala	Thr	Gly	Gly	Thr	Asp		
		160			165					170			175				
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Gly	Tyr	Val	Arg	Val	Trp	Lys	Val	Pro	Ser	Leu	Glu	Lys	Val	Leu	Glu		
			180					185					190				
ttc aaa gcc cac gaa ggg gag att gaa gac ctg gct tta ggg cct gat 805																	
Phe	Lys	Ala	His	Glu	Gly	Glu	Ile	Glu	Asp	Leu	Ala	Leu	Gly	Pro	Asp		
			195					200					205				
ggc aag ttg gta acc gtg ggc cgg gac ctt aag gcc tct gtg tgg cag 853																	
Gly	Lys	Leu	Val	Thr	Val	Gly	Arg	Asp	Leu	Lys	Ala	Ser	Val	Trp	Gln		
			210				215					220					
aag gat cag ctg gtg aca cag ctg cac tgg caa gaa aat gga ccc acc 901																	
Lys	Asp	Gln	Leu	Val	Thr	Gln	Leu	His	Trp	Gln	Glu	Asn	Gly	Pro	Thr		
		225					230					235					
ttt tcc agc aca cct tac cgc tac cag gcc tgc agg ttt ggg cag gtt 949																	
Phe	Ser	Ser	Thr	Pro	Tyr	Arg	Tyr	Gln	Ala	Cys	Arg	Phe	Gly	Gln	Val		
		240			245				250				255				
cca gac cag cct gct ggc ctg cga ctc ttc aca gtg caa att ccc cac 997																	
Pro	Asp	Gln	Pro	Ala	Gly	Leu	Arg	Leu	Phe	Thr	Val	Gln	Ile	Pro	His		
			260					265					270				
aag cgc ctg cgc cag ccc cct ccc tgc tac ctc aca gcc tgg gat ggc 1045																	
Lys	Arg	Leu	Arg	Gln	Pro	Pro	Pro	Cys	Tyr	Leu	Thr	Ala	Trp	Asp	Gly		
			275				280						285				
tcc aac ttc ttg ccc ctt cgg acc aag tcc tgt ggc cat gaa gtc gtc 1093																	
Ser	Asn	Phe	Leu	Pro	Leu	Arg	Thr	Lys	Ser	Cys	Gly	His	Glu	Val	Val		
		290					295					300					
tcc tgc ctc gat gtc agt gaa tcc ggc acc ttc cta ggc ctg ggc aca 1141																	
Ser	Cys	Leu	Asp	Val	Ser	Glu	Ser	Gly	Thr	Phe	Leu	Gly	Leu	Gly	Thr		
		305				310					315						
gtc act ggc tct gtt gcc atc tac ata gct ttc tct ctc cag tgc ctc 1189																	

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Val Thr Gly Ser Val Ala Ile Tyr Ile Ala Phe Ser Leu Gln Cys Leu
320                               325                               330                               335

tac tac gtg agg gag gcc cat ggc att gtg gtg acg gat gtg gcc ttt      1237
Tyr Tyr Val Arg Glu Ala His Gly Ile Val Val Thr Asp Val Ala Phe
                               340                               345                               350

cta cct gag aag ggt cgt ggt cca gag ctc ctt ggg tcc cat gaa act      1285
Leu Pro Glu Lys Gly Arg Gly Pro Glu Leu Leu Gly Ser His Glu Thr
                               355                               360                               365

gcc ctg ttc tct gtg gct gtg gac agt cgt tgc cag ctg cat ctg ttg      1333
Ala Leu Phe Ser Val Ala Val Asp Ser Arg Cys Gln Leu His Leu Leu
                               370                               375                               380

ccc tca cgg cgg agt gtt cct gtg tgg ctc ctg ctc ctg ctg tgt gtc      1381
Pro Ser Arg Arg Ser Val Pro Val Trp Leu Leu Leu Leu Leu Cys Val
                               385                               390                               395

ggg ctt att att gtg acc atc ctg ctg ctc cag agt gcc ttt cca ggt      1429
Gly Leu Ile Ile Ile Thr Thr Ile Leu Leu Leu Gln Ser Ala Phe Pro Gly
400                               405                               410                               415

ttc ctt tag cttccct gcttcctggg aatcaggagc ctggacactg ccatctctag      1485
Phe Leu *

agcagagtgg aggcctggac tccctttgct cactccattc ggggccacag ctgaggttgc      1545
ctctgacaag atgaatgggc actgcctgcc cttctagtga aaaggcttgg ctatggccct      1605
gtgtgactcc aggtcccagg aaccttgcc tgcgtcatctg tggatccatc cagaacagcg      1665
gtatctgaag cccaggccat actccctgcc tcctttcttc tgcctaccag aggctccaga      1725
gttgagcttg tccttttatct agaaacatgt gaagatgccc aagagcctgg aggcactgct      1785
gtccttcctg cagaaacagt ttctcctcct ccctcagcc ttgtggccag ttcctcttga      1845
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aaggggcaaa aggaagactt gggtagtaat ctgggggttc agatgggtag cactaagcca      1965
gctggcctaa agatgcaata agttcctagg tagtctaccc ttaccttgag gaatgggaaa      2025
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tgagaaaaaa aaaaaa                                           2101

<210> 680
<211> 1851
<212> DNA
<213> Homo sapiens

<220>
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<222> (1063)..(1815)

<400> 680
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ggcggttagca ggtggtcctg cagcaggttg tctggccaca gctggggcgg cagcaggttg	180
gctggcagta cacagactgg cagcactggg gtctgaagca gctggacaca cagcagctgg	240
gacggcagca ggtggtcctg cagcaagtgg tctggcagca gctggggctg cagcaggttg	300
gctggcagca cacagactgg cagcactgcg gtctgcagca gctggacaca cagcagctgg	360
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gacggcagca gctggacata ccacagctgg ggtggcaggt ggtctgacag cagagtgggc	660
ggcagcagct ggacacacca cagctggggc ggcaggtggc ctgacaacag actgggtggc	720
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agcaggtctc ttggcagagg ccttgatcac agccctgggc agagcagaca gagccacaac	900
aagagttaac catggtgtca gaggggtggag gttagaagct gcggcagcag caagcggtct	960
tgcagcaggt ggtctggcag cagctgggat ggcagcagat ctcttggcag aggtcttaac	1020
cacacctctc tgaacaggag cccacccttc acccctgaca cc atg acc cac tgc	1074
	Met Thr His Cys
	1
tgt tcc cct tgc tgt cag cct aca tgc tgc agg acc acc tgc tgc agg	1122
Cys Ser Pro Cys Cys Gln Pro Thr Cys Cys Arg Thr Thr Cys Cys Arg	
5 10 15 20	
aca acc tgc tgg aag ccc acc act gtg acc acc tgc agc agc aca ccc	1170
Thr Thr Cys Trp Lys Pro Thr Thr Val Thr Thr Cys Ser Ser Thr Pro	
25 30 35	
tgt tgc cag ccc tcc tgc tgt gtg ccc agc tgc tgc cag cct tgc tgc	1218
Cys Cys Gln Pro Ser Cys Cys Val Pro Ser Cys Cys Gln Pro Cys Cys	
40 45 50	
cac cca act tgc tgt caa aac acc tgc tgc agg acc acc tgc tgc cag	1266
His Pro Thr Cys Cys Gln Asn Thr Cys Cys Arg Thr Thr Cys Cys Gln	
55 60 65	
ccc act tgt gtg gcc agc tgc tgc cag cct tcc tgc tgc agc aca ccc	1314
Pro Thr Cys Val Ala Ser Cys Cys Gln Pro Ser Cys Cys Ser Thr Pro	
70 75 80	
tgc tgc cag ccc acc tgc tgt ggg tcc agc tgc tgt ggc caa acc agc	1362
Cys Cys Gln Pro Thr Cys Cys Gly Ser Ser Cys Cys Gly Gln Thr Ser	
85 90 95 100	
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Cys Gly Ser Ser Cys Cys Gln Pro Ile Cys Gly Ser Ser Cys Cys Gln	
105 110 115	

cct tgc tgt cac ccg act tgc tat caa act atc tgc ttc agg acc acc	1458
Pro Cys Cys His Pro Thr Cys Tyr Gln Thr Ile Cys Phe Arg Thr Thr	
120 125 130	
tgc tgc cag cct acc tgc tgc cag ccc acc tgc tgc agg aac acc tct	1506
Cys Cys Gln Pro Thr Cys Cys Gln Pro Thr Cys Cys Arg Asn Thr Ser	
135 140 145	
tgc cag ccc acc tgc tgt ggg tcc agc tgc tgc cag cct tgc tgc cac	1554
Cys Gln Pro Thr Cys Cys Gly Ser Ser Cys Cys Gln Pro Cys Cys His	
150 155 160	
cca aca tgc tgt caa acc att tgt aga tcc acc tgc tgc caa cca tcc	1602
Pro Thr Cys Cys Gln Thr Ile Cys Arg Ser Thr Cys Cys Gln Pro Ser	
165 170 175 180	
tgt gtg acc aga tgc tgc agc aca ccc tgt tgc cag cca acc tgt ggt	1650
Cys Val Thr Arg Cys Cys Ser Thr Pro Cys Cys Gln Pro Thr Cys Gly	
185 190 195	
ggg tcc agc tgc tgt agc caa acc tgc aat gag tcc agc tat tgt ctg	1698
Gly Ser Ser Cys Cys Ser Gln Thr Cys Asn Glu Ser Ser Tyr Cys Leu	
200 205 210	
cct tgc tgc cgt ccc acc tgc tgc cag acc acc tgc tac agg acc acc	1746
Pro Cys Cys Arg Pro Thr Cys Cys Gln Thr Thr Cys Tyr Arg Thr Thr	
215 220 225	
tgt tgc cgc ccc agc tgt tgc tgc agt cct tgc tgt gtc tcc agc tgc	1794
Cys Cys Arg Pro Ser Cys Cys Cys Ser Pro Cys Cys Val Ser Ser Cys	
230 235 240	
tgc cag cct tcc tgc tgc taa tc cacttgctgc agaccaccca cccaccagag	1847
Cys Gln Pro Ser Cys Cys *	
245 250	
acat	1851

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 <212> DNA
 <213> Homo sapiens

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 <222> (1050) .. (3260)

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agcctcccaa aaagggtgga ttacagggtt tagccccgc gcccggcctg caaaaccctt	180
ttttactttt ggggccccaa aagatcccc atttccccgt ccttttccgg tagactattc	240
gctactgaaa cgattttttt ttttttttga gacgagggtg aggggcgggg gttctcgcta	300
tcttgctcaa gctgatctcg aactcctggg ttcgatcaat actcagacaa tcttggcagg	360
cgcaggagga ccaaattcta gtgaatgaga tcgagtctct cggtcttttc ccttccatgt	420

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tttctttttg attgcccctc gacgatcctc agtgacgcct cccgcaccgc ctcacccgag      480
agtcagccgc cctcgctttt ccgtgcgcac gcgcagtatc ccgattggct ctgccctagc      540
ggattgacgg gcaggtttagc caatggtctc gtaatatagg tggagcgagc cctcgaggat      600
gtccacgacc cggcctctcg ctgaatatct atgagggagg cgggtcgacc ccgctgcaca      660
gtccggccgg cgccatgaag tgagaagggg gctgggggtc gcgctcgcta gcgggcgcgg      720
gggggtcttga agatggggtc atcggtgggc gcgcctgggt cccaagggg gcgaggggag      780
ggtgaagggg tgggacgggg gcagccgcag ggagcagcag tgatagcgag gagacactga      840
ggggggccccg aggcctctga ggacctgagg gttaccgggg gcgccggggc cgtcacccctt      900
ctctggggctc gacgaccggg cactgtggag gcgggagagg ggctgagggg acgggaactg      960
accagcagc ccctgccgcc aggcctcaacg tggacgggct cctggtctac ttcccgtagc     1020
actacatcta ccccgagcag ttctcctac  atg  cgg  gag  ctc  aaa  cgc  acg  ctg      1073
                               Met Arg Glu Leu Lys Arg Thr Leu
                               1                               5

gac gcc aag ggt cat gga gtc ctg gag atg ccc tca ggc acc ggg aag      1121
Asp Ala Lys Gly His Gly Val Leu Glu Met Pro Ser Gly Thr Gly Lys
    10                               15                               20

aca gta tcc ctg ttg gcc ctg atc atg gca tac cag aga gca tat ccg      1169
Thr Val Ser Leu Leu Ala Leu Ile Met Ala Tyr Gln Arg Ala Tyr Pro
    25                               30                               35                               40

ctg gag gtg acc aaa ctc atc tac tgc tca aga act gtg cca gag att      1217
Leu Glu Val Thr Lys Leu Ile Tyr Cys Ser Arg Thr Val Pro Glu Ile
                               45                               50                               55

gag aag gtg att gaa gag ctt cga aag ttg ctc aac ttc tat gag aag      1265
Glu Lys Val Ile Glu Glu Leu Arg Lys Leu Leu Asn Phe Tyr Glu Lys
    60                               65                               70

cag gag ggc gag aag ctg ccg ttt ctg gga ctg gct ctg agc tcc cgc      1313
Gln Glu Gly Glu Lys Leu Pro Phe Leu Gly Leu Ala Leu Ser Ser Arg
    75                               80                               85

aaa aac ttg tgt att cac cct gag gtg aca ccc ctg cgc ttt ggg aag      1361
Lys Asn Leu Cys Ile His Pro Glu Val Thr Pro Leu Arg Phe Gly Lys
    90                               95                               100

gac gtc gat ggg aaa tgc cac agc ctc aca gcc tcc tat gtg cgg gcg      1409
Asp Val Asp Gly Lys Cys His Ser Leu Thr Ala Ser Tyr Val Arg Ala
    105                               110                               115                               120

cag tac cag cat gac acc agc ctg ccc cac tgc cga ttc tat gag gaa      1457
Gln Tyr Gln His Asp Thr Ser Leu Pro His Cys Arg Phe Tyr Glu Glu
    125                               130                               135

ttt gat gcc cat ggg cgt gag gtg ccc ctc ccc gct ggc atc tac aac      1505
Phe Asp Ala His Gly Arg Glu Val Pro Leu Pro Ala Gly Ile Tyr Asn
    140                               145                               150

ctg gat gac ctg aag gcc ctg ggg cgg cgc cag ggc tgg tgc cca tac      1553
Leu Asp Asp Leu Lys Ala Leu Gly Arg Arg Gln Gly Trp Cys Pro Tyr
    155                               160                               165

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ttc ctt gct cga tac tca atc ctg cat gcc aat gtg gtg gtt tat agc	1601
Phe Leu Ala Arg Tyr Ser Ile Leu His Ala Asn Val Val Val Tyr Ser	
170 175 180	
tac cac tac ctc ctg gac ccc aag att gca gac ctg gtg tcc aag gaa	1649
Tyr His Tyr Leu Leu Asp Pro Lys Ile Ala Asp Leu Val Ser Lys Glu	
185 190 195 200	
ctg gcc cgc aag gcc gtc gtg gtc ttc gac gag gcc cac aac att gac	1697
Leu Ala Arg Lys Ala Val Val Val Phe Asp Glu Ala His Asn Ile Asp	
205 210 215	
aac gtc tgc atc gac tcc atg agc gtc aac ctc acc cgc cgg acc ctt	1745
Asn Val Cys Ile Asp Ser Met Ser Val Asn Leu Thr Arg Arg Thr Leu	
220 225 230	
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Asp Arg Cys Gln Gly Asn Leu Glu Thr Leu Gln Lys Thr Val Leu Arg	
235 240 245	
atc aaa gag aca gac gag cag cgc ctg cgg gac gag tac cgg cgt ctg	1841
Ile Lys Glu Thr Asp Glu Gln Arg Leu Arg Asp Glu Tyr Arg Arg Leu	
250 255 260	
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Val Glu Gly Leu Arg Glu Ala Ser Ala Ala Arg Glu Thr Asp Ala His	
265 270 275 280	
ctg gcc aac ccc gtg ctg ccc gac gaa gtg ctg cag gag gca gtg cct	1937
Leu Ala Asn Pro Val Leu Pro Asp Glu Val Leu Gln Glu Ala Val Pro	
285 290 295	
ggc tcc atc cgc acg gcc gag cat ttc ctg ggc ttc ctg agg cgg ctg	1985
Gly Ser Ile Arg Thr Ala Glu His Phe Leu Gly Phe Leu Arg Arg Leu	
300 305 310	
ctg gag tac gtg aag tgg cgg ctg cgt gtg cag cat gtg gtg cag gag	2033
Leu Glu Tyr Val Lys Trp Arg Leu Arg Val Gln His Val Val Gln Glu	
315 320 325	
agc ccg ccc gcc ttc ctg agc ggc ctg gcc cag cgc gtg tgc atc cag	2081
Ser Pro Pro Ala Phe Leu Ser Gly Leu Ala Gln Arg Val Cys Ile Gln	
330 335 340	
cgc aag ccc ctc aga ttc tgt gct gaa cgc ctc cgg tcc ctg ctg cat	2129
Arg Lys Pro Leu Arg Phe Cys Ala Glu Arg Leu Arg Ser Leu Leu His	
345 350 355 360	
act ctg gag atc acc gac ctt gct gac ttc tcc ccg ctc acc ctc ctt	2177
Thr Leu Glu Ile Thr Asp Leu Ala Asp Phe Ser Pro Leu Thr Leu Leu	
365 370 375	
gct aac ttt gcc acc ctt gtc agc acc tac gcc aaa ggc ttc acc atc	2225
Ala Asn Phe Ala Thr Leu Val Ser Thr Tyr Ala Lys Gly Phe Thr Ile	
380 385 390	
atc atc gag ccc ttt gac gac aga acc ccg acc att gcc aac ccc atc	2273
Ile Ile Glu Pro Phe Asp Asp Arg Thr Pro Thr Ile Ala Asn Pro Ile	
395 400 405	
ctg cac ttc agc tgc atg gac gcc tcg ctg gcc atc aaa ccc gta ttt	2321
Leu His Phe Ser Cys Met Asp Ala Ser Leu Ala Ile Lys Pro Val Phe	
410 415 420	

gag cgt ttc cag tct gtc atc atc aca tct ggg aca ctg tcc ccg ctg	2369
Glu Arg Phe Gln Ser Val Ile Ile Thr Ser Gly Thr Leu Ser Pro Leu	
425 430 435 440	
gac atc tac ccc aag atc ctg gac ttc cac ccc gtc acc atg gca acc	2417
Asp Ile Tyr Pro Lys Ile Leu Asp Phe His Pro Val Thr Met Ala Thr	
445 450 455	
ttc acc atg acg ctg gca cgg gtc tgc ctc tgc cct atg atc atc ggc	2465
Phe Thr Met Thr Leu Ala Arg Val Cys Leu Cys Pro Met Ile Ile Gly	
460 465 470	
cgt ggc aat gac cag gtg gcc atc agc tcc aaa ttt gag acc cgg gag	2513
Arg Gly Asn Asp Gln Val Ala Ile Ser Ser Lys Phe Glu Thr Arg Glu	
475 480 485	
gat att gct gtg atc cgg aac tat ggg aac ctc ctg ctg gag atg tcc	2561
Asp Ile Ala Val Ile Arg Asn Tyr Gly Asn Leu Leu Leu Glu Met Ser	
490 495 500	
gct gtg gtc cct gat ggc atc gtg gcc ttc ttc acc agc tac cag tac	2609
Ala Val Val Pro Asp Gly Ile Val Ala Phe Phe Thr Ser Tyr Gln Tyr	
505 510 515 520	
atg gag agc acc gtg gcc tcc tgg tat gag cag ggg atc ctt gag aac	2657
Met Glu Ser Thr Val Ala Ser Trp Tyr Glu Gln Gly Ile Leu Glu Asn	
525 530 535	
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Ile Gln Arg Asn Lys Leu Leu Phe Ile Glu Thr Gln Asp Gly Ala Glu	
540 545 550	
acc agt gtc gcc ctg gag aag tac cag gag gcc tgc gag aat ggc cgc	2753
Thr Ser Val Ala Leu Glu Lys Tyr Gln Glu Ala Cys Glu Asn Gly Arg	
555 560 565	
ggg gcc atc ctg ctg tca gtg gcc cgg ggc aaa gtg tcc gag gga atc	2801
Gly Ala Ile Leu Leu Ser Val Ala Arg Gly Lys Val Ser Glu Gly Ile	
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gac ttt gtg cac cac tac ggg cgg gcc gtc atc atg ttt ggc gtc ccc	2849
Asp Phe Val His His Tyr Gly Arg Ala Val Ile Met Phe Gly Val Pro	
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tac gtc tac aca cag agc cgc att ctc aag gcg cgg ctg gaa tac ctg	2897
Tyr Val Tyr Thr Gln Ser Arg Ile Leu Lys Ala Arg Leu Glu Tyr Leu	
605 610 615	
cgg gac cag ttc cag att cgt gag aat gac ttt ctt acc ttc gat gcc	2945
Arg Asp Gln Phe Gln Ile Arg Glu Asn Asp Phe Leu Thr Phe Asp Ala	
620 625 630	
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Met Arg His Ala Ala Gln Cys Val Gly Arg Ala Ile Arg Gly Lys Thr	
635 640 645	
gac tac ggc ctc atg gtc ttt gcc gac aag cgg ttt gcc cgt ggg gac	3041
Asp Tyr Gly Leu Met Val Phe Ala Asp Lys Arg Phe Ala Arg Gly Asp	
650 655 660	
aag cgg ggg aag ctg ccc cgc tgg atc cag gag cac ctc aca gat gcc	3089
Lys Arg Gly Lys Leu Pro Arg Trp Ile Gln Glu His Leu Thr Asp Ala	
665 670 675 680	

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Asn Leu Asn Leu Thr Val Asp Glu Gly Val Gln Val Ala Lys Tyr Phe
      685                                690                                695

ctg cgg cag atg gca cag ccc ttc cac cgg gag gat cag ctg ggc ctg      3185
Leu Arg Gln Met Ala Gln Pro Phe His Arg Glu Asp Gln Leu Gly Leu
      700                                705                                710

tcc ctg ctc agc ctg gag cag cta gaa tca gag gag acg ctg aag agg      3233
Ser Leu Leu Ser Leu Glu Gln Leu Glu Ser Glu Glu Thr Leu Lys Arg
      715                                720                                725

ata gag cag att gct cag cag ctc tga gtggg gcgggtgggg ccataaacgg      3285
Ile Glu Gln Ile Ala Gln Gln Leu *
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gaggaggaga ggctcggagcc gtctccagga gcccttagag accgagtcgc gccggcgacg      180
gcgggggcagc gcaccggcag gcggattcat tccacttaaa acctgaaaac attggaccac      240
acaaagtctt actgatttca ggtaaaaaca ataattgaag  atg tcc agc aaa aca      295
                                         Met Ser Ser Lys Thr
                                         1             5

gca agc acc aac aat ata gcc cag gca agg aga act gtg cag cag tta      343
Ala Ser Thr Asn Asn Ile Ala Gln Ala Arg Arg Thr Val Gln Gln Leu
      10                                15                                20

aga tta gaa gcc tcc att gaa aga ata aag gtt tcg aag gca tca gcg      391
Arg Leu Glu Ala Ser Ile Glu Arg Ile Lys Val Ser Lys Ala Ser Ala
      25                                30                                35

gac ctc atg tcc tac tgt gag gaa cat gcc agg agt gac cct ttg ctg      439
Asp Leu Met Ser Tyr Cys Glu Glu His Ala Arg Ser Asp Pro Leu Leu
      40                                45                                50

ata gga ata cca act tca gaa aac cct ttc aag gat aaa aaa act tgc      487
Ile Gly Ile Pro Thr Ser Glu Asn Pro Phe Lys Asp Lys Lys Thr Cys
      55                                60                                65

atc atc tta tag tgg aatagagaaa cagctcctcg cctctttcca acaacgcaaa      542
Ile Ile Leu *
      70

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ttatgagcag ctcccttgaag agatttacct tcagcttatt tggtaaccac tgctaataac 602
 taaaatgttc tcagcttgga ataatggact ctgaagtctc tattttccaa gttgtccttt 662
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 Arg Lys Ser Lys Arg Lys Pro Pro Pro Lys Lys Lys Met Thr Gly Thr
 5 10 15
 ctc gag acc cag ttc acc tgc ccc ttc tgc aac cac gag aaa tcc tgt 151
 Leu Glu Thr Gln Phe Thr Cys Pro Phe Cys Asn His Glu Lys Ser Cys
 20 25 30 35
 gat gtg aaa atg gac cgt gcc cgc aac acc gga gtc atc tct tgt acc 199
 Asp Val Lys Met Asp Arg Ala Arg Asn Thr Gly Val Ile Ser Cys Thr
 40 45 50
 gtg tgc cta gag gaa ttc cag acg ccc ata acg tgt atc ctt gga aac 247
 Val Cys Leu Glu Glu Phe Gln Thr Pro Ile Thr Cys Ile Leu Gly Asn
 55 60 65
 ctg ggc ttt ttc cag agg gtg ggg agg ggg ctg gag tcc gga ccc tgc 295
 Leu Gly Phe Phe Gln Arg Val Gly Arg Gly Leu Glu Ser Gly Pro Cys
 70 75 80
 tca tct ggc cca ctg tgt gcc ctg gtg cag ggc caa agc cgt cca gag 343
 Ser Ser Gly Pro Leu Cys Ala Leu Val Gln Gly Gln Ser Arg Pro Glu
 85 90 95
 gaa cag gtg cca cct agt gat ttc tgt ggg gtg aga aga tgc agg gca 391
 Glu Gln Val Pro Pro Ser Asp Phe Cys Gly Val Arg Arg Cys Arg Ala
 100 105 110 115
 ggg ttc caa tgc caa tga tcgccc ttgacctatg tgggccagat ctgtcagaac 445
 Gly Phe Gln Cys Gln *
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 gagga 510

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Met Lys Arg Phe Leu Phe Leu Leu Leu Thr
1 5 10

atc agc ctc ctg gtt atg gta cag ata caa act gga ctc tca gga caa 160
Ile Ser Leu Leu Val Met Val Gln Ile Gln Thr Gly Leu Ser Gly Gln
15 20 25

aac gac acc agc caa acc agc agc ccc tca gca tcc agc agc atg agc 208
Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser Ala Ser Ser Ser Met Ser
30 35 40

gga ggc att ttc ctt ttc ttc gtg gcc aat gcc ata atc cac ctc ttc 256
Gly Gly Ile Phe Leu Phe Phe Val Ala Asn Ala Ile Ile His Leu Phe
45 50 55

tgc ttc agt tga ggg gacacgtctc agccttagcc ctgtgcccc tgaacacgct 311
Cys Phe Ser *
60

gccaccatca ctgcgaagag aatccccctcc atctttggga ggggttgatg ccagacatca 371

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gatgtagggg ccaagcactg cccagctg 459

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gaagatggcg ctggccgg atg gaa atc cta atg aca gtc tcc aaa ttc gcc 171
Met Glu Ile Leu Met Thr Val Ser Lys Phe Ala
1 5 10

tcc atc tgt acc atg ggc gcc aat gct tcg gca tta gag aaa gag att 219
Ser Ile Cys Thr Met Gly Ala Asn Ala Ser Ala Leu Glu Lys Glu Ile
15 20 25

ggt cca gaa cag ttt ccg gtc aat gag cac tat ttt gga tta gtc aat 267
Gly Pro Glu Gln Phe Pro Val Asn Glu His Tyr Phe Gly Leu Val Asn
30 35 40

ttt ggg aat acc tgc tac tgc aat tca gtt ctt caa gca ctt tat ttt	315
Phe Gly Asn Thr Cys Tyr Cys Asn Ser Val Leu Gln Ala Leu Tyr Phe	
45 50 55	
tgt cgt cca ttt cgg gaa aaa gtt ctt gcg tat aag agt caa cct agg	363
Cys Arg Pro Phe Arg Glu Lys Val Leu Ala Tyr Lys Ser Gln Pro Arg	
60 65 70 75	
aaa aag gag agc ctt ctt aca tgc tta gca gat ctc ttc cat agc ata	411
Lys Lys Glu Ser Leu Leu Thr Cys Leu Ala Asp Leu Phe His Ser Ile	
80 85 90	
gcc act cag aag aaa aag gtt gga gta ata ccc cct aag aag ttc atc	459
Ala Thr Gln Lys Lys Lys Val Gly Val Ile Pro Pro Lys Lys Phe Ile	
95 100 105	
aca aga tta cgg aaa gaa aat gag ctt ttt gac aac tac atg caa caa	507
Thr Arg Leu Arg Lys Glu Asn Glu Leu Phe Asp Asn Tyr Met Gln Gln	
110 115 120	
gat gcc cat gaa ttc tta aat tac cta cta aat aca att gct gat att	555
Asp Ala His Glu Phe Leu Asn Tyr Leu Leu Asn Thr Ile Ala Asp Ile	
125 130 135	
tta caa gaa gag aga aag cag gaa aaa caa aat ggt cgt tta cct aat	603
Leu Gln Glu Glu Arg Lys Gln Glu Lys Gln Asn Gly Arg Leu Pro Asn	
140 145 150 155	
ggg aat att gat aat gaa aat aat aac agc aca cca gac cca acg tgg	651
Gly Asn Ile Asp Asn Glu Asn Asn Asn Ser Thr Pro Asp Pro Thr Trp	
160 165 170	
gtt cat gag att ttt cag gga aca tta act aat gaa acc aga tgt ctt	699
Val His Glu Ile Phe Gln Gly Thr Leu Thr Asn Glu Thr Arg Cys Leu	
175 180 185	
act tgt gaa act ata agc agc aaa gat gaa gat ttt tta gac ctt tct	747
Thr Cys Glu Thr Ile Ser Ser Lys Asp Glu Asp Phe Leu Asp Leu Ser	
190 195 200	
gtt gac gtg gaa caa aat aca tca att act cac tgc tta agg ggt ttc	795
Val Asp Val Glu Gln Asn Thr Ser Ile Thr His Cys Leu Arg Gly Phe	
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Ser Asn Thr Glu Thr Leu Cys Ser Glu Tyr Lys Tyr Tyr Cys Glu Glu	
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tgt cgc agc aaa cag gaa gca cac aaa cgg atg aaa gtt aaa aaa ctg	891
Cys Arg Ser Lys Gln Glu Ala His Lys Arg Met Lys Val Lys Lys Leu	
240 245 250	
ccc atg att cta gct cta cac ctg aag aga ttt aaa tat atg gat caa	939
Pro Met Ile Leu Ala Leu His Leu Lys Arg Phe Lys Tyr Met Asp Gln	
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Leu His Arg Tyr Thr Lys Leu Ser Tyr Arg Val Val Phe Pro Leu Glu	
270 275 280	
ctt cgt ctg ttt aac act tca ggt gat gcc acc aat cca gac aga atg	1035
Leu Arg Leu Phe Asn Thr Ser Gly Asp Ala Thr Asn Pro Asp Arg Met	
285 290 295	

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Tyr Asp Leu Val Ala Val Val Val His Cys Gly Ser Gly Pro Asn Arg	
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Gly His Tyr Ile Ala Ile Val Lys Ser His Asp Phe Trp Leu Leu Phe	
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Asp Asp Asp Ile Val Glu Lys Ile Asp Ala Gln Ala Ile Glu Glu Phe	
335 340 345	
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Tyr Gly Leu Thr Ser Asp Ile Ser Lys Asn Ser Glu Ser Gly Tyr Ile	
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Leu Phe Tyr Gln Ser Arg Asp *	
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c g g a c c t t a c t a g a a a a a t g a a a c c t g a t g a a a c t c c t a t g t t t g a c c c a	110
Met Lys Pro Asp Glu Thr Pro Met Phe Asp Pro	
1 5 10	
a a t c t a c t c a a a g a a g t g g a c t g g a g t c a g a a t a c a g c t a c a t t t t c t	158
Asn Leu Leu Lys Glu Val Asp Trp Ser Gln Asn Thr Ala Thr Phe Ser	
15 20 25	
c c a g c c a t t t c c c c a a c a c a t c c t g g a g a a g g c t t g g t t t t g a g g c c t	206
Pro Ala Ile Ser Pro Thr His Pro Gly Glu Gly Leu Val Leu Arg Pro	
30 35 40	
c t t t g t a c t g c t g a c t t a a a t a g a g g t t t t t t t a a g g t a t t g g g t c a g	254
Leu Cys Thr Ala Asp Leu Asn Arg Gly Phe Phe Lys Val Leu Gly Gln	
45 50 55	
c t a a c a g a g a c t g g a g t t g t c a g c c c t g a a c a a t t t a t g a a a t c t t t t	302
Leu Thr Glu Thr Gly Val Val Ser Pro Glu Gln Phe Met Lys Ser Phe	
60 65 70 75	
g a g c a t a t g a a g a a a t c t g g g g a t t a t t a t g t t a c a g t t g t a g a a g a t	350
Glu His Met Lys Lys Ser Gly Asp Tyr Tyr Val Thr Val Val Glu Asp	
80 85 90	
g t g a c t c t a g g a c a g a t t g t t g c t a c g g c a a c t c t g a t t a t a g a a c a t	398
Val Thr Leu Gly Gln Ile Val Ala Thr Ala Thr Leu Ile Ile Glu His	
95 100 105	
a a a t t c a t c c a t t c c t g t g c t a a g a g a g g a a g a g t a g a a g a t g t t g t t	446
Lys Phe Ile His Ser Cys Ala Lys Arg Gly Arg Val Glu Asp Val Val	
110 115 120	
g c t a g t g a t g a a t g c a g a g g a a a g c a g c t t g g c a a c t t g t t a t t a t c a	494
Ala Ser Asp Glu Cys Arg Gly Lys Gln Leu Gly Asn Leu Leu Leu Ser	
125 130 135	
a c c c t t a c t t t g c t a a g c a a g a a a c t g a a c t g t t a c a a g a t t a c c c t t	542
Thr Leu Thr Leu Leu Ser Lys Lys Leu Asn Cys Tyr Lys Ile Thr Leu	
140 145 150 155	
g a a t g t c t a c c a c a a a a t g t t g g t t t c t a t a a a a a g t t t g g a t a t a c t	590
Glu Cys Leu Pro Gln Asn Val Gly Phe Tyr Lys Lys Phe Gly Tyr Thr	
160 165 170	
g t a t c t g a a g a a a a c t a c a t g t g t c g g a g g t t t c t a a a g t a a a a a t c t t	639
Val Ser Glu Glu Asn Tyr Met Cys Arg Arg Phe Leu Lys *	
175 180 185	
g t a a g a a a a t t g t c a a a g g g g c t a a t g c t a c a a g g c t a c a c t c t t c c t a g a g t t g a a a t a	699
t t t t g t t g c t q c a q c c q a g t q a c c t c c a t a a a t a c t q q a c t q a a a a a a c a t t q t a a t a c t	759

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 Met Lys Ser
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 ccg ttc tac cgc tgc cag aac acc acc tct gtg gaa aaa ggc aac tcg 222
 Pro Phe Tyr Arg Cys Gln Asn Thr Thr Ser Val Glu Lys Gly Asn Ser
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 gcg gtg atg ggc ggg gtg ctc ttc agc acc ggc ctc ctg ggc aac ctg 270
 Ala Val Met Gly Gly Val Leu Phe Ser Thr Gly Leu Leu Gly Asn Leu
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 ctg gcc ctg ggc ctg ctg gcg cgc tog ggg ctg ggg tgg tgc tcg cgg 318
 Leu Ala Leu Gly Leu Leu Ala Arg Ser Gly Leu Gly Trp Cys Ser Arg
 40 45 50
 cgt cca ctg cgc ccg ctg ccc tcg gtc ttc tac atg ctg gtg tgt ggc 366
 Arg Pro Leu Arg Pro Leu Pro Ser Val Phe Tyr Met Leu Val Cys Gly
 55 60 65
 ctg acg gtc acc gac ttg ctg ggc aag tgc ctc cta agc ccg gtg gtg 414
 Leu Thr Val Thr Asp Leu Leu Gly Lys Cys Leu Leu Ser Pro Val Val
 70 75 80
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 Leu Ala Ala Tyr Ala Gln Asn Arg Ser Leu Arg Val Leu Ala Pro Ala
 85 90 95
 ttg gac aac tcg ttg tgc caa gcc ttc gcc ttc ttc atg tcc ttc ttt 510
 Leu Asp Asn Ser Leu Cys Gln Ala Phe Ala Phe Phe Met Ser Phe Phe
 100 105 110 115
 ggg ctc tcc tcg aca ctg caa ctc ctg gcc atg gca ctg gag tgc tgg 558
 Gly Leu Ser Ser Thr Leu Gln Leu Leu Ala Met Ala Leu Glu Cys Trp
 120 125 130
 ctc tcc cta ggg cac cct ttc ttc tac cga cgg cac atc acc ctg cgc 606
 Leu Ser Leu Gly His Pro Phe Phe Tyr Arg Arg His Ile Thr Leu Arg
 135 140 145
 ctg ggc gca ctg gtg gcc ccg gtg gtg agc gcc ttc tcc ctg gct ttc 654

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Leu Gly Ala Leu Val Ala Pro Val Val Ser Ala Phe Ser Leu Ala Phe
      150                      155                      160

tgc gcg cta cct ttc atg ggc ttc ggg aag ttc gtg cag tac tgc ccc      702
Cys Ala Leu Pro Phe Met Gly Phe Gly Lys Phe Val Gln Tyr Cys Pro
      165                      170                      175

ggc acc tgg tgc ttt atc cag atg gtc cac gag gag ggc tcg ctg tcg      750
Gly Thr Trp Cys Phe Ile Gln Met Val His Glu Glu Gly Ser Leu Ser
      180                      185                      190

gtg ctg ggg tac tct gtg ctc tac tcc agc ctc atg gcg ctg ctg gtc      798
Val Leu Gly Tyr Ser Val Leu Tyr Ser Ser Leu Met Ala Leu Leu Val
      200                      205                      210

ctc gcc acc gtg ctg tgc aac ctc ggc gcc atg cgc aac ctc tat gcg      846
Leu Ala Thr Val Leu Cys Asn Leu Gly Ala Met Arg Asn Leu Tyr Ala
      215                      220                      225

atg cac cgg cgg ctg cag cgg cac ccg cgc tcc tgc acc agg gac tgt      894
Met His Arg Arg Leu Gln Arg His Pro Arg Ser Cys Thr Arg Asp Cys
      230                      235                      240

gcc gag ccg cgc gcg gac ggg agg gaa gcg tcc cct cag ccc ctg gag      942
Ala Glu Pro Arg Ala Asp Gly Arg Glu Ala Ser Pro Gln Pro Leu Glu
      245                      250                      255

gag ctg gat cac ctc ctg ctg ctg gcg ctg atg acc gtg ctc ttc act      990
Glu Leu Asp His Leu Leu Leu Leu Ala Leu Met Thr Val Leu Phe Thr
      260                      265                      270

atg tgt tct ctg ccc gta att tat cgc gct tac tat gga gca ttt aag      1038
Met Cys Ser Leu Pro Val Ile Tyr Arg Ala Tyr Tyr Gly Ala Phe Lys
      280                      285                      290

gat gtc aag gag aaa aac agg acc tct gaa gaa gca gaa gac ctc cga      1086
Asp Val Lys Glu Lys Asn Arg Thr Ser Glu Glu Ala Glu Asp Leu Arg
      295                      300                      305

gcc ttg cga ttt cta tct gtg att tca att gtg gac cct tgg att ttt      1134
Ala Leu Arg Phe Leu Ser Val Ile Ser Ile Val Asp Pro Trp Ile Phe
      310                      315                      320

atc att ttc aga tct cca gta ttt cgg ata ttt ttt cac aag att ttc      1182
Ile Ile Phe Arg Ser Pro Val Phe Arg Ile Phe Phe His Lys Ile Phe
      325                      330                      335

att aga cct ctt agg tac agg agc cgg tgc agc aat tcc act aac atg      1230
Ile Arg Pro Leu Arg Tyr Arg Ser Arg Cys Ser Asn Ser Thr Asn Met
      340                      345                      350

gaa tcc agt ctg tga cagtgttttt cactctgtgg taagctgagg aatatgtcac      1285
Glu Ser Ser Leu *
      360

attttcagcg gcaccagc      1303

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<210> 688
 <211> 1023
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (121) .. (846)

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 ggtggagtcg tgttggtcct cagaatcccc gcgtagccgc tgccctctcc taccctcgcc 120
 atg ttt ctt acc cgg tct gag tac gac agg ggc gtg aat act ttt tct 168
 Met Phe Leu Thr Arg Ser Glu Tyr Asp Arg Gly Val Asn Thr Phe Ser
 1 5 10 15
 ccc gaa gga aga tta ttt caa gtg gaa tat gcc att gag gct atc aag 216
 Pro Glu Gly Arg Leu Phe Gln Val Glu Tyr Ala Ile Glu Ala Ile Lys
 20 25 30
 ctt ggt tct aca gcc att ggg atc cag aca tca gag ggt gtg tgc cta 264
 Leu Gly Ser Thr Ala Ile Gly Ile Gln Thr Ser Glu Gly Val Cys Leu
 35 40 45
 gct gtg gag aag aga att act tcc cca ctg atg gag ccc agc agc att 312
 Ala Val Glu Lys Arg Ile Thr Ser Pro Leu Met Glu Pro Ser Ser Ile
 50 55 60
 gag aaa att gta gag att gat gct cac ata ggt tgt gcc atg agt ggg 360
 Glu Lys Ile Val Glu Ile Asp Ala His Ile Gly Cys Ala Met Ser Gly
 65 70 75 80
 cta att gct gat gct aag act tta att gat aaa gcc aga gtg gag aca 408
 Leu Ile Ala Asp Ala Lys Thr Leu Ile Asp Lys Ala Arg Val Glu Thr
 85 90 95
 cag aac cac tgg ttc acc tac aat gag aca atg aca gtg gag agt gtg 456
 Gln Asn His Trp Phe Thr Tyr Asn Glu Thr Met Thr Val Glu Ser Val
 100 105 110
 acc caa gct gtg tcc aat ctg gct ttg cag ttt gga gaa gaa gat gca 504
 Thr Gln Ala Val Ser Asn Leu Ala Leu Gln Phe Gly Glu Glu Asp Ala
 115 120 125
 gat cca ggt gcc atg tct cgt ccc ttt gga gta gca tta tta ttt gga 552
 Asp Pro Gly Ala Met Ser Arg Pro Phe Gly Val Ala Leu Leu Phe Gly
 130 135 140
 gga gtt gat gag aaa gga ccc cag ctg ttt cat atg gac cca tct ggg 600
 Gly Val Asp Glu Lys Gly Pro Gln Leu Phe His Met Asp Pro Ser Gly
 145 150 155 160
 acc ttt gta cag tgt gat gct cga gca att ggc tct gct tca gag ggt 648
 Thr Phe Val Gln Cys Asp Ala Arg Ala Ile Gly Ser Ala Ser Glu Gly
 165 170 175
 gcc cag agc tcc ttg caa gaa gtt tac cac aag tct atg act ttg aaa 696
 Ala Gln Ser Ser Leu Gln Glu Val Tyr His Lys Ser Met Thr Leu Lys
 180 185 190
 gaa gcc atc aag tct tca ctc atc atc ctc aaa caa gta atg gag gag 744
 Glu Ala Ile Lys Ser Ser Leu Ile Ile Leu Lys Gln Val Met Glu Glu
 195 200 205
 aag ctg aat gca aca aac att gag cta gcc aca gtg cag cct ggc cag 792
 Lys Leu Asn Ala Thr Asn Ile Glu Leu Ala Thr Val Gln Pro Gly Gln

210	215	220	
aat ttc cac atg ttc aca aag gaa gaa ctt gaa gag gtt atc aag gac			840
Asn Phe His Met Phe Thr Lys Glu Glu Leu Glu Glu Val Ile Lys Asp			
225	230	235	240
att taa ggaatcctga tcctcagaac ttctctggga caatttcagt tctaataatg			896
Ile *			
tccttaaatt ttatttccag ctctgttcc ttggaaaatc tccattgtat gtgcattttt			956
taa atgatgt ctgtacataa aggcagttct gaaataaaga aaattttaaa atattaaaaa			1016
aaaaaaaa			1023

<210> 689
 <211> 2132
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (59)..(1255)

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atg ctc ggc agg tct ggg tac cgg gcg ctg ccc ctg ggt gat ttt gac	106
Met Leu Gly Arg Ser Gly Tyr Arg Ala Leu Pro Leu Gly Asp Phe Asp	
1 5 10 15	
cgc ttc cag cag tcg agc ttc ggc ttt ctg ggc tcg cag aag ggc tgc	154
Arg Phe Gln Gln Ser Ser Phe Gly Phe Leu Gly Ser Gln Lys Gly Cys	
20 25 30	
ttg tcc ccg gag cgg ggc ggc gtg ggg aca ggg gcc gat gta ccc cag	202
Leu Ser Pro Glu Arg Gly Gly Val Gly Thr Gly Ala Asp Val Pro Gln	
35 40 45	
agc tgg ccc tcc tgc ctc tgt cat ggc ctc atc agt ttc ctg ggg ttc	250
Ser Trp Pro Ser Cys Leu Cys His Gly Leu Ile Ser Phe Leu Gly Phe	
50 55 60	
ttg ctg ctg ttg gtc acc ttc ccc att tct ggc tgg ttt gcc ctg aag	298
Leu Leu Leu Leu Val Thr Phe Pro Ile Ser Gly Trp Phe Ala Leu Lys	
65 70 75 80	
att gtg ccc acc tac gag cgg atg att gtg ttc cgc ctg ggc cgg atc	346
Ile Val Pro Thr Tyr Glu Arg Met Ile Val Phe Arg Leu Gly Arg Ile	
85 90 95	
cgc acc ccc cag gga cct ggc atg gtt ctg ctc ttg ccc ttc att gac	394
Arg Thr Pro Gln Gly Pro Gly Met Val Leu Leu Leu Pro Phe Ile Asp	
100 105 110	
tcc ttt cag agg gtg gat ctg agg aca cga gcc ttc aac gtc cct ccc	442
Ser Phe Gln Arg Val Asp Leu Arg Thr Arg Ala Phe Asn Val Pro Pro	
115 120 125	
tgc aag ctg gcc tct aag gac ggg gct gtg ctg tcc gtg gga gcc gat	490
Cys Lys Leu Ala Ser Lys Asp Gly Ala Val Leu Ser Val Gly Ala Asp	

130	135	140	
gtc cag ttt cgc atc tgg gac ccg gtg ctg tgc gtg atg act gtg aaa			538
Val Gln Phe Arg Ile Trp Asp Pro Val Leu Ser Val Met Thr Val Lys			
145	150	155	160
gac ctg aac aca gcc aca cgc atg aca gcc cag aac gcc atg acc aag			586
Asp Leu Asn Thr Ala Thr Arg Met Thr Ala Gln Asn Ala Met Thr Lys			
	165	170	175
gcc ctg ctc aag agg ccg ctg cgg gag atc cag atg gag aag ctc aag			634
Ala Leu Leu Lys Arg Pro Leu Arg Glu Ile Gln Met Glu Lys Leu Lys			
	180	185	190
atc agc gac cag ctt ctg ctg gag atc aac gat gtg acc agg gcc tgg			682
Ile Ser Asp Gln Leu Leu Leu Glu Ile Asn Asp Val Thr Arg Ala Trp			
	195	200	205
ggg ctg gag gta gac cgc gtg gag ctg gca gtg gag gcc gtg ctc cag			730
Gly Leu Glu Val Asp Arg Val Glu Leu Ala Val Glu Ala Val Leu Gln			
	210	215	220
ccg ccc cag gac agc cca gct ggg ccc aac ctg gac agc acc ctc cag			778
Pro Pro Gln Asp Ser Pro Ala Gly Pro Asn Leu Asp Ser Thr Leu Gln			
	225	230	235
cag ctg gcc ctg cac ttc ctg gga gga agc atg aac tca atg gca gga			826
Gln Leu Ala Leu His Phe Leu Gly Gly Ser Met Asn Ser Met Ala Gly			
	245	250	255
ggt gcc ccg tcc ccg ggg cca gca gac acc gtg gag atg gtg agt gaa			874
Gly Ala Pro Ser Pro Gly Pro Ala Asp Thr Val Glu Met Val Ser Glu			
	260	265	270
gtt gag cca cct gcc cct caa gtt ggt gcc agg tcc agt ccg aag cag			922
Val Glu Pro Pro Ala Pro Gln Val Gly Ala Arg Ser Ser Pro Lys Gln			
	275	280	285
cct ctg gcg gag ggg cta ctg act gct cta cag ccc ttc ctg tct gag			970
Pro Leu Ala Glu Gly Leu Leu Thr Ala Leu Gln Pro Phe Leu Ser Glu			
	290	295	300
gcc ctg gtc agc caa gtc ggg gcc tgc tac cag ttc aat gtc gtc ctg			1018
Ala Leu Val Ser Gln Val Gly Ala Cys Tyr Gln Phe Asn Val Val Leu			
	305	310	315
ccc agc ggc acc caa agc gcc tac ttc ctg gac ctc act aca gga cga			1066
Pro Ser Gly Thr Gln Ser Ala Tyr Phe Leu Asp Leu Thr Thr Gly Arg			
	325	330	335
gga aga gtg gga cac ggg gtg cct gat ggc atc cct gat gtg gtg gtg			1114
Gly Arg Val Gly His Gly Val Pro Asp Gly Ile Pro Asp Val Val Val			
	340	345	350
gag atg gcc gag gca gac ctg cgg gcc ctg cta tgc aga gag ctg cgg			1162
Glu Met Ala Glu Ala Asp Leu Arg Ala Leu Leu Cys Arg Glu Leu Arg			
	355	360	365
ccc ctg ggg gcc tac atg agt gga cgg ctg aag gtg aag ggc gac ctg			1210
Pro Leu Gly Ala Tyr Met Ser Gly Arg Leu Lys Val Lys Gly Asp Leu			
	370	375	380
gct atg gcc atg aag ctg gag gct gtc ctc agg gcc ttg aag tag cag			1258
Ala Met Ala Met Lys Leu Glu Ala Val Leu Arg Ala Leu Lys *			

385

390

395

ccttggctga ctttccagag cccagtccca agcctggcac caagcctgag gggcctcttg 1318
 gaggaggagg tgttcatctg caccacagag agttgaggcc ctaacaaatt tcaggcccag 1378
 ccaagagccc atgaatggag gctgcaggag gctgagtccg gctgccatgc acgtctcccc 1438
 tacagtgggtt ctctggacaa ggctttgtcc atcccggccc ccagctgagt gccagcgct 1498
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 cctgactgga gagacaggac ccacagaaac agcctgacag cagctggttt ggtccttgtg 1618
 tgagggacca agcatgtggc ccaggctcta agctctgcgg ggattggaga gggatgggga 1678
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 tggcccaact tcctggctgc agtccaggcc cgtgctggcg ggattgggca tgggaaggag 1798
 cagggcctgc tgcttccctg gcgctgctcc caaagatttc tgactcatct gccagctccg 1858
 tcctgcatgc ctggcgagct ggggcccagg gcagcatgaa ggagagccct gcgttctgtg 1918
 cttcttacca gaggtttgca agcctcagac aaataaatgt ggtgtttaca atgtaaaaa 1978
 aagacttcag tcatcccagc aatcgcttgg ttcagtttca ttcagctctc tatggaccag 2038
 taatctgata aataaccgag ctcttctttg gggatcacta cttcttgact tgtagtaact 2098
 gccaccaatc aagcagtctc tcccctgcaa aaca 2132

<210> 690

<211> 575

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (134) .. (499)

<400> 690

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 tgggtgaaata gat atg gcg acc gag ggg gat gtg gag ctg gag ttg gag 169
 Met Ala Thr Glu Gly Asp Val Glu Leu Glu Leu Glu
 1 5 10
 act gag acc agt gga cca gag cgg cct ccg gag aag cca cgg aaa cat 217
 Thr Glu Thr Ser Gly Pro Glu Arg Pro Pro Glu Lys Pro Arg Lys His
 15 20 25
 gac agc ggt gcg gcg gac ttg gag cgg gtc acc gac tat gca gag gag 265
 Asp Ser Gly Ala Ala Asp Leu Glu Arg Val Thr Asp Tyr Ala Glu Glu
 30 35 40
 aag gag atc cag agt tcc aat ctg gag acg gcc atg tct gtg att gga 313
 Lys Glu Ile Gln Ser Ser Asn Leu Glu Thr Ala Met Ser Val Ile Gly
 45 50 55 60

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gac aga agg tcc cgg gag cag aaa gcc aaa cag gag cgg gag aaa gaa      361
Asp Arg Arg Ser Arg Glu Gln Lys Ala Lys Gln Glu Arg Glu Lys Glu
      65                      70                      75

ctg gca aaa gtc act atc aag aag gaa gat ctg gag cta ata atg act      409
Leu Ala Lys Val Thr Ile Lys Lys Glu Asp Leu Glu Leu Ile Met Thr
      80                      85                      90

gag atg gag ata tct cga gca gca gca gaa cgc agt ttg cgg gaa cac      457
Glu Met Glu Ile Ser Arg Ala Ala Ala Glu Arg Ser Leu Arg Glu His
      95                      100                     105

atg ggc aac gtg gta gag gcg ctt att gcc cta acc aac tga tgcgtgc      506
Met Gly Asn Val Val Glu Ala Leu Ile Ala Leu Thr Asn *
      110                     115                     120

tttctcaaat atacctactg gattaattta tggcaataaa attttttttt gtcttttaaa      566

aaaaaaaaa                                                                575

<210> 691
<211> 642
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (52)..(471)

<400> 691
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Met Glu
1

gcg gtg gtg ttc gtc ttc tct ctc ctc gat tgt tgc gcg ctc atc ttc      105
Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys Ala Leu Ile Phe
      5                      10                      15

ctc tcg gtc tac ttc ata att aca ttg tct gat tta gaa tgt gat tac      153
Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu Glu Cys Asp Tyr
      20                      25                      30

att aat gct aga tca tgt tgc tca aaa tta aac aag tgg gta att cca      201
Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys Trp Val Ile Pro
      35                      40                      45                      50

gaa ttg att ggc cat acc att gtc act gta tta ctg ctc atg tca ttg      249
Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu Leu Met Ser Leu
      55                      60                      65

cac tgg ttc atc ttc ctt ctc aac tta cct gtt gcc act tgg aat ata      297
His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala Thr Trp Asn Ile
      70                      75                      80

tat cga tac att atg gtg ccg agt ggt aac atg gga gtg ttt gat cca      345
Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly Val Phe Asp Pro
      85                      90                      95

aca gaa ata cac aat cga ggg cag ctg aag tca cac atg aaa gaa gcc      393
Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His Met Lys Glu Ala

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100	105	110	
atg atc aag ctt ggt ttc cac ttg ctc tgc ttc ttc atg tat ctt tat			441
Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe Met Tyr Leu Tyr			
115	120	125	130
agt atg atc tta gct ttg ata aat gac tga a gccgtggttg aagtcagcct			492
Ser Met Ile Leu Ala Leu Ile Asn Asp *			
	135	140	
acactacagt gcacagttga ggagccagag acttcttaaa tcatccttag aaccgtgacc			552
atagcagtat atattttcct cttggaacaa aaaactatctt ttgctgtatt ttaccatat			612
aaagtatttta aaaaacataa aaaaaaaaaa			642

<210> 692
 <211> 3135
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (489)..(2900)

<400> 692	
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ccgcaatgct ttttttaggtg tttttttttg gggctggggg gtgtttattt gggatatatac	120
aatgagtcac ggattaaaat tgcttcacgc ggatagatac ctaggtgttc cacagcatta	180
ctgaacaagc tgctgtcatt tccccattac ctgagaagac ccccttaatt acttacttat	240
attaactgta gaacgtattt atgcatacca ggctctacct ctgggctttc tattctgttc	300
cagagaccca gtaccagaat atttaaatca ctgggggcgt taaatacgtt ttaatatctg	360
atagggccag tttctgcgca ttgcacattt ttttttcccc ttccaggaac gtgttcaggc	420
ccgcggcagg gggcgggatc ggcctcctc ctgggctctg gttccagccg agcctctcgg	480
acgcagag atg gaa atc ccg aag ctg ctc ccg gct cgc ggg aca cta cag	530
Met Glu Ile Pro Lys Leu Leu Pro Ala Arg Gly Thr Leu Gln	
1 5 10	
ggc ggc ggc ggc ggc ggt atc ccc gcg ggt ggc ggc cga gtc cac cga	578
Gly Gly Gly Gly Gly Gly Ile Pro Ala Gly Gly Gly Arg Val His Arg	
15 20 25 30	
ggc cct gac tcg ccg gct ggc cag gtc ccc acg cgc cgc ctg ctg	626
Gly Pro Asp Ser Pro Ala Gly Gln Val Pro Thr Arg Arg Leu Leu Leu	
35 40 45	
ctc cgg ggc ccc caa gat ggc ggg ccc ggg cgg cgg cgc gag gag gcc	674
Leu Arg Gly Pro Gln Asp Gly Gly Pro Gly Arg Arg Arg Glu Glu Ala	
50 55 60	
agc acg gca tca cgg ggc cct ggc cca agc ctg ttg gcg ccg agg acc	722
Ser Thr Ala Ser Arg Gly Pro Gly Pro Ser Leu Leu Ala Pro Arg Thr	
65 70 75	

gat caa cct agc ggc ggc ggc ggc ggc ggc ggc gac gac ttc ttc ctg	770
Asp Gln Pro Ser Gly Gly Gly Gly Gly Gly Gly Gly Asp Asp Phe Phe Leu	
80 85 90	
gtg ctg ctt gac ccg gtg ggt ggc gac gtg gag acc gcg ggc tcc ggt	818
Val Leu Leu Asp Pro Val Gly Gly Asp Val Glu Thr Ala Gly Ser Gly	
95 100 105 110	
cag gcc gca ggg cct gtg ttg agg gag gag gcc gag gag ggc ccg ggg	866
Gln Ala Ala Gly Pro Val Leu Arg Glu Glu Ala Glu Glu Gly Pro Gly	
115 120 125	
ctc cag ggg ggc gag agc ggc gcg aat ccc gcg ggg ccc act gcg cta	914
Leu Gln Gly Gly Glu Ser Gly Ala Asn Pro Ala Gly Pro Thr Ala Leu	
130 135 140	
ggc ccc cgc tgc ctg tcc gcg gtt ccc act ccg gcc ccg atc tcc gcc	962
Gly Pro Arg Cys Leu Ser Ala Val Pro Thr Pro Ala Pro Ile Ser Ala	
145 150 155	
ccc ggc ccc gcc gcg gcc ttc gcg ggc aca gtc act atc cac aac cag	1010
Pro Gly Pro Ala Ala Ala Phe Ala Gly Thr Val Thr Ile His Asn Gln	
160 165 170	
gac ctg ctg ttg cgc ttt gag aac ggc gtc ctc acc ctg gcc acg ccc	1058
Asp Leu Leu Leu Arg Phe Glu Asn Gly Val Leu Thr Leu Ala Thr Pro	
175 180 185 190	
cca cca cac gcc tgg gag cca ggg gcc gct cct gcc cag cag ccc ggg	1106
Pro Pro His Ala Trp Glu Pro Gly Ala Ala Pro Ala Gln Gln Pro Gly	
195 200 205	
tgt ctg atc gcc ccg caa gct ggg ttc ccg cat gcc gcg cac ccg ggt	1154
Cys Leu Ile Ala Pro Gln Ala Gly Phe Pro His Ala Ala His Pro Gly	
210 215 220	
gac tgc cca gag ctg ccg cca gac ctc ctg cta gct gag ccg gcc gaa	1202
Asp Cys Pro Glu Leu Pro Pro Asp Leu Leu Leu Ala Glu Pro Ala Glu	
225 230 235	
ccc gcg cca gct ccg gcg cct gag gag gag gcg gag ggc ccg gcc gcc	1250
Pro Ala Pro Ala Pro Ala Pro Glu Glu Glu Ala Glu Gly Pro Ala Ala	
240 245 250	
gcc ctg ggc ccc cgc gga ccg ctg ggc tcc ggc cca ggc gtg gtg ctg	1298
Ala Leu Gly Pro Arg Gly Pro Leu Gly Ser Gly Pro Gly Val Val Leu	
255 260 265 270	
tac ttg tgc ccc gag gcg cag tgc ggg caa acc ttc gcc aag aag cac	1346
Tyr Leu Cys Pro Glu Ala Gln Cys Gly Gln Thr Phe Ala Lys Lys His	
275 280 285	
cag ctg aag gtg cac ctg ctg acg cac agc agc agc cag ggc cag agg	1394
Gln Leu Lys Val His Leu Leu Thr His Ser Ser Ser Gln Gly Gln Arg	
290 295 300	
ccc ttc aaa tgc ccc ctg ggt ggc tgc ggc tgg acc ttc acc acc tct	1442
Pro Phe Lys Cys Pro Leu Gly Gly Cys Gly Trp Thr Phe Thr Thr Ser	
305 310 315	
tac aag ctc aag agg cac ctg cag tcg cac gac aaa ctg cgg ccc ttt	1490
Tyr Lys Leu Lys Arg His Leu Gln Ser His Asp Lys Leu Arg Pro Phe	
320 325 330	

ggc tgc ccg gca gag ggc tgt ggc aag agc ttc acc aca gtg tac aac	1538
Gly Cys Pro Ala Glu Gly Cys Gly Lys Ser Phe Thr Thr Val Tyr Asn	
335 340 345 350	
ctc aag gcg cac atg aag ggc cat gag cag gag aac tca ttc aaa tgc	1586
Leu Lys Ala His Met Lys Gly His Glu Gln Glu Asn Ser Phe Lys Cys	
355 360 365	
gag gtg tgc gag gag agc ttc ccc acg cag gcc aaa ctc agc gcc cac	1634
Glu Val Cys Glu Glu Ser Phe Pro Thr Gln Ala Lys Leu Ser Ala His	
370 375 380	
cag cgc agc cac ttc gaa ccg gag agg cct tac cag tgc gcg ttt tct	1682
Gln Arg Ser His Phe Glu Pro Glu Arg Pro Tyr Gln Cys Ala Phe Ser	
385 390 395	
ggc tgc aag aag aca ttt atc aca gtg agt gct ctg ttt tcc cat aac	1730
Gly Cys Lys Lys Thr Phe Ile Thr Val Ser Ala Leu Phe Ser His Asn	
400 405 410	
cgc gcc cat ttc agg gaa cag gaa ctg ttt tcc tgc tct ttt cct ggc	1778
Arg Ala His Phe Arg Glu Gln Glu Leu Phe Ser Cys Ser Phe Pro Gly	
415 420 425 430	
tgc agc aaa caa tat gac aag gct tgt agg ctg aaa att cac ctg cgg	1826
Cys Ser Lys Gln Tyr Asp Lys Ala Cys Arg Leu Lys Ile His Leu Arg	
435 440 445	
agt cac acc ggc gag aga cct ttc ctt tgt gac ttt gat ggc tgt ggc	1874
Ser His Thr Gly Glu Arg Pro Phe Leu Cys Asp Phe Asp Gly Cys Gly	
450 455 460	
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Trp Asn Phe Thr Ser Met Ser Lys Leu Leu Arg His Lys Arg Lys His	
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gac gat gac cgg agg ttc atg tgc cct gtg gaa ggc tgt ggg aaa tct	1970
Asp Asp Asp Arg Arg Phe Met Cys Pro Val Glu Gly Cys Gly Lys Ser	
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Phe Thr Arg Ala Glu His Leu Lys Gly His Ser Ile Thr His Leu Gly	
495 500 505 510	
aca aag cct ttc gtg tgt cct gtg gca ggc tgc tgt gcc agg ttc tct	2066
Thr Lys Pro Phe Val Cys Pro Val Ala Gly Cys Cys Ala Arg Phe Ser	
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Ala Arg Ser Ser Leu Tyr Ile His Ser Lys Lys His Leu Gln Asp Val	
530 535 540	
gac act tgg aaa agc cgt tgc ccg atc tcc tct tgt aat aaa ctc ttc	2162
Asp Thr Trp Lys Ser Arg Cys Pro Ile Ser Ser Cys Asn Lys Leu Phe	
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aca tcc aag cac agc atg aag acg cac atg gtt aaa agg cat aag gtg	2210
Thr Ser Lys His Ser Met Lys Thr His Met Val Lys Arg His Lys Val	
560 565 570	
ggc cag gat ctc tta gct cag cta gaa gca gca aat tct ctc aca ccc	2258
Gly Gln Asp Leu Leu Ala Gln Leu Glu Ala Ala Asn Ser Leu Thr Pro	
575 580 585 590	

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ata gtg tct ctc ttc tct gat gta cct gac agt act tct gct gca ttg Ile Val Ser Leu Phe Ser Asp Val Pro Asp Ser Thr Ser Ala Ala Leu 610 615 620	2354
ctg gac aca gca ttg gtg aac tct gga atc ttg act att gat gtg gct Leu Asp Thr Ala Leu Val Asn Ser Gly Ile Leu Thr Ile Asp Val Ala 625 630 635	2402
tct gtg agc tcg act ctg gca ggg cac ctc cct gct aat aat aat aat Ser Val Ser Ser Thr Leu Ala Gly His Leu Pro Ala Asn Asn Asn Asn 640 645 650	2450
tcc gta ggg cag gct gtg gac cct ccg tcc ttg atg gcc acc agc gac Ser Val Gly Gln Ala Val Asp Pro Pro Ser Leu Met Ala Thr Ser Asp 655 660 665 670	2498
cct cct caa agt ctg gat acc tct ctc ttt ttt gga acg gcg gcc act Pro Pro Gln Ser Leu Asp Thr Ser Leu Phe Phe Gly Thr Ala Ala Thr 675 680 685	2546
ggc ttt cag cag agc tcc tta aat atg gat gag gtc tca agt gta agt Gly Phe Gln Gln Ser Ser Leu Asn Met Asp Glu Val Ser Ser Val Ser 690 695 700	2594
gtg ggg cca ttg gga tct ctg gac tct ttg gcc atg aaa aac tcc agt Val Gly Pro Leu Gly Ser Leu Asp Ser Leu Ala Met Lys Asn Ser Ser 705 710 715	2642
cca gag cct cag gct ttg aca ccc agc agt aag cta aca gtg gac aca Pro Glu Pro Gln Ala Leu Thr Pro Ser Ser Lys Leu Thr Val Asp Thr 720 725 730	2690
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cta ctg aca cca acc aaa gcg gag tgg aac gta cat cct gac tct gac Leu Leu Thr Pro Thr Lys Ala Glu Trp Asn Val His Pro Asp Ser Asp 755 760 765	2786
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gga aac cat ggt tct cag aaa gaa aca gat ctt atc act gtg act ggc Gly Asn His Gly Ser Gln Lys Glu Thr Asp Leu Ile Thr Val Thr Gly 785 790 795	2882
agc tca ttt ttg gta tga accaac tctattcatt cctcatcatg tggcttactt Ser Ser Phe Leu Val * 800	2936
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gtgaacagtc tccttcaca aaacc atg gcg tcg ctc aaa tgt agc acc gtc      172
                Met Ala Ser Leu Lys Cys Ser Thr Val
                1                      5

gtc tgc gtg atc tgc ttg gag aag ccc aaa tac cgc tgt cca gcc tgc      220
Val Cys Val Ile Cys Leu Glu Lys Pro Lys Tyr Arg Cys Pro Ala Cys
    10                      15                      20                      25

cgc gtg ccc tac tgc tcg gta gtc tgc ttc cgg aag cac aaa gaa cag      268
Arg Val Pro Tyr Cys Ser Val Val Cys Phe Arg Lys His Lys Glu Gln
                30                      35                      40

tgc aac cct gaa act cgt cct gtt gag aaa aaa ata aga tca gct ctt      316
Cys Asn Pro Glu Thr Arg Pro Val Glu Lys Lys Ile Arg Ser Ala Leu
                45                      50                      55

cct acc aaa acc gta aag cct gtg gaa aac aaa gat gat gat gac tct      364
Pro Thr Lys Thr Val Lys Pro Val Glu Asn Lys Asp Asp Asp Asp Ser
                60                      65                      70

ata gct gat ttt ctc aat agt gat gag gaa gaa gac aga gtt tct ttg      412
Ile Ala Asp Phe Leu Asn Ser Asp Glu Glu Glu Asp Arg Val Ser Leu
    75                      80                      85

cag aat tta aag aat tta ggg gaa tct gca aca tta aga agc tta ttg      460
Gln Asn Leu Lys Asn Leu Gly Glu Ser Ala Thr Leu Arg Ser Leu Leu
    90                      95                      100                      105

ctc aat cca cac ctc agg cag ttg atg gtc aac ctc gat cag gga gaa      508
Leu Asn Pro His Leu Arg Gln Leu Met Val Asn Leu Asp Gln Gly Glu
                110                      115                      120

gac aaa gca aag ctc atg aga gct tac atg caa gag cct ttg ttt gtg      556
Asp Lys Ala Lys Leu Met Arg Ala Tyr Met Gln Glu Pro Leu Phe Val
                125                      130                      135

gag ttt gca gac tgc tgt tta gga att gtg gag cca tcc cag aat gag      604
Glu Phe Ala Asp Cys Cys Leu Gly Ile Val Glu Pro Ser Gln Asn Glu
    140                      145                      150

gag tct taa gatggat tattgtgctg cttgctcaag cgtgtgcttg actcctggaa      660

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Glu Ser *
155

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aggcagactt ggggtcctta aggtggcaag tcctttatgg agagaaaact tgacattcag 840
atgattgttt ttaaattgtt tacttttggg acagttgata gacatcataa acgatatcaa 900
gcttacactt catatggagt taaacttggg cagtgttaat aaaatcaaaa cgtgattcta 960
ctgtacattg cattattcat aattttaattg tttgaaatta cattaaataa atcaactaat 1020
taaataactaa agttttgttc ctttttaaag gaaataacca caagattttt ccagagccaa 1080
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gaaacaaagg caccaaggat caccacagcc cagtgaaggc agaagaggtc acgtggatca 1500
gcctgtgtct ttccagcaga atctgattaa agcctgtaat gctgtagggt gaaggttcag 1560
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accgcacgcg atcgat 1636

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acc cag gcc atg agg gac aaa tgt gga gca agg gat gga gct gga act 96
Thr Gln Ala Met Arg Asp Lys Cys Gly Ala Arg Asp Gly Ala Gly Thr
20 25 30

tgc tat tat ggg acg tta aag ctg gca gga cct gag agc ctt aga tgg 144
Cys Tyr Tyr Gly Thr Leu Lys Leu Ala Gly Pro Glu Ser Leu Arg Trp
35 40 45

ctt gcc tta gat ggc gaa agg gat gtt gca gat aca atg aag aat ttt 192
Leu Ala Leu Asp Gly Glu Arg Asp Val Ala Asp Thr Met Lys Asn Phe

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50	55	60	
gag atg cgg att ctc ctg gat tac cca ggt ggg ccc agc aca atc act			240
Glu Met Arg Ile Leu Leu Asp Tyr Pro Gly Gly Pro Ser Thr Ile Thr			
65	70	75	80
gga tca gag aga gta gaa gat gcc tct ttg ctg gct ttg aag atg gag			288
Gly Ser Glu Arg Val Glu Asp Ala Ser Leu Leu Ala Leu Lys Met Glu			
	85	90	95
gaa ggg gct atg agt gaa gga gga ggg aag aat agc cac tgt cta ctg			336
Glu Gly Ala Met Ser Glu Gly Gly Gly Lys Asn Ser His Cys Leu Leu			
	100	105	110
acc tct acc gtg agg ccc aga gca aca gct tac gga gcc agt ggc cca			384
Thr Ser Thr Val Arg Pro Arg Ala Thr Ala Tyr Gly Ala Ser Gly Pro			
	115	120	125
gac cct ggc cca gcc cgt gtg gcc tcc aga cgt ctg ggg gcc gca gtt			432
Asp Pro Gly Pro Ala Arg Val Ala Ser Arg Arg Leu Gly Ala Ala Val			
	130	135	140
ggg ctt ctg agt gca gac acg ctg tgg cct ctc aat ggc ctt gcc agg			480
Gly Leu Leu Ser Ala Asp Thr Leu Trp Pro Leu Asn Gly Leu Ala Arg			
	145	150	155
gca ata gat gag gaa att gag gct ctg aga gat gac tct ggg gac gac			528
Ala Ile Asp Glu Glu Ile Glu Ala Leu Arg Asp Asp Ser Gly Asp Asp			
	165	170	175
gac gag gct acc acc cca gcc gac aag agc gag ctg cac cac acc ctg			576
Asp Glu Ala Thr Thr Pro Ala Asp Lys Ser Glu Leu His His Thr Leu			
	180	185	190
aag aat ctt tcc ctg aag tta gat gac ctc agc acg tgc aat gac ctc			624
Lys Asn Leu Ser Leu Lys Leu Asp Asp Leu Ser Thr Cys Asn Asp Leu			
	195	200	205
atc gcc aag cac ggc gct gca ctc cag cgc tcc ctg aca gag ctg gac			672
Ile Ala Lys His Gly Ala Ala Leu Gln Arg Ser Leu Thr Glu Leu Asp			
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ggc ctc aag atc cca tct gag agt ggg gag aag ctg aag gtg gtg aat			720
Gly Leu Lys Ile Pro Ser Glu Ser Gly Glu Lys Leu Lys Val Val Asn			
	225	230	235
gag cgg gcc acc ctc ttc cgc atc aca tcc aat gct atg atc aac ggc			768
Glu Arg Ala Thr Leu Phe Arg Ile Thr Ser Asn Ala Met Ile Asn Gly			
	245	250	255
gct gca gcc atc ctc acc tca tat cag gaa tgg ctt cag ccc cag ggg			816
Ala Ala Ala Ile Leu Thr Ser Tyr Gln Glu Trp Leu Gln Pro Gln Gly			
	260	265	270
ttt gag gga aca agg tgc tca gag gtg gtt tct gga ttg gga atc tgg			864
Phe Glu Gly Thr Arg Cys Ser Glu Val Val Ser Gly Leu Gly Ile Trp			
	275	280	285
aac agc aac gct gtg ttt caa ccc ccc acg cct tta cca gtg ctg tac			912
Asn Ser Asn Ala Val Phe Gln Pro Pro Thr Pro Leu Pro Val Leu Tyr			
	290	295	300
ctt cta gaa cac ccc ttc ctc acc ctt cag cac agc cag gat ggg gcc			960
Leu Leu Glu His Pro Phe Leu Thr Leu Gln His Ser Gln Asp Gly Ala			

305	310	315	320	
tgg aga agg ccg gca gca gca gag gag acc ctg gga gtc agg gat gga				1008
Trp Arg Arg Pro Ala Ala Ala Glu Glu Thr Leu Gly Val Arg Asp Gly				
	325	330	335	
cac cag gtg agg act ggt gtg ccc atc ttc ctc ctt tgg ggt ggg aca				1056
His Gln Val Arg Thr Gly Val Pro Ile Phe Leu Leu Trp Gly Gly Thr				
	340	345	350	
gcc tgt gat gtg cat gga gct cag tgg gtg ctc cag gcc tgc agg gac				1104
Ala Cys Asp Val His Gly Ala Gln Trp Val Leu Gln Ala Cys Arg Asp				
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ttc ttg gaa cta gca gag ata cac agt cgg aaa tgg cag cgg gca ctg				1152
Phe Leu Glu Leu Ala Glu Ile His Ser Arg Lys Trp Gln Arg Ala Leu				
	370	375	380	
cag tat gag cag gag cag cgc gtg cac ttg gag gaa acc att gag cag				1200
Gln Tyr Glu Gln Glu Gln Arg Val His Leu Glu Glu Thr Ile Glu Gln				
	385	390	395	400
ctg gcg aag cag cac aac agc ctc gag cgg gcc ttc cac agt gcc cct				1248
Leu Ala Lys Gln His Asn Ser Leu Glu Arg Ala Phe His Ser Ala Pro				
	405	410	415	
ggc cgg ccg gcc aac ccc tcc aag agc ttc att gag gga agc ctc ttg				1296
Gly Arg Pro Ala Asn Pro Ser Lys Ser Phe Ile Glu Gly Ser Leu Leu				
	420	425	430	
act ccc aaa gga gag gac agt gag gaa gat gaa gat acc gag tac ttt				1344
Thr Pro Lys Gly Glu Asp Ser Glu Glu Asp Glu Asp Thr Glu Tyr Phe				
	435	440	445	
gat gcc atg gaa gac tcc aca tcc ttc atc acc gtg atc acc gag gcc				1392
Asp Ala Met Glu Asp Ser Thr Ser Phe Ile Thr Val Ile Thr Glu Ala				
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aag gaa gac agc aga aaa gct gaa ggt agc acc ggg aca agt tcc gtg				1440
Lys Glu Asp Ser Arg Lys Ala Glu Gly Ser Thr Gly Thr Ser Ser Val				
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gac tgg agc tca gca gac aat gta cta gat ggt gcc tcg ctc gtg ccc				1488
Asp Trp Ser Ser Ala Asp Asn Val Leu Asp Gly Ala Ser Leu Val Pro				
	485	490	495	
aag ggt tca tcc aaa gtc aag agg cga gtc cgc att ccc aac aag ccc				1536
Lys Gly Ser Ser Lys Val Lys Arg Arg Val Arg Ile Pro Asn Lys Pro				
	500	505	510	
aac tac agc ctt aac ctc tgg agc atc atg aag aac tgc atc ggc cgg				1584
Asn Tyr Ser Leu Asn Leu Trp Ser Ile Met Lys Asn Cys Ile Gly Arg				
	515	520	525	
gag ctc tcc agg atc ccc atg ccg gtg aac ttc aat gag ccc ctg tcc				1632
Glu Leu Ser Arg Ile Pro Met Pro Val Asn Phe Asn Glu Pro Leu Ser				
	530	535	540	
atg ctc cag cgg ctg aca gag gac ctg gag tac cac cac ctg ctg gac				1680
Met Leu Gln Arg Leu Thr Glu Asp Leu Glu Tyr His His Leu Leu Asp				
	545	550	555	560
aag gca gtg cac tgc acc agc tca gtg gag cag atg tgc ctg gtg gcc				1728
Lys Ala Val His Cys Thr Ser Ser Val Glu Gln Met Cys Leu Val Ala				

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gcc ttc tct gtg tcc tcc tac tcc acc aca gtg cac cgc atc gcc aag Ala Phe Ser Val Ser Ser Tyr Ser Thr Thr Val His Arg Ile Ala Lys 580 585 590			1776
ccc ttc aac ccc atg ctg ggg gag acc ttc gag ctg gac cgc ctc gac Pro Phe Asn Pro Met Leu Gly Glu Thr Phe Glu Leu Asp Arg Leu Asp 595 600 605			1824
gac atg ggc ctg cgc tcc ctc tgt gag cag gtg agc cac cac ccc ccc Asp Met Gly Leu Arg Ser Leu Cys Glu Gln Val Ser His His Pro Pro 610 615 620			1872
tca gct gcg cac tac gtg ttc tcc aag cat ggc tgg agc ctc tgg cag Ser Ala Ala His Tyr Val Phe Ser Lys His Gly Trp Ser Leu Trp Gln 625 630 635 640			1920
gag atc acc atc tcc agc aag ttc cgg gga aaa tac atc tcc atc atg Glu Ile Thr Ile Ser Ser Lys Phe Arg Gly Lys Tyr Ile Ser Ile Met 645 650 655			1968
ccg cta ggt gcc atc cac tta gaa ttc cag gcc agt ggg aat cac tac Pro Leu Gly Ala Ile His Leu Glu Phe Gln Ala Ser Gly Asn His Tyr 660 665 670			2016
gtg tgg agg aag agc acc tca act gtt cac aac atc atc gtg ggc aag Val Trp Arg Lys Ser Thr Ser Thr Val His Asn Ile Ile Val Gly Lys 675 680 685			2064
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ctg cgg ccc gac cag cgg ctg atg gag aag ggc cgt tgg gac gag gcc Leu Arg Pro Asp Gln Arg Leu Met Glu Lys Gly Arg Trp Asp Glu Ala			2496

820	825	830	
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Asn Thr Glu Lys Gln Arg Leu Glu Glu Lys Gln Arg Leu Ser Arg Arg			
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cgg cgg ctg gag gcc tgc ggg ccg ggc agc agc tgc agc tcg gag gaa			2592
Arg Arg Leu Glu Ala Cys Gly Pro Gly Ser Ser Cys Ser Ser Glu Glu			
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gaa ggt gta aag gca ttt gac aaa att cag cca gtt tcc agg ggg cac			2640
Glu Gly Val Lys Ala Phe Asp Lys Ile Gln Pro Val Ser Arg Gly His			
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Ser Pro Arg Phe Ile Leu Cys Asp Cys Cys Pro Leu Ala Pro Asn Ser			
885	890	895	
ggc agg act ggc aac tac cgg aag ctc gcg agg ctt cca aag cgc atg			2736
Gly Arg Thr Gly Asn Tyr Arg Lys Leu Ala Arg Leu Pro Lys Arg Met			
900	905	910	
cgc agg tca cgg tac ggg cac gtg cgg cgc gcc agc aaa acc acg cag			2784
Arg Arg Ser Arg Tyr Gly His Val Arg Arg Ala Ser Lys Thr Thr Gln			
915	920	925	
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Ala Ser Cys Arg Phe Arg Leu Glu Arg Val Ala Gly Leu Arg Lys Pro			
930	935	940	
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	Met Gly Ile
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Phe Val Lys Thr Ile Phe Pro Asn Gly Ser Ala Ala Glu Asp Gly Arg	
5	10
ctt aaa gaa ggg gat gaa atc cta gat gta aat gga ata cca ata aag	273
Leu Lys Glu Gly Asp Glu Ile Leu Asp Val Asn Gly Ile Pro Ile Lys	
20	25
	30
	35

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gga tta ttt gtt tta acg gta cgc aca aag ttg gtg agc ccc agc ctc	369
Gly Leu Phe Val Leu Thr Val Arg Thr Lys Leu Val Ser Pro Ser Leu	
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Thr Pro Cys Ser Thr Pro Thr His Met Ser Arg Ser Ala Ser Pro Asn	
70 75 80	
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Phe Asn Thr Ser Gly Gly Ala Ser Ala Gly Gly Ser Asp Glu Gly Ser	
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Ser Ser Ser Leu Gly Arg Lys Thr Pro Gly Pro Lys Asp Arg Ile Val	
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Met Glu Val Thr Leu Asn Lys Glu Pro Arg Val Gly Leu Gly Ile Gly	
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Ala Cys Cys Leu Ala Leu Glu Asn Ser Pro Pro Gly Ile Tyr Ile His	
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Ser Leu Ala Pro Gly Ser Val Ala Lys Met Glu Ser Asn Leu Ser Arg	
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Gly Asp Gln Ile Leu Glu Val Asn Ser Val Asn Val Arg His Ala Ala	
165 170 175	
tta agc aaa gtc cac gcc atc ttg agt aaa tgc cct cca gga ccc gtt	753
Leu Ser Lys Val His Ala Ile Leu Ser Lys Cys Pro Pro Gly Pro Val	
180 185 190 195	
cgc ctt gtc atc ggc cgg cac cct aat cca aag gac tcc ctt att tct	801
Arg Leu Val Ile Gly Arg His Pro Asn Pro Lys Asp Ser Leu Ile Ser	
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gaa tct gaa ctc tcc cag tac ttt gcc cac gat gtc cct ggc ccc ttg	849
Glu Ser Glu Leu Ser Gln Tyr Phe Ala His Asp Val Pro Gly Pro Leu	
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tca gac ttc atg gtg gcc ggt tct gag gac gag gat cac ccg gga agt	897
Ser Asp Phe Met Val Ala Gly Ser Glu Asp Glu Asp His Pro Gly Ser	
230 235 240	
ggc tgc agc acg tgc gag gag ggc agc ctg cct ccc agc acc tcc act	945
Gly Cys Ser Thr Ser Glu Glu Gly Ser Leu Pro Pro Ser Thr Ser Thr	
245 250 255	
cac aag gag cct gga aaa ccc aga gcc aac agc ctc gtg act ctt ggg	993
His Lys Glu Pro Gly Lys Pro Arg Ala Asn Ser Leu Val Thr Leu Gly	
260 265 270 275	
agc cat cgg gct tct ggg ctc ttc cac aag cag gtg aca gtt gcc aga	1041
Ser His Arg Ala Ser Gly Leu Phe His Lys Gln Val Thr Val Ala Arg	
280 285 290	

caa gcc agt ctc ccc gga agc cca cag gcc ctc cga aac cct ctc ctc	1089
Gln Ala Ser Leu Pro Gly Ser Pro Gln Ala Leu Arg Asn Pro Leu Leu	
295 300 305	
cgc cag agg aag gta ggc tgc tac gat gcc aac gat gcc agt gat gag	1137
Arg Gln Arg Lys Val Gly Cys Tyr Asp Ala Asn Asp Ala Ser Asp Glu	
310 315 320	
gaa gag ttt gac aga gaa ggg gac tgc att tca ctc cca ggg gcc ctc	1185
Glu Glu Phe Asp Arg Glu Gly Asp Cys Ile Ser Leu Pro Gly Ala Leu	
325 330 335	
ccg ggt ccc atc agg cct ctg tca gag gat gac ccg agg cgt gtc tca	1233
Pro Gly Pro Ile Arg Pro Leu Ser Glu Asp Pro Arg Arg Val Ser	
340 345 350 355	
att tcc tct tcc aag ggc atg gac gtc cac aac caa gag gaa cga ccc	1281
Ile Ser Ser Ser Lys Gly Met Asp Val His Asn Gln Glu Glu Arg Pro	
360 365 370	
cgg aaa aca ctg gtg agc aag gcc atc tcg gca cct ctt ctt ggt agc	1329
Arg Lys Thr Leu Val Ser Lys Ala Ile Ser Ala Pro Leu Leu Gly Ser	
375 380 385	
tca gtg gac tta gag gag agt atc cca gag ggc atg gtg gat gct gcg	1377
Ser Val Asp Leu Glu Glu Ser Ile Pro Glu Gly Met Val Asp Ala Ala	
390 395 400	
tcc tat gca gcc aac ctc acg gac tct gca gag gcc ccc aag ggg agc	1425
Ser Tyr Ala Ala Asn Leu Thr Asp Ser Ala Glu Ala Pro Lys Gly Ser	
405 410 415	
cct gga agc tgg tgg aag aag gaa ctg tca gga tca agt agc gca ccc	1473
Pro Gly Ser Trp Trp Lys Lys Glu Leu Ser Gly Ser Ser Ser Ala Pro	
420 425 430 435	
aaa ttg gaa tac aca gtc cgt aca gac acc cag agt ccg acg aac act	1521
Lys Leu Glu Tyr Thr Val Arg Thr Asp Thr Gln Ser Pro Thr Asn Thr	
440 445 450	
ggg agc ccc agt tcc ccc cag cag aaa agt gaa ggc ctg ggc tcc agg	1569
Gly Ser Pro Ser Ser Pro Gln Gln Lys Ser Glu Gly Leu Gly Ser Arg	
455 460 465	
cac aga cca gtg gcc agg gta agc ccc cac tgc aag aga tcc gag gct	1617
His Arg Pro Val Ala Arg Val Ser Pro His Cys Lys Arg Ser Glu Ala	
470 475 480	
gag gcc aag ccc agt ggc tca cag aca gtg aac ctg act ggc aga gcc	1665
Glu Ala Lys Pro Ser Gly Ser Gln Thr Val Asn Leu Thr Gly Arg Ala	
485 490 495	
aat gat cca tgc gat ctg gac tcg aga gtc cag gcc act tct gtc aaa	1713
Asn Asp Pro Cys Asp Leu Asp Ser Arg Val Gln Ala Thr Ser Val Lys	
500 505 510 515	
gtg act gtc gct ggc ttt cag cca ggt gga gct gtg gag aag gaa tct	1761
Val Thr Val Ala Gly Phe Gln Pro Gly Gly Ala Val Glu Lys Glu Ser	
520 525 530	
ctg gga aag ctg acc act gga gat gct tgt gtc tct acc agc tgt gaa	1809
Leu Gly Lys Leu Thr Thr Gly Asp Ala Cys Val Ser Thr Ser Cys Glu	
535 540 545	

cta gcc agt gct ctg tcc cat ctg gat gcc agc cac ctc aca gag aac	1857
Leu Ala Ser Ala Leu Ser His Leu Asp Ala Ser His Leu Thr Glu Asn	
550 555 560	
ctg ccc aaa gct gca tca gag ctg ggg caa caa ccc atg act gaa ctg	1905
Leu Pro Lys Ala Ala Ser Glu Leu Gly Gln Gln Pro Met Thr Glu Leu	
565 570 575	
gac agc tcc tcg gac ctc atc tct tcc cca ggg aag aag ggg gcc gct	1953
Asp Ser Ser Ser Asp Leu Ile Ser Ser Pro Gly Lys Lys Gly Ala Ala	
580 585 590 595	
cat cct gac ccc agc aag acc tct gta gac aca ggg aaa gtc agt cgg	2001
His Pro Asp Pro Ser Lys Thr Ser Val Asp Thr Gly Lys Val Ser Arg	
600 605 610	
cca gag aat ccc agc cag cct gca tcg ccc agg gtc gcc aag tgc aag	2049
Pro Glu Asn Pro Ser Gln Pro Ala Ser Pro Arg Val Ala Lys Cys Lys	
615 620 625	
gcc agg tct cca gtc agg ctc ccc cat gag ggc agc ccc tcc cca ggg	2097
Ala Arg Ser Pro Val Arg Leu Pro His Glu Gly Ser Pro Ser Pro Gly	
630 635 640	
gag aaa gca gcg gct ccc cct gac tac agc aag act cga tca gca tcg	2145
Glu Lys Ala Ala Ala Pro Pro Asp Tyr Ser Lys Thr Arg Ser Ala Ser	
645 650 655	
gaa acc agc aca ccc cac aat acc agg agg gtg gct gcc ctc agg gga	2193
Glu Thr Ser Thr Pro His Asn Thr Arg Arg Val Ala Ala Leu Arg Gly	
660 665 670 675	
gcg gga cct gga gca gag gga atg aca cca gct ggt gct gtc ctg cca	2241
Ala Gly Pro Gly Ala Glu Gly Met Thr Pro Ala Gly Ala Val Leu Pro	
680 685 690	
gga gac ccc ctc aca tcc cag gag cag aga cag gga gct cca ggt aac	2289
Gly Asp Pro Leu Thr Ser Gln Glu Gln Arg Gln Gly Ala Pro Gly Asn	
695 700 705	
cac agt aag gct ctg gaa atg aca gga atc cat gca cct gaa agc tcc	2337
His Ser Lys Ala Leu Glu Met Thr Gly Ile His Ala Pro Glu Ser Ser	
710 715 720	
cag gag cct tcc ctg ctg gag gga gca gat tct gtg tcc tca agg gca	2385
Gln Glu Pro Ser Leu Leu Glu Gly Ala Asp Ser Val Ser Ser Arg Ala	
725 730 735	
ccg cag gcc agc ctc tcc atg ctg cca tcc act gac aac acc aaa gaa	2433
Pro Gln Ala Ser Leu Ser Met Leu Pro Ser Thr Asp Asn Thr Lys Glu	
740 745 750 755	
gca tgt ggc cat gtc tcg ggg cac tgc tgc ccg ggg ggg agt aga gag	2481
Ala Cys Gly His Val Ser Gly His Cys Cys Pro Gly Gly Ser Arg Glu	
760 765 770	
agc cct gtg acg gac att gac agc ttc atc aag gag ctg gat gct tct	2529
Ser Pro Val Thr Asp Ile Asp Ser Phe Ile Lys Glu Leu Asp Ala Ser	
775 780 785	
gca gca agg tct ccg tct tcc cag acg ggg gac agt ggc tct cag gag	2577
Ala Ala Arg Ser Pro Ser Ser Gln Thr Gly Asp Ser Gly Ser Gln Glu	
790 795 800	

ggc agt gct cag ggc cac cca cca gcc ggg gct gga ggt ggg agc tcc Gly Ser Ala Gln Gly His Pro Pro Ala Gly Ala Gly Gly Gly Ser Ser 805 810 815	2625
tgc cgt gcc gaa cca gtc ccg ggg ggc cag acc tcc tcc ccg agg agg Cys Arg Ala Glu Pro Val Pro Gly Gly Gln Thr Ser Ser Pro Arg Arg 820 825 830 835	2673
gcc tgg gct gct ggt gcc ccc gcc tac cca caa tgg gcc tcc cag cct Ala Trp Ala Ala Gly Ala Pro Ala Tyr Pro Gln Trp Ala Ser Gln Pro 840 845 850	2721
tcg gtt tta gat tca att aat ccc gac aaa cat ttt act gtg aac aaa Ser Val Leu Asp Ser Ile Asn Pro Asp Lys His Phe Thr Val Asn Lys 855 860 865	2769
aac ttt ctg agc aac tac tct aga aat ttt agc agt ttt cat gaa gac Asn Phe Leu Ser Asn Tyr Ser Arg Asn Phe Ser Ser Phe His Glu Asp 870 875 880	2817
agc acc tcc cta tca gcc ctg ggt gac agc acg gag ccg tct ctg tca Ser Thr Ser Leu Ser Gly Leu Gly Asp Ser Thr Glu Pro Ser Leu Ser 885 890 895	2865
tcc atg tat ggc gat gct gag gat tct tct tct gac cct gag tca ctc Ser Met Tyr Gly Asp Ala Glu Asp Ser Ser Ser Asp Pro Glu Ser Leu 900 905 910 915	2913
act gaa gcc cca cga gct tct gcc agg gac ggc tgg tcc cct cct cgt Thr Glu Ala Pro Arg Ala Ser Ala Arg Asp Gly Trp Ser Pro Pro Arg 920 925 930	2961
tcc cgt gtg tct ttg cac aag gaa gat cct tcg gag tca gaa gag gaa Ser Arg Val Ser Leu His Lys Glu Asp Pro Ser Glu Ser Glu Glu Glu 935 940 945	3009
cag att gag att tgt tcc aca cgt ggc tgc ccc aat cca ccc tcg agt Gln Ile Glu Ile Cys Ser Thr Arg Gly Cys Pro Asn Pro Pro Ser Ser 950 955 960	3057
cct gct cat ctt ccc acc cag gct gcc atc tgt cct gcc tca gcc aaa Pro Ala His Leu Pro Thr Gln Ala Ala Ile Cys Pro Ala Ser Ala Lys 965 970 975	3105
gtt ctg tca tta aaa tac agc act ccg aga gag tcg gtg gcc agt ccc Val Leu Ser Leu Lys Tyr Ser Thr Pro Arg Glu Ser Val Ala Ser Pro 980 985 990 995	3153
cgt gag aag gcc gcc tgc ttg cca ggc tca tac act tca ggc cca gac Arg Glu Lys Ala Ala Cys Leu Pro Gly Ser Tyr Thr Ser Gly Pro Asp 1000 1005 1010	3201
tct tcc cag cca tca tca ctc ttg gag atg agc tct cag gag cat gaa Ser Ser Gln Pro Ser Ser Leu Leu Glu Met Ser Ser Gln Glu His Glu 1015 1020 1025	3249
act cat gcg gac ata agc act tca cag aac cac agg ccc tcg tgt gca Thr His Ala Asp Ile Ser Thr Ser Gln Asn His Arg Pro Ser Cys Ala 1030 1035 1040	3297
gaa gaa acc aca gaa gtc acc agc gct agc tca gcc atg gaa aac agt Glu Glu Thr Thr Glu Val Thr Ser Ala Ser Ser Ala Met Glu Asn Ser 1045 1050 1055	3345

ccg ctg tct aaa gta gcc agg cat ttt cac agt ccg ccc atc att ctc	3393
Pro Leu Ser Lys Val Ala Arg His Phe His Ser Pro Pro Ile Ile Leu	
1060 1065 1070 1075	
agc tcc ccc aac atg gta aat ggc ttg gaa cat gac ctg cta gat gac	3441
Ser Ser Pro Asn Met Val Asn Gly Leu Glu His Asp Leu Leu Asp Asp	
1080 1085 1090	
gaa acc ctg aat caa tac gaa aca agc att aat gca gct gcc agt ctg	3489
Glu Thr Leu Asn Gln Tyr Glu Thr Ser Ile Asn Ala Ala Ala Ser Leu	
1095 1100 1105	
tcc tcc ttc agt gtg gat gtc cct aag aat gga gaa tct gtt ttg gaa	3537
Ser Ser Phe Ser Val Asp Val Pro Lys Asn Gly Glu Ser Val Leu Glu	
1110 1115 1120	
aac ctc cac atc tct gaa agt caa gac ctg gat gac ttg cta cag aaa	3585
Asn Leu His Ile Ser Glu Ser Gln Asp Leu Asp Asp Leu Leu Gln Lys	
1125 1130 1135	
cca aaa atg atc gct agg agg ccc atc atg gcc tgg ttt aaa gaa ata	3633
Pro Lys Met Ile Ala Arg Arg Pro Ile Met Ala Trp Phe Lys Glu Ile	
1140 1145 1150 1155	
aat aaa cat aac caa ggc aca cat ttg agg agc aaa acc gag aag gaa	3681
Asn Lys His Asn Gln Gly Thr His Leu Arg Ser Lys Thr Glu Lys Glu	
1160 1165 1170	
caa cct cta atg cct gcc aga agt ccc gac tcc aag att cag atg gtg	3729
Gln Pro Leu Met Pro Ala Arg Ser Pro Asp Ser Lys Ile Gln Met Val	
1175 1180 1185	
agt tca agc caa aaa aag ggc gtt act gtg cct cat agc cct cct cag	3777
Ser Ser Ser Gln Lys Lys Gly Val Thr Val Pro His Ser Pro Pro Gln	
1190 1195 1200	
ccg aaa aca aac ctg gaa aat aag gac ctg tct aag aag agt ccg gca	3825
Pro Lys Thr Asn Leu Glu Asn Lys Asp Leu Ser Lys Lys Ser Pro Ala	
1205 1210 1215	
gaa atg ctt ctg act aat ggt cag aag gca aag tgt ggt ccg aag ctg	3873
Glu Met Leu Leu Thr Asn Gly Gln Lys Ala Lys Cys Gly Pro Lys Leu	
1220 1225 1230 1235	
aag agg ctc agc ctc aag ggc aag gcc aaa gtc aac tct gag gcc cct	3921
Lys Arg Leu Ser Leu Lys Gly Lys Ala Lys Val Asn Ser Glu Ala Pro	
1240 1245 1250	
gct gcg aat gct gtg aag gct ggg ggg acg gac cac agg aaa ccc ttg	3969
Ala Ala Asn Ala Val Lys Ala Gly Gly Thr Asp His Arg Lys Pro Leu	
1255 1260 1265	
atc tca ccc cag acc tcc cac aaa aca ctt tct aag gca gtg tca cag	4017
Ile Ser Pro Gln Thr Ser His Lys Thr Leu Ser Lys Ala Val Ser Gln	
1270 1275 1280	
cgg ctc cat gta gcc gac cac gag gac cct gac aga aac acc aca gct	4065
Arg Leu His Val Ala Asp His Glu Asp Pro Asp Arg Asn Thr Thr Ala	
1285 1290 1295	
gcc ccc agg tcc ccc cag tgt gtg ctg gaa agc aag cca cct ctt gcc	4113
Ala Pro Arg Ser Pro Gln Cys Val Leu Glu Ser Lys Pro Pro Leu Ala	
1300 1305 1310 1315	

acc tct ggg cca ctg aaa ccc tca gtg tct gac acg agc atc agg aca Thr Ser Gly Pro Leu Lys Pro Ser Val Ser Asp Thr Ser Ile Arg Thr 1320 1325 1330	4161
ttt gtc tcg ccc ctg acc tct ccc aag cct gtt cct gag caa ggc atg Phe Val Ser Pro Leu Thr Ser Pro Lys Pro Val Pro Glu Gln Gly Met 1335 1340 1345	4209
tgg agc agg ttc cac atg gct gtc ctc tct gaa ccc gac aga ggt tgc Trp Ser Arg Phe His Met Ala Val Leu Ser Glu Pro Asp Arg Gly Cys 1350 1355 1360	4257
cca acc acc cct aaa tct cct aag tgt aga gca gag ggc agg gcg ccc Pro Thr Thr Pro Lys Ser Pro Lys Cys Arg Ala Glu Gly Arg Ala Pro 1365 1370 1375	4305
cgt gct gac tcc ggg ccg gtg agt ccg gca gcg tct agg aac ggc atg Arg Ala Asp Ser Gly Pro Val Ser Pro Ala Ala Ser Arg Asn Gly Met 1380 1385 1390 1395	4353
tcc gtg gca ggg aac aga cag agt gag ccg cgc ctg gcc agc cat gtg Ser Val Ala Gly Asn Arg Gln Ser Glu Pro Arg Leu Ala Ser His Val 1400 1405 1410	4401
gca gca gac aca gcc caa ccc agg ccg act ggc gaa aaa gga ggc aac Ala Ala Asp Thr Ala Gln Pro Arg Pro Thr Gly Glu Lys Gly Gly Asn 1415 1420 1425	4449
ata atg gcc agc gat cgc ctc gaa aga aca aac cag ctg aaa atc gtg Ile Met Ala Ser Asp Arg Leu Glu Arg Thr Asn Gln Leu Lys Ile Val 1430 1435 1440	4497
gag att tct gct gaa gca gtg tca gag act gta tgt ggt aac aag cca Glu Ile Ser Ala Glu Ala Val Ser Glu Thr Val Cys Gly Asn Lys Pro 1445 1450 1455	4545
gct gaa agc gac aga ccg gga ggg tgc ttg gcc cag ggc aac tgt cag Ala Glu Ser Asp Arg Arg Gly Gly Cys Leu Ala Gln Gly Asn Cys Gln 1460 1465 1470 1475	4593
gag aag agt gaa atc agg ctc tat cgc cag gtc gca gaa tca tcc aca Glu Lys Ser Glu Ile Arg Leu Tyr Arg Gln Val Ala Glu Ser Ser Thr 1480 1485 1490	4641
agt cat cca tcc tca ctc cca tct cat gcc tcc cag gca gag cag gaa Ser His Pro Ser Ser Leu Pro Ser His Ala Ser Gln Ala Glu Gln Glu 1495 1500 1505	4689
atg tca cga tca ttc agc atg aca aaa ctg gcg tcc tcc tcc tcc tcc Met Ser Arg Ser Phe Ser Met Thr Lys Leu Ala Ser Ser Ser Ser Ser 1510 1515 1520	4737
ctt caa aca gcc att aga aag gca gaa tac tcc cag gga aaa tca agc Leu Gln Thr Ala Ile Arg Lys Ala Glu Tyr Ser Gln Gly Lys Ser Ser 1525 1530 1535	4785
ctg atg tca gac tcc cga ggg gtg ccc aga aac agc att cca ggg ggc Leu Met Ser Asp Ser Arg Gly Val Pro Arg Asn Ser Ile Pro Gly Gly 1540 1545 1550 1555	4833
ccc tcg ggg gag gac cat ctc tac ttc acc cca agg cca gcg acc agg Pro Ser Gly Glu Asp His Leu Tyr Phe Thr Pro Arg Pro Ala Thr Arg 1560 1565 1570	4881

acc tac tcc atg cca gcc cag ttc tca agc cat ttt gga cgg gag ggt	4929
Thr Tyr Ser Met Pro Ala Gln Phe Ser Ser His Phe Gly Arg Glu Gly	
1575 1580 1585	
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His Pro Pro His Ser Leu Gly Arg Ser Arg Asp Ser Gln Val Pro Val	
1590 1595 1600	
aca agc agt gtt gtc ccc gag gca aag gca tcc aga ggt ggt ctt ccc	5025
Thr Ser Ser Val Val Pro Glu Ala Lys Ala Ser Arg Gly Gly Leu Pro	
1605 1610 1615	
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Ser Leu Ala Asn Gly Gln Gly Ile Tyr Ser Val Lys Pro Leu Leu Asp	
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Thr Ser Arg Asn Leu Pro Ala Thr Asp Glu Gly Asp Ile Ile Ser Val	
1640 1645 1650	
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Gln Glu Thr Ser Cys Leu Val Thr Asp Lys Ile Lys Val Thr Arg Arg	
1655 1660 1665	
cac tac tgc tat gag cag aac tgg ccc cat gaa tct acc tca ttt ttc	5217
His Tyr Cys Tyr Glu Gln Asn Trp Pro His Glu Ser Thr Ser Phe Phe	
1670 1675 1680	
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Ser Val Lys Gln Arg Ile Lys Ser Phe Glu Asn Leu Ala Asn Ala Asp	
1685 1690 1695	
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Arg Pro Val Ala Lys Ser Gly Ala Ser Pro Phe Leu Ser Val Ser Ser	
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Lys Pro Pro Ile Gly Arg Arg Ser Ser Gly Ser Ile Val Ser Gly Ser	
1720 1725 1730	
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Leu Gly His Pro Gly Asp Ala Ala Ala Arg Leu Leu Arg Arg Ser Leu	
1735 1740 1745	
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Ser Ser Cys Ser Glu Asn Gln Ser Glu Ala Gly Thr Leu Leu Pro Gln	
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Met Ala Lys Ser Pro Ser Ile Met Thr Leu Thr Ile Ser Arg Gln Asn	
1765 1770 1775	
cca cca gag acc agt agc aag ggc tct gat tcg gaa cta aag aaa tca	5553
Pro Pro Glu Thr Ser Ser Lys Gly Ser Asp Ser Glu Leu Lys Lys Ser	
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Leu Gly Pro Leu Gly Ile Pro Thr Pro Thr Met Thr Leu Ala Ser Pro	
1800 1805 1810	
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Val Lys Arg Asn Lys Ser Ser Val Arg His Thr Gln Pro Ser Pro Val	
1815 1820 1825	

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ttc aaa act gag ctg gag atc acc ccc agg agg tca cct ggc cct cct Phe Lys Thr Glu Leu Glu Ile Thr Pro Arg Arg Ser Pro Gly Pro Pro 1860 1865 1870 1875	5793
gct gga ggc gtt tcg tgt ccc gag aag ggc ggg aac agg gcc tgt cca Ala Gly Gly Val Ser Cys Pro Glu Lys Gly Gly Asn Arg Ala Cys Pro 1880 1885 1890	5841
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gtg gtc atc aag aaa ggg atg gat cag ccc agg ccc tct gcc cgg cag Val Val Ile Lys Lys Gly Met Asp Gln Pro Arg Pro Ser Ala Arg Gln 2055 2060 2065	6369
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tgt gtt gaa gtg ctg aag acc tcg gct ggg ctg gga ctg agt ctg gat Cys Val Glu Val Leu Lys Thr Ser Ala Gly Leu Gly Leu Ser Leu Asp 2100 2105 2110 2115	6513
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ttt gat gcc tgg aat att atg aag tct gtc cca gaa gga cct gtg cag Phe Asp Ala Trp Asn Ile Met Lys Ser Val Pro Glu Gly Pro Val Gln 2165 2170 2175	6705
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<213> Homo sapiens

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<222> (361)..(1566)

<400> 696

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ctgctccagg ccaggcactg ttctaggagc caggatacag aggtggagac agaaacaaac      180
aaaccgataa ctgtatacaa tactctaacg tcagagggac cacagagcac cagcctgcat      240
ggaacttcct tcctcactca gcttcccacg ttgccagctg ggacagggga gatggagtaa      300
ttttgctgtg gaaagacttc acgtcttgcc gaatgaaagt cccgcctgtc tgtcacgctg      360

atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct atg cac      408
Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His
   1             5             10             15

tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc atg acc      456
Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr
           20             25             30

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Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr
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ttc ttt gtg ggt gcc gcc atc ctc tgg ctg ctc tgc tcc cac cgc ccg      552
Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro
           50             55             60

gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg ctc ggc      600
Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly
           65             70             75             80

cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct ccc cca      648
Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro
           85             90             95

caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc gca gac      696
Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp
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ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc agt tac      744
Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr
           115            120            125

ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag gtg gcc      792
Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala
           130            135            140

gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg gcg gag      840
Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu
           145            150            155            160

aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat ggg aaa      888
Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys
           165            170            175

ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc gaa ggc      936

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Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val	
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Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Lys Asp Glu Arg Leu	
210 215 220	
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Tyr Val Gly Gly Leu Lys Glu Trp Thr Thr Thr Gly Asp Val	
225 230 235 240	
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Val Asn Glu Asn Pro Glu Trp Val Lys Val Val Gly Tyr Lys Gly Ser	
245 250 255	
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Val Asp His Glu Asn Trp Val Ser Asn Tyr Asn Ala Leu Arg Ala Ala	
260 265 270	
gcc ggc atc cag ccg cca ggc tac ctc atc cat gag tct gcc tgc tgg	1224
Ala Gly Ile Gln Pro Pro Gly Tyr Leu Ile His Glu Ser Ala Cys Trp	
275 280 285	
agt gac acg ctg cag cgc tgg ttc ttc ctg ccg cgc cgc gcc agc cag	1272
Ser Asp Thr Leu Gln Arg Trp Phe Phe Leu Pro Arg Arg Ala Ser Gln	
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gag cgc tac agc gag aag gac gac gag cgc aag ggc gcc aac ctg ctg	1320
Glu Arg Tyr Ser Glu Lys Asp Asp Glu Arg Lys Gly Ala Asn Leu Leu	
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Leu Ser Ala Ser Pro Asp Phe Gly Asp Ile Ala Val Ser His Val Gly	
325 330 335	
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Ala Val Val Pro Thr His Gly Phe Ser Ser Phe Lys Phe Ile Pro Asn	
340 345 350	
acc gac gac cag atc att gtg gcc ctc aaa tcc gag gag gac agc ggc	1464
Thr Asp Asp Gln Ile Ile Val Ala Leu Lys Ser Glu Glu Asp Ser Gly	
355 360 365	
aga gtc gcc tcc tac atc atg gcc ttc acg ctg gac ggg cgc ttc ctg	1512
Arg Val Ala Ser Tyr Ile Met Ala Phe Thr Leu Asp Gly Arg Phe Leu	
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Leu Pro Glu Thr Lys Ile Gly Ser Val Lys Tyr Glu Gly Ile Glu Phe	
385 390 395 400	
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Ile *	
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tctggacagg gagcccagtc ccgggccccca tagtggtgag ggcactggac ccccgggccc	1736
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<210> 697
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<213> Homo sapiens

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<220>
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<222> (262) .. (1260)

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gatccagaca aaagagaagt aaacctcttc tgttacaatc agttcaggcc aatcactcca 180
caactctgcc ctcccccttac ttgccaagggt tctagcccag tccagagagg tgatgtcaga 240
tccttcagaa actggtctga g atg aat gga gaa gaa gaa tac gga agc gga 291
Met Asn Gly Glu Glu Glu Tyr Gly Ser Gly
1 5 10

agt gcc ggt gga gcg cga gta gga agt ggt gag ttc gga gta gag atg 339
Ser Ala Gly Gly Ala Arg Val Gly Ser Gly Glu Phe Gly Val Glu Met
15 20 25

gcc gcg ctt gca ccg ctg ccc ccg ctc ccc gca cag ttc aag agc ata 387
Ala Ala Leu Ala Pro Leu Pro Pro Leu Pro Ala Gln Phe Lys Ser Ile
30 35 40

cag cat cat ctg agg acg gct cag gag cat gac aag cga gac cct gtg 435
Gln His His Leu Arg Thr Ala Gln Glu His Asp Lys Arg Asp Pro Val
45 50 55

gtg gct tat tac tgt cgt tta tac gca atg cag act gga atg aag atc 483
Val Ala Tyr Tyr Cys Arg Leu Tyr Ala Met Gln Thr Gly Met Lys Ile
60 65 70

gat agt aaa act cct gaa tgt cgc aaa ttt tta tca aag tta atg gat 531
Asp Ser Lys Thr Pro Glu Cys Arg Lys Phe Leu Ser Lys Leu Met Asp
75 80 85 90

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cag tta gaa gct cta aag aag cag ttg ggt gat aat gaa gct att act Gln Leu Glu Ala Leu Lys Lys Gln Leu Gly Asp Asn Glu Ala Ile Thr 95 100 105	579
caa gaa ata gtg ggc tgt gcc cat ttg gag aat tat gct ttg aaa atg Gln Glu Ile Val Gly Cys Ala His Leu Glu Asn Tyr Ala Leu Lys Met 110 115 120	627
ttt ttg tat gca gac aat gaa gat cgt gct gga cga ttt cac aaa aac Phe Leu Tyr Ala Asp Asn Glu Asp Arg Ala Gly Arg Phe His Lys Asn 125 130 135	675
atg atc aag tcc ttc tat act gca agt ctt ttg ata gat gtc ata aca Met Ile Lys Ser Phe Tyr Thr Ala Ser Leu Leu Ile Asp Val Ile Thr 140 145 150	723
gta ttt gga gaa ctc act gat gaa aat gtg aaa cac agg aag tat gcc Val Phe Gly Glu Leu Thr Asp Glu Asn Val Lys His Arg Lys Tyr Ala 155 160 165 170	771
aga tgg aag gca aca tac atc cat aat tgt tta aag aat ggg gag act Arg Trp Lys Ala Thr Tyr Ile His Asn Cys Leu Lys Asn Gly Glu Thr 175 180 185	819
cct caa gca ggc cct gtt gga att gaa gaa gat aat gat att gaa gaa Pro Gln Ala Gly Pro Val Gly Ile Glu Glu Asp Asn Asp Ile Glu Glu 190 195 200	867
aat gaa gat gct gga gca gcc tct ctg ccc act cag cca act cag cca Asn Glu Asp Ala Gly Ala Ala Ser Leu Pro Thr Gln Pro Thr Gln Pro 205 210 215	915
tca tca tct tca act tat gac cca agc aac atg cca tca ggc aac tat Ser Ser Ser Thr Tyr Asp Pro Ser Asn Met Pro Ser Gly Asn Tyr 220 225 230	963
act gga ata cag att cct ccg ggt gca cac gct cca gct aat aca cca Thr Gly Ile Gln Ile Pro Pro Gly Ala His Ala Pro Ala Asn Thr Pro 235 240 245 250	1011
gca gaa gtg cct cac agc aca ggt gta gca agt aat act atc caa cct Ala Glu Val Pro His Ser Thr Gly Val Ala Ser Asn Thr Ile Gln Pro 255 260 265	1059
act cca cag act ata cct gcc att gat ccc gca ctt ttc aat aca att Thr Pro Gln Thr Ile Pro Ala Ile Asp Pro Ala Leu Phe Asn Thr Ile 270 275 280	1107
tcc cag ggg gat gtt cgt cta acc cca gaa gac ttt gct aga gct cag Ser Gln Gly Asp Val Arg Leu Thr Pro Glu Asp Phe Ala Arg Ala Gln 285 290 295	1155
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act gct gtc cag aat cta caa aag gct ctc aag tta ctg acg aca ggc Thr Ala Val Gln Asn Leu Gln Lys Ala Leu Lys Leu Leu Thr Thr Gly 315 320 325 330	1251
aga gaa tga agccttt gtatgacaga cccatgtatt tttggcatga ggaactaaca Arg Glu *	1307

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<212> DNA
<213> Homo sapiens
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<222> (23) .. (964)
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			1				5				10						
tgg	cag	cag	tgg	cgg	cga	tgt	ttg	tcg	gct	cgg	gat	ggg	tcc	agg	agg		100
Trp	Gln	Gln	Trp	Arg	Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Arg		
				15					20					25			
tta	ctc	ctt	ctt	ctt	ttg	ttg	ggg	tct	ggg	cag	ggg	cca	cag	caa	gtc		148
Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val		
				30				35					40				
ggg	gcg	ggt	caa	acg	ttc	gag	tac	ttg	aaa	cgg	gag	cac	tcg	ctg	tcg		196
Gly	Ala	Gly	Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser		
			45				50					55					
aag	ccc	tac	cag	ggt	gag	gcg	ccc	agg	cca	tgt	ttc	ctg	aga	gac	tgg		244
Lys	Pro	Tyr	Gln	Gly	Glu	Ala	Pro	Arg	Pro	Cys	Phe	Leu	Arg	Asp	Trp		
	60					65					70						

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Glu Leu Gln Val His Phe Lys Ile His Gly Gln Gly Lys Lys Asn Leu	
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cat ggg gat ggc ttg gca atc tgg tac aca aag gat cgg atg cag cca	340
His Gly Asp Gly Leu Ala Ile Trp Tyr Thr Lys Asp Arg Met Gln Pro	
95 100 105	
ggg cct gtg ttt gga aac atg gac aaa ttt gtg ggg ctg gga gta ttt	388
Gly Pro Val Phe Gly Asn Met Asp Lys Phe Val Gly Leu Gly Val Phe	
110 115 120	
gta gac acc tac ccc aat gag gag aag cag caa gag cgg gta ttc ccc	436
Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg Val Phe Pro	
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Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Glu	
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cgg gat ggg cgg cct aca gag ctg gga ggc tgc aca gcc att gtc cgc	532
Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala Ile Val Arg	
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Asn Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His	
175 180 185	
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Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys	
190 195 200	
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Ile Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr	
205 210 215	
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Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu	
220 225 230	
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Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu	
235 240 245 250	
cat cga gat gtg ttc ttg ccc tca gtg gac aat atg aag ctg cct gag	820
His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro Glu	
255 260 265	
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Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile	
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Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val Ile Gly Ile	
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Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys Arg Phe Tyr *	
300 305 310	
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 <213> Homo sapiens

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 Met Gln Pro Pro Pro Gly Pro Leu Gly Asp Cys Leu Arg Asp Trp
 1 5 10 15
 gag gat cta cag cag gac ttc cag aac atc cag gag acc cat cgg ctc 152
 Glu Asp Leu Gln Gln Asp Phe Gln Asn Ile Gln Glu Thr His Arg Leu
 20 25 30
 tac cgc ctg aag ctg gag gag ctg acc aaa ctt cag aac aat tgc acc 200
 Tyr Arg Leu Lys Leu Glu Glu Leu Thr Lys Leu Gln Asn Asn Cys Thr
 35 40 45
 agc tcc atc acg cgg cag aag aag cgg ctc cag gag ctg gcc ctc gcc 248
 Ser Ser Ile Thr Arg Gln Lys Lys Arg Leu Gln Glu Leu Ala Leu Ala
 50 55 60
 ctg aag aaa tgc aaa ccc tcc ctc cca gca gag gcc gag ggg gcc gca 296
 Leu Lys Lys Cys Lys Pro Ser Leu Pro Ala Glu Ala Glu Gly Ala Ala
 65 70 75 80
 cag gag ctg gag aac cag atg aaa gag cgc caa ggc ctc ttc ttt gac 344
 Gln Glu Leu Glu Asn Gln Met Lys Glu Arg Gln Gly Leu Phe Phe Asp
 85 90 95
 atg gag gcc tat ttg cct aag aag aat gga ttg tac ctg agc ctg gtt 392
 Met Glu Ala Tyr Leu Pro Lys Lys Asn Gly Leu Tyr Leu Ser Leu Val
 100 105 110
 ctg ggg aac gtc aac gtc acg ctc ctg agc aag cag gct aag ttt gcc 440
 Leu Gly Asn Val Asn Val Thr Leu Leu Ser Lys Gln Ala Lys Phe Ala
 115 120 125
 tac aag gac gag tat gag aag ttc aag ctc tac ctc acc atc atc ctc 488
 Tyr Lys Asp Glu Tyr Glu Lys Phe Lys Leu Tyr Leu Thr Ile Ile Leu
 130 135 140
 atc ctc atc tcc ttc act tgc cgc ttc ctg ctc aac tcc agg gtg aca 536
 Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu Leu Asn Ser Arg Val Thr
 145 150 155 160

gat gct gcc ttc aac ttc ctg ctg gtc tgg tac tac tgc acc ctg acc	584
Asp Ala Ala Phe Asn Phe Leu Leu Val Trp Tyr Tyr Cys Thr Leu Thr	
165 170 175	
atc cgg gag agc atc ctc atc aac aac ggc tcc cgg atc aaa ggc tgg	632
Ile Arg Glu Ser Ile Leu Ile Asn Asn Gly Ser Arg Ile Lys Gly Trp	
180 185 190	
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Trp Val Phe His His Tyr Val Ser Thr Phe Leu Ser Gly Val Met Leu	
195 200 205	
acg tgg ccc gac ggt ctc atg tac cag aaa ttc cgg aac caa ttc ctc	728
Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys Phe Arg Asn Gln Phe Leu	
210 215 220	
tcc ttt tcc atg tac cag agc ttc gtg cag ttt ctc cag tac tac tac	776
Ser Phe Ser Met Tyr Gln Ser Phe Val Gln Phe Leu Gln Tyr Tyr Tyr	
225 230 235 240	
cag agc ggc tgc ctc tac cgc ctg cgg gcg ctg ggc gag cgg cac acc	824
Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala Leu Gly Glu Arg His Thr	
245 250 255	
atg gac ctc act gtg gag ggc ttc cag tcc tgg atg tgg cgg ggc ctc	872
Met Asp Leu Thr Val Glu Gly Phe Gln Ser Trp Met Trp Arg Gly Leu	
260 265 270	
acc ttc ctg ctg cct ttt ctt ttc ttt gga cac ttc tgg cag ctt ttt	920
Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly His Phe Trp Gln Leu Phe	
275 280 285	
aac gcg ctg acg ttg ttc aac ctg gcc cag gac cct cag tgc aag gag	968
Asn Ala Leu Thr Leu Phe Asn Leu Ala Gln Asp Pro Gln Cys Lys Glu	
290 295 300	
tgg cag gtg ctt atg tgc ggc ttt ccc ttc ctc ctc ctt ttc ctc ggc	1016
Trp Gln Val Leu Met Cys Gly Phe Pro Phe Leu Leu Leu Phe Leu Gly	
305 310 315 320	
aat ttc ttc acc acc ctg agg gtt gtg cac cag ctc cat cac gcg gca	1064
Asn Phe Phe Thr Thr Leu Arg Val Val His Gln Leu His His Ala Ala	
325 330 335	
gaa gaa gcg gct cca gga gct ggg cct tcc cct gaa gaa atg caa acc	1112
Glu Glu Ala Ala Pro Gly Ala Gly Pro Ser Pro Glu Glu Met Gln Thr	
340 345 350	
ctc cct ccc agc aga ggc cga ggg ggc cgc aca gga gct gga gaa cca	1160
Leu Pro Pro Ser Arg Gly Arg Gly Gly Arg Thr Gly Ala Gly Glu Pro	
355 360 365	
gat gaa aga gcg cca agg cct ctt ctt tga c atggaggcct atttgcctaa	1211
Asp Glu Arg Ala Pro Arg Pro Leu Leu *	
370 375	
gaagaatgga ttgtacctga gcttggttct gggaacgtc aacgtcacgc tcctgagcaa	1271
gcaggctaag ttgtacctga aggacgagta tgagaagttc aagctctacc tcaccatcat	1331
cctcatcctc atctccttca cttgccgctt cctgctcaac tccaggggtga cagatgctgc	1391
cttcaacttc ctgctggtct ggtactactg caccctgacc atccgggaga gcacccatcat	1451

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caacaacggc tcccgggtggg cagggcgggc cctgagggag gggagcatgg aatgggggtgc 1511
caggaccctc cggaagcag gaacaggcgc tgggggtgat ggtggctctc tgctccagga 1571
tcaaaggctg gtgggtgttc catcactacg tgtccacctt cctgtcggga gtcattgtga 1631
cgtggcccgga cggtctcatg taccagaaat tccggaacca attcctctcc ttttccatgt 1691
accagagctt cgtcgagtgt ctccagtact actaccagag cggctgcctc taccgcctgc 1751
ggcgctgggc gagcggcaca ccatggacct cactgtggag ggcttccagt cctggatgtg 1811
gcggggcctc accttctgc tgctttttct tttctttgga cacttctggc agcttttttaa 1871
cgcgctgacg ttgttcaacc tggcccagga ccctcagtgc aaggagtggc aggtgcttat 1931
gtgcggcttt cccttccttc tccttttctt cggcaatttc ttcaccaccc tgtgtgttgt 1991
gcaccacaag tttcacagtc agcggcacgg gagcaagaag gattgaggct gggccttccc 2051
ctgccggccc agaggggctt ctgtcctgtg tgttgtggga ggggatggga ggcgccctc 2111
gagtgtgcgt gtatcagggg gtctcttcta ttctccttg ggttttatgg gcgctgtggg 2171
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aaaaa 2236

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<210> 700
<211> 963
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (214) .. (798)

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cattatgcct taaaaactta cacagtgttt tgggaattcc aaagtactca gtggagagag 180
gtgtttcagg agccgtagag ccagatcgtc atc atg tct gca ttg tgg ctg ctg 234
                               Met Ser Ala Leu Trp Leu Leu
                               1                               5
ctg ggc ctc ctt gcc ctg atg gac ttg tct gaa agc agc aac tgg gga 282
Leu Gly Leu Leu Ala Leu Met Asp Leu Ser Glu Ser Ser Asn Trp Gly
      10                      15                      20
tgc tat gga aac atc caa agc ctg gac acc cct gga gca tct tgt ggg 330
Cys Tyr Gly Asn Ile Gln Ser Leu Asp Thr Pro Gly Ala Ser Cys Gly
      25                      30                      35
att gga aga cgt cac ggc ctg aac tac tgt gga gtt cgt gct tct gaa 378
Ile Gly Arg Arg His Gly Leu Asn Tyr Cys Gly Val Arg Ala Ser Glu
      40                      45                      50                      55

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agg ctg gct gaa ata gac atg cca tac ctc ctg aaa tat caa ccc atg      426
Arg Leu Ala Glu Ile Asp Met Pro Tyr Leu Leu Lys Tyr Gln Pro Met
          60                      65                      70

atg caa acc att ggc caa aag tac tgc atg gat cct gcc gtg atc gct      474
Met Gln Thr Ile Gly Gln Lys Tyr Cys Met Asp Pro Ala Val Ile Ala
          75                      80                      85

ggg gtc ttg tcc agg aag tct ccc ggt gac aaa att ctg gtc aac atg      522
Gly Val Leu Ser Arg Lys Ser Pro Gly Asp Lys Ile Leu Val Asn Met
          90                      95                      100

ggc gat agg act agc atg gtg cag gac cct ggc tct caa gct ccc aca      570
Gly Asp Arg Thr Ser Met Val Gln Asp Pro Gly Ser Gln Ala Pro Thr
        105                      110                      115

tcc tgg att agt gag tct cag gtt tcc cag aca act gaa gtt ctg act      618
Ser Trp Ile Ser Glu Ser Gln Val Ser Gln Thr Thr Glu Val Leu Thr
        120                      125                      130                      135

act aga atc aaa gaa atc cag agg agg ttt cca acc tgg acc cct gac      666
Thr Arg Ile Lys Glu Ile Gln Arg Arg Phe Pro Thr Trp Thr Pro Asp
          140                      145                      150

cag tac ctg aga ggt gga ctc tgt gcc tac agt ggg ggt gct ggc tat      714
Gln Tyr Leu Arg Gly Gly Leu Cys Ala Tyr Ser Gly Gly Ala Gly Tyr
          155                      160                      165

gtc cga agc agc cag gac ctg agc tgt gac ttc tgc aat gat gtc ctt      762
Val Arg Ser Ser Gln Asp Leu Ser Cys Asp Phe Cys Asn Asp Val Leu
        170                      175                      180

gca cga gcc aag tac ctc aag aga cat ggc ttc taa catc tcagatgaaa      812
Ala Arg Ala Lys Tyr Leu Lys Arg His Gly Phe *
        185                      190                      195

cccaagacca tgatcacata tgcagcctca aatgttacac agataaaaact agccaagggc      872

acctgtaact gggaatctga gtttgaccta aaagtcatta aaataacatg aatcacatta      932

aaggaagaat tttgacctgc aaaaaaaaaa a      963

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<210> 701
 <211> 975
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (28)..(714)

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Met Lys Ile Lys Pro Gly Phe Met
          1                      5

ggg aag gcc act cca ccc tat gac gtc cag ttt cat atg gag gcc tca      99
Gly Lys Ala Thr Pro Pro Tyr Asp Val Gln Phe His Met Glu Ala Ser
        10                      15                      20

gtt gaa aac tgc att att gtg agc atg aac acc gct gac cct ggc agc      147

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Val	Glu	Asn	Cys	Ile	Ile	Val	Ser	Met	Asn	Thr	Ala	Asp	Pro	Gly	Ser		
25					30					35					40		
cag	ggc	atc	aca	cac	agc	ctc	ttg	cta	cag	gtc	att	gat	gac	aag	ggc	195	
Gln	Gly	Ile	Thr	His	Ser	Leu	Leu	Leu	Gln	Val	Ile	Asp	Asp	Lys	Gly		
				45					50					55			
agc	atc	ctg	cca	cct	aac	aca	gaa	gga	aac	att	ggc	atc	aga	atc	aaa	243	
Ser	Ile	Leu	Pro	Pro	Asn	Thr	Glu	Gly	Asn	Ile	Gly	Ile	Arg	Ile	Lys		
			60					65					70				
cct	gtc	agg	cct	gtg	agc	ctc	ttc	atg	tgc	tat	gag	ggg	gac	cca	gag	291	
Pro	Val	Arg	Pro	Val	Ser	Leu	Phe	Met	Cys	Tyr	Glu	Gly	Asp	Pro	Glu		
		75					80					85					
aag	aca	gct	aaa	gtg	gaa	tgt	ggg	gac	ttc	tac	aac	act	ggg	gac	aga	339	
Lys	Thr	Ala	Lys	Val	Glu	Cys	Gly	Asp	Phe	Tyr	Asn	Thr	Gly	Asp	Arg		
	90					95					100						
gga	aag	atg	gat	gaa	gag	ggc	tac	att	tgt	ttc	ctg	ggg	agg	agt	gat	387	
Gly	Lys	Met	Asp	Glu	Glu	Gly	Tyr	Ile	Cys	Phe	Leu	Gly	Arg	Ser	Asp		
105					110					115				120			
gac	atc	att	aat	gcc	tct	ggg	tat	cgc	atc	ggg	cct	gca	gag	gtt	gaa	435	
Asp	Ile	Ile	Asn	Ala	Ser	Gly	Tyr	Arg	Ile	Gly	Pro	Ala	Glu	Val	Glu		
				125				130						135			
agc	gct	ttg	gtg	gag	cac	cca	gcg	gtg	gcg	gag	tca	gcc	gtg	gtg	ggc	483	
Ser	Ala	Leu	Val	Glu	His	Pro	Ala	Val	Ala	Glu	Ser	Ala	Val	Val	Gly		
			140					145					150				
agc	cca	gac	ccg	att	cga	ggg	gag	gtg	gtg	aag	gcc	ttt	att	gtc	ctg	531	
Ser	Pro	Asp	Pro	Ile	Arg	Gly	Glu	Val	Val	Lys	Ala	Phe	Ile	Val	Leu		
		155					160					165					
acc	cca	cag	ttc	ctg	tcc	cat	gac	aag	gat	cag	ctg	acc	aag	gaa	ctg	579	
Thr	Pro	Gln	Phe	Leu	Ser	His	Asp	Lys	Asp	Gln	Leu	Thr	Lys	Glu	Leu		
		170				175					180						
cag	cag	cat	gtc	aag	tca	gtg	aca	gcc	cca	tac	aag	tac	cca	agg	aag	627	
Gln	Gln	His	Val	Lys	Ser	Val	Thr	Ala	Pro	Tyr	Lys	Tyr	Pro	Arg	Lys		
185					190					195				200			
gtg	gag	ttt	gtc	tca	gag	ctg	cca	aaa	acc	atc	act	ggc	aag	att	gaa	675	
Val	Glu	Phe	Val	Ser	Glu	Leu	Pro	Lys	Thr	Ile	Thr	Gly	Lys	Ile	Glu		
				205					210					215			
cgg	aag	gaa	ctt	cgg	aaa	aag	gag	act	ggg	cag	atg	taa	tcggcagtga			724	
Arg	Lys	Glu	Leu	Arg	Lys	Lys	Glu	Thr	Gly	Gln	Met	*					
			220					225									
actcagaacg	cactgcacac	ctgaggcaaa	tccttgccca	ctttagtctc	cccactatgg											784	
tgaggacgag	ggtggggcat	tgagagtgtt	gatttgggaa	agtatcagga	gtgccatgat											844	
tccaatgttt	tccttctttt	aaattaaatt	cagttgctct	gcttctctca	agtcctctgt											904	
atcttttagaa	tttcccaggt	gagcactcat	aacgcaagta	ataaaaatact	gatatcaaca											964	
aaaaaaaaa	a															975	

<210> 702
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (224) .. (811)

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 aatgaccaaa agcatcaggt tccctgccct ggagcactgc tatactggcg gggagggtcgt 120
 gttgcccaag gatcaggagg agtggaaaag acggacgggc cttctgctct acgagaacta 180
 tgggcagtcg gaaacgggac taatttgtgc cacctactgg gga atg aag atc aag 235
 Met Lys Ile Lys
 1
 ccg ggt ttc atg ggg aag gcc act cca ccc tat gac gtc cag gtc att 283
 Pro Gly Phe Met Gly Lys Ala Thr Pro Pro Tyr Asp Val Gln Val Ile
 5 10 15 20
 gat gac aag ggc agc atc ctg cca cct aac aca gaa gga aac att ggc 331
 Asp Asp Lys Gly Ser Ile Leu Pro Pro Asn Thr Glu Gly Asn Ile Gly
 25 30 35
 atc aga atc aaa cct gtc agg cct gtg agc ctc ttc atg tgc tat gag 379
 Ile Arg Ile Lys Pro Val Arg Pro Val Ser Leu Phe Met Cys Tyr Glu
 40 45 50
 ggt gac cca gag aag aca gct aaa gtg gaa tgt ggg gac ttc tac aac 427
 Gly Asp Pro Glu Lys Thr Ala Lys Val Glu Cys Gly Asp Phe Tyr Asn
 55 60 65
 act ggg gac aga gga aag atg gat gaa gag ggc tac att tgt ttc ctg 475
 Thr Gly Asp Arg Gly Lys Met Asp Glu Glu Gly Tyr Ile Cys Phe Leu
 70 75 80
 ggg agg agt gat gac atc att aat gcc tct ggg tat cgc atc ggg cct 523
 Gly Arg Ser Asp Asp Ile Ile Asn Ala Ser Gly Tyr Arg Ile Gly Pro
 85 90 95 100
 gca gag gtt gaa agc gct ttg gtg gag cac cca gcg gtg gcg gag tca 571
 Ala Glu Val Glu Ser Ala Leu Val Glu His Pro Ala Val Ala Glu Ser
 105 110 115
 gcc gtg gtg ggc agc cca gac ccg att cga ggg gag gtg gtg aag gcc 619
 Ala Val Val Gly Ser Pro Asp Pro Ile Arg Gly Glu Val Val Lys Ala
 120 125 130
 ttt att gtc ctg acc cca cag ttc ctg tcc cat gac aag gat cag ctg 667
 Phe Ile Val Leu Thr Pro Gln Phe Leu Ser His Asp Lys Asp Gln Leu
 135 140 145
 acc aag gaa ctg cag cag cat gtc aag tca gtg aca gcc cca tac aag 715
 Thr Lys Glu Leu Gln Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys
 150 155 160
 tac cca agg aag gtg gag ttt gtc tca gag ctg cca aaa acc atc act 763
 Tyr Pro Arg Lys Val Glu Phe Val Ser Glu Leu Pro Lys Thr Ile Thr
 165 170 175 180

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ggc aag att gaa cgg aag gaa ctt cgg aaa aag gag act ggt cag atg      811
Gly Lys Ile Glu Arg Lys Glu Leu Arg Lys Lys Glu Thr Gly Gln Met
185                               190                               195

taatcggcag tgaactcaga acgcactgca cacctgagggc aaatccctgg ccactttagt    871

ctccccacta tgggtgaggac gaggggtgggg cattgagagt gttgatttgg gaaagtatca    931

ggagtgccat gattccaatg ttttccttct tttaaattaa attcagttgc tctgcttctt    991

ccaagtcttc tgtatcttta gaatttccca ggtgagcact cataacgcaa gtaataaaat    1051

actgatatca acaaaaaaaaa aaaa                                           1075

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<210> 703
<211> 2338
<212> DNA
<213> Homo sapiens

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<220>
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<222> (104)..(2212)

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<400> 703
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gcctcgggggc tcattgtgcgg agcccacttt tactgatacg gga  atg gtg gct cac    115
Met Val Ala His
1

ata aac aac agc cgg ctc aag gcc aag ggc gtg ggc cag cac gac aac    163
Ile Asn Asn Ser Arg Leu Lys Ala Lys Gly Val Gly Gln His Asp Asn
5 10 15 20

gcc cag aac ttt ggt aac cag agc ttt gag gag ctg cga gca gcc tgt    211
Ala Gln Asn Phe Gly Asn Gln Ser Phe Glu Glu Leu Arg Ala Ala Cys
25 30 35

cta aga aag ggg gag ctc ttc gag gac ccc tta ttc cct gct gaa ccc    259
Leu Arg Lys Gly Glu Leu Phe Glu Asp Pro Leu Phe Pro Ala Glu Pro
40 45 50

agc tca ctg ggc ttc aag gac ctg ggc ccc aac tcc aaa aat gtg cag    307
Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser Lys Asn Val Gln
55 60 65

aac atc tcc tgg cag cgg ccc aag gat atc ata aac aac cct cta ttc    355
Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn Asn Pro Leu Phe
70 75 80

atc atg gat ggg att tct cca aca gac atc tgc cag ggg atc ctc ggg    403
Ile Met Asp Gly Ile Ser Pro Thr Asp Ile Cys Gln Gly Ile Leu Gly
85 90 95 100

gac tgc tgg ctg ctg gct gcc atc ggc tcc ctt acc acc tgc ccc aaa    451
Asp Cys Trp Leu Leu Ala Ala Ile Gly Ser Leu Thr Thr Cys Pro Lys
105 110 115

ctg cta tac cgc gtg gtg ccc aga gga cag agc ttc aag aaa aac tat    499
Leu Leu Tyr Arg Val Val Pro Arg Gly Gln Ser Phe Lys Lys Asn Tyr
120 125 130

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gct ggc atc ttc cat ttt cag att tgg cag ttt gga cag tgg gtg aac	547
Ala Gly Ile Phe His Phe Gln Ile Trp Gln Phe Gly Gln Trp Val Asn	
135 140 145	
gtg gtg gta gat gac cgg ctg ccc aca aag aat gac aag ctg gtg ttt	595
Val Val Val Asp Asp Arg Leu Pro Thr Lys Asn Asp Lys Leu Val Phe	
150 155 160	
gtg cac tca acc gaa cgc agt gag ttc tgg agt gcc ctg ctg gag aag	643
Val His Ser Thr Glu Arg Ser Glu Phe Trp Ser Ala Leu Leu Glu Lys	
165 170 175 180	
gcg tat gcc aag ctg agt ggg tcc tat gaa gca ttg tca ggg ggc agt	691
Ala Tyr Ala Lys Leu Ser Gly Ser Tyr Glu Ala Leu Ser Gly Gly Ser	
185 190 195	
acc atg gag ggc ctt gag gac ttc aca gga ggc gtg gcc cag agc ttc	739
Thr Met Glu Gly Leu Glu Asp Phe Thr Gly Gly Val Ala Gln Ser Phe	
200 205 210	
caa ctc cag agg ccc cct cag aac ctg ctc agg ctc ctt agg aag gcc	787
Gln Leu Gln Arg Pro Pro Gln Asn Leu Leu Arg Leu Leu Arg Lys Ala	
215 220 225	
gtg gag cga tcc tcc ctc atg ggt tgc tcc att gaa gtc acc agt gat	835
Val Glu Arg Ser Ser Leu Met Gly Cys Ser Ile Glu Val Thr Ser Asp	
230 235 240	
agt gaa ctg gaa tcc atg act gac aag atg ctg gtg aga ggg cac gct	883
Ser Glu Leu Glu Ser Met Thr Asp Lys Met Leu Val Arg Gly His Ala	
245 250 255 260	
tac tct gtg act ggc ctt cag gat gtc cac tac aga ggc aaa atg gaa	931
Tyr Ser Val Thr Gly Leu Gln Asp Val His Tyr Arg Gly Lys Met Glu	
265 270 275	
aca ctg att cgg gtc cgg aat ccc tgg ggc cgg att gag tgg aat gga	979
Thr Leu Ile Arg Val Arg Asn Pro Trp Gly Arg Ile Glu Trp Asn Gly	
280 285 290	
gct tgg agt gac agt gcc agg gag tgg gaa gag gtg gcc tca gac atc	1027
Ala Trp Ser Asp Ser Ala Arg Glu Trp Glu Glu Val Ala Ser Asp Ile	
295 300 305	
cag atg cag ctg ctg cac aag acg gag gac ggg gag ttc tgg atg tcc	1075
Gln Met Gln Leu Leu His Lys Thr Glu Asp Gly Glu Phe Trp Met Ser	
310 315 320	
tac caa gat ttc ctg aac aac ttc acg ctc ctg gag atc tgc aac ctc	1123
Tyr Gln Asp Phe Leu Asn Asn Phe Thr Leu Leu Glu Ile Cys Asn Leu	
325 330 335 340	
acg cct gat aca ctc tct ggg gac tac aag agc tac tgg cac acc acc	1171
Thr Pro Asp Thr Leu Ser Gly Asp Tyr Lys Ser Tyr Trp His Thr Thr	
345 350 355	
ttc tac gag ggc agc tgg cgc aga ggc agc tcc gca ggg ggc tgc agg	1219
Phe Tyr Glu Gly Ser Trp Arg Arg Gly Ser Ser Ala Gly Gly Cys Arg	
360 365 370	
aac cac cct ggc acg ttc tgg acc aac ccc cag ttt aag atc tct ctt	1267
Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe Lys Ile Ser Leu	
375 380 385	

cct gag ggg gat gac cca gag gat gac gca gag ggc aat gtt gtg gtc	1315
Pro Glu Gly Asp Asp Pro Glu Asp Asp Ala Glu Gly Asn Val Val Val	
390 395 400	
tgc acc tgc ctg gtg gcc cta atg cag aag aac tgg cgg cat gca cgg	1363
Cys Thr Cys Leu Val Ala Leu Met Gln Lys Asn Trp Arg His Ala Arg	
405 410 415 420	
cag cag gga gcc cag ctg cag acc att ggc ttt gtc ctc tac gcg gtc	1411
Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly Phe Val Leu Tyr Ala Val	
425 430 435	
cca aaa gag ttt cag aac att cag gat gtc cac ttg aag aag gaa ttc	1459
Pro Lys Glu Phe Gln Asn Ile Gln Asp Val His Leu Lys Lys Glu Phe	
440 445 450	
ttc acg aag tat cag gac cac ggc ttc tca gag atc ttc acc aac tca	1507
Phe Thr Lys Tyr Gln Asp His Gly Phe Ser Glu Ile Phe Thr Asn Ser	
455 460 465	
cgg gag gtg agc agc caa ctc cgg ctg cct ccg ggg gaa tat atc att	1555
Arg Glu Val Ser Ser Gln Leu Arg Leu Pro Pro Gly Glu Tyr Ile Ile	
470 475 480	
att ccc tcc acc ttt gag cca cac aga gat gct gac ttc ctg ctt cgg	1603
Ile Pro Ser Thr Phe Gln Pro His Arg Asp Ala Asp Phe Leu Leu Arg	
485 490 495 500	
gtc ttc acc gag aag cac agc gag tca tgg gaa ttg gat gaa gtc aac	1651
Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu Asp Glu Val Asn	
505 510 515	
tat gct gag caa ctc caa gag gaa aag gtc tct gag gat gac atg gac	1699
Tyr Ala Glu Gln Leu Gln Glu Glu Lys Val Ser Glu Asp Asp Met Asp	
520 525 530	
cag gac ttc cta cat ttg ttt aag ata gtg gca gga gag ggc aag gag	1747
Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly Glu Gly Lys Glu	
535 540 545	
ata ggg gtg tat gag ctc cag agg ctg ctc aac agg atg gcc atc aaa	1795
Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg Met Ala Ile Lys	
550 555 560	
ttc aaa agc ttc aag acc aag ggc ttt ggc ctg gat gct tgc cgc tgc	1843
Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp Ala Cys Arg Cys	
565 570 575 580	
atg atc aac ctc atg gat aaa gat ggc tct ggc aag ctg ggg ctt cta	1891
Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys Leu Gly Leu Leu	
585 590 595	
gag ttc aag atc ctg tgg aaa aaa ctc aag aaa tgg atg gac atc ttc	1939
Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys Lys Trp Met Asp Ile Phe	
600 605 610	
aga gag tgt gac cag gac cat tca ggc acc ttg aac tcc tat gag atg	1987
Arg Glu Cys Asp Gln Asp His Ser Gly Thr Leu Asn Ser Tyr Glu Met	
615 620 625	
cgc ctg gtt att gag aaa gca ggc atc aag ctg aac aac aag gta atg	2035
Arg Leu Val Ile Glu Lys Ala Gly Ile Lys Leu Asn Asn Lys Val Met	
630 635 640	

cag gtc ctg gtg gcc agg tat gca gat gat gac ctg atc ata gac ttt 2083
 Gln Val Leu Val Ala Arg Tyr Ala Asp Asp Asp Leu Ile Ile Asp Phe
 645 650 655 660
 gac agc ttc atc agc tgt ttc ctg agg cta aag acc atg ttc aca ttc 2131
 Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu Lys Thr Met Phe Thr Phe
 665 670 675
 ttt cta acc atg gac ccc aag aat act ggc cat att tgc ttg agc ctg 2179
 Phe Leu Thr Met Asp Pro Lys Asn Thr Gly His Ile Cys Leu Ser Leu
 680 685 690
 gaa cag tgg ctg cag atg acc atg tgg gga tag aggcgctg taggagcctg 2230
 Glu Gln Trp Leu Gln Met Thr Met Trp Gly *
 695 700
 gtcattctcta ccagcagcag cagcagcgag gttctagccc aggagggtgg ggtgcttctt 2290
 gtagccctca gctctccagt ctctgctgat gaaatgggat ccagggtgg 2338

<210> 704
 <211> 1541
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (81) .. (173)

<400> 704
 cccctctgtg cactcattac ctgcttctctg agctccccga gaagtcattcc aggacctccc 60
 cgagaagccg tccaggaaac atg ctc tca ggg gac ccc cat ctg cct cag 110
 Met Leu Ser Gly Asp Pro His Leu Pro Gln
 1 5 10
 cct ctt tgt cac tgc ctg gac cat tgt ccc tgc tgt ttc tca ggc acc 158
 Pro Leu Cys His Cys Leu Asp His Cys Pro Cys Cys Phe Ser Gly Thr
 15 20 25
 acc agg acc agc tga tcattccagc ccacagcaat ggagccacat gactcctccc 213
 Thr Arg Thr Ser *
 30
 acatggactc tgagttccga tacactctct tcccatttgt ttacagcatc atctttgtgc 273
 tcgggggtcat tgctaattggc tacgtgctgt gggctctttgc ccgcctgtac ccttgcaaga 333
 aattcaatga gataaagatc ttcattggtga acctcaccat ggcggacatg ctcttcttga 393
 tcacctgccc actttggatt gtctactacc aaaaccaggg caactggata ctccccaat 453
 tcctgtgcaa cgtggctggc tgccctttct tcatcaacac ctactgctct gtggccttcc 513
 tgggggtcat cacttataac cgcttccagg cagtaactcg gcccatcaag actgctcagg 573
 ccaacacccg caagcgtggc atctctttgt ccttggtcat ctgggtggcc attgtgggag 633
 ctgcattcta ctctctcatc ctggactcca ccaacacagt gcccgacagt gctggctcag 693

```

gcaacgtcac tcgctgcttt gagcattacg agaagggcag cgtgccagtc ctcatcatcc 753
acatcttcat cgtgttcagc ttcttctcgg tcttctcat catcctcttc tgcaacctgg 813
tcacatccg taccttgctc atgcagccgg tgcagcagca gcgcaacgct gaagtcaagc 873
gccgggcgct gtggatgggtg tgcacggctc' tggcgggtgtt catcatctgc ttcgtgcccc 933
accacgtggt gcagctgccc tggacccttg ctgagctggg cttccaggac agcaaattcc 993
accaggccat taatgatgca catcagggtca ccctctgcct ccttagcacc aactgtgtct 1053
tagaccctgt tatctactgt ttctcacca aaaagttccg caagcacctc accgaaaagt 1113
tctacagcat gcgcagtagc cggaattgct cccgggccac cacggatacg gtcactgaag 1173
tggttgtgcc attcaaccag atccctggca attccctcaa aaattagtc ctgcttccat 1233
gcctgaagtc ttctcctcca tgaacatcat ggactgagct gggggaagaa gggatatcta 1293
ctgtgggtct gggcaccacc tctgtgggt ctggtgggcc attagatttg gaggtacct 1353
cacctgggca gggatgatgg cagagccagg ctgttggaat atccagaact caaatgagcc 1413
ccttcacccg cctgtgggcg catactacag taactgtgac tgatgacttt atcctgagtc 1473
ccttaatctt atggggccgg aaggaatgtc agggccaggt gcagacctg ggggaagact 1533
ttaaacca 1541

```

<210> 705
 <211> 523
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (71)..(445)

```

<400> 705
gacacgcgtt cgaacctatg caaatgccca ctccctgccca acctacgtga agagcccagc 60

tccctgccag  atg acc tac atc aaa agt cca gct ccc tgc cag acc cag 109
              Met Thr Tyr Ile Lys Ser Pro Ala Pro Cys Gln Thr Gln
                1             5             10

acg tgc tat gtc cag ggt gct tct cct tgc cag agc tat tat gtt caa 157
Thr Cys Tyr Val Gln Gly Ala Ser Pro Cys Gln Ser Tyr Tyr Val Gln
  15             20             25

gct cct gca agt ggc tca acc tcc cag tac tgt gtc act gac cca tgc 205
Ala Pro Ala Ser Gly Ser Thr Ser Gln Tyr Cys Val Thr Asp Pro Cys
  30             35             40             45

tct gct ccc tgt tcc acc agc tac tgc tgt ctg gct ccc cgg acc ttc 253
Ser Ala Pro Cys Ser Thr Ser Tyr Cys Cys Leu Ala Pro Arg Thr Phe
          50             55             60

ggg gtg agt ccc ctg aga cgc tgg att cag cgg ccc cag aac tgc aac 301
Gly Val Ser Pro Leu Arg Arg Trp Ile Gln Arg Pro Gln Asn Cys Asn
          65             70             75

```

```

aca gga tca tct ggc tgc tgt gag aat tgc gga agc tct ggg tgc tgt      349
Thr Gly Ser Ser Gly Cys Cys Glu Asn Ser Gly Ser Ser Gly Cys Cys
      80                      85                      90

ggt tct ggg ggc tgt ggc tgc agc tgt gga tgt ggc agc tct ggg tgc      397
Gly Ser Gly Gly Cys Gly Cys Ser Cys Gly Cys Gly Ser Ser Gly Cys
      95                      100                     105

tgc tgt ttg gga att atc ccc atg aag tcc cga agt cct gcg ttg ctg      445
Cys Cys Leu Gly Ile Ile Pro Met Lys Ser Arg Ser Pro Ala Leu Leu
110                      115                      120                     125

tgaccatgag gatgactgct gctgctaaac atacgacagc tcaactccag aatgcactgc      505

cccgcacccc ctctggaa                                                    523

```

```

<210> 706
<211> 1783
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (133) .. (1548)

```

```

<220>
<221> misc_feature
<222> (1) ... (1783)
<223> n = a,t,c or g

```

```

<400> 706
gagggtcanag cactggagcc aacaccgccc caggatgggg tataaaaggg ttgggaggag      60

aggaggcttc agtctcagtg gctcagcctt cccagctgat ctgaagctcc tgtgcagcct      120

cagccctaca cc      atg acc tcc ttc tac agc acc tcc tca tgc cct ctg      168
                  Met Thr Ser Phe Tyr Ser Thr Ser Ser Cys Pro Leu
                  1                      5                      10

ggt tgc acc atg gct cct gga gca aga aat gtc ttt gtc tct cct atc      216
Gly Cys Thr Met Ala Pro Gly Ala Arg Asn Val Phe Val Ser Pro Ile
      15                      20                      25

gat gtt ggg tgc cag cct gtg gca gag gcc aat gct gcc tcc atg tgc      264
Asp Val Gly Cys Gln Pro Val Ala Glu Ala Asn Ala Ala Ser Met Cys
      30                      35                      40

ctc ttg gcc aac gtg gca cac gcc aac aga gtc cgt gtg ggg tgc act      312
Leu Leu Ala Asn Val Ala His Ala Asn Arg Val Arg Val Gly Ser Thr
      45                      50                      55                     60

ccc ctg ggc cgc ccc agc ctc tgt ctg ccc cca acc agt cac act gct      360
Pro Leu Gly Arg Pro Ser Leu Cys Leu Pro Pro Thr Ser His Thr Ala
      65                      70                      75

tgt ccc ttg cca ggg acc tgt cac att ccc ggc aac atc gga atc tgt      408
Cys Pro Leu Pro Gly Thr Cys His Ile Pro Gly Asn Ile Gly Ile Cys
      80                      85                      90

ggg gcc tac ggc aaa aac acc ctg aat ggc cat gag aag gag acc atg      456

```

Gly	Ala	Tyr	Gly	Lys	Asn	Thr	Leu	Asn	Gly	His	Glu	Lys	Glu	Thr	Met	
95							100					105				
aag	ttc	ctg	aat	gac	cgc	ctg	gcc	aac	tac	ctg	gag	aag	gtg	cgc	cag	504
Lys	Phe	Leu	Asn	Asp	Arg	Leu	Ala	Asn	Tyr	Leu	Glu	Lys	Val	Arg	Gln	
110						115					120					
ctg	gag	cag	gag	aat	gca	gag	ctg	gag	acc	aca	ctc	ctc	gag	agg	agc	552
Leu	Glu	Gln	Glu	Asn	Ala	Glu	Leu	Glu	Thr	Thr	Leu	Leu	Glu	Arg	Ser	
125					130					135					140	
aag	tgc	cac	gag	tcc	acc	gtg	tgc	ccc	gac	tac	cag	tcc	tac	ttc	cgt	600
Lys	Cys	His	Glu	Ser	Thr	Val	Cys	Pro	Asp	Tyr	Gln	Ser	Tyr	Phe	Arg	
				145					150					155		
aca	atc	gag	gag	ctc	cag	cag	aag	atc	ctg	tgc	agc	aag	gct	gag	aat	648
Thr	Ile	Glu	Glu	Leu	Gln	Gln	Lys	Ile	Leu	Cys	Ser	Lys	Ala	Glu	Asn	
			160					165					170			
gcc	agg	ctg	att	gta	caa	att	gac	aac	gcg	aag	ctg	gct	gct	gat	gac	696
Ala	Arg	Leu	Ile	Val	Gln	Ile	Asp	Asn	Ala	Lys	Leu	Ala	Ala	Asp	Asp	
		175					180					185				
ttt	agg	atc	aag	ctg	gag	agt	gag	cgc	tcc	ctt	cac	cag	ctg	gtg	gag	744
Phe	Arg	Ile	Lys	Leu	Glu	Ser	Glu	Arg	Ser	Leu	His	Gln	Leu	Val	Glu	
190						195					200					
gcg	gac	aag	tgc	ggg	acg	cag	aag	ctc	ctg	gat	gac	gcg	acc	ctg	gcc	792
Ala	Asp	Lys	Cys	Gly	Thr	Gln	Lys	Leu	Leu	Asp	Asp	Ala	Thr	Leu	Ala	
205					210					215				220		
aag	gcc	gac	ctg	gag	gcc	cag	cag	gag	tcc	ctg	aag	gag	gag	cag	ctc	840
Lys	Ala	Asp	Leu	Glu	Ala	Gln	Gln	Glu	Ser	Leu	Lys	Glu	Glu	Gln	Leu	
			225					230						235		
tcc	ctc	aag	agc	aac	cac	gag	cag	gaa	gta	aag	att	ctg	agg	agt	cag	888
Ser	Leu	Lys	Ser	Asn	His	Glu	Gln	Glu	Val	Lys	Ile	Leu	Arg	Ser	Gln	
			240					245					250			
ctg	ggg	gag	aag	ttc	cgg	atc	gag	ctg	gac	att	gag	ccc	acc	att	gac	936
Leu	Gly	Glu	Lys	Phe	Arg	Ile	Glu	Leu	Asp	Ile	Glu	Pro	Thr	Ile	Asp	
		255					260					265				
ctg	aac	agg	gtg	ttg	ggg	gag	atg	cgg	gct	cag	tac	gag	gcc	atg	gtg	984
Leu	Asn	Arg	Val	Leu	Gly	Glu	Met	Arg	Ala	Gln	Tyr	Glu	Ala	Met	Val	
	270					275					280					
gag	acc	aac	cac	cag	gat	gtg	gaa	cag	tgg	ttc	caa	gcc	cag	tct	gaa	1032
Glu	Thr	Asn	His	Gln	Asp	Val	Glu	Gln	Trp	Phe	Gln	Ala	Gln	Ser	Glu	
285					290					295				300		
ggc	atc	agc	ctg	cag	gcc	atg	tcc	tgc	tcc	gag	gag	ctg	cag	tgc	tgc	1080
Gly	Ile	Ser	Leu	Gln	Ala	Met	Ser	Cys	Ser	Glu	Glu	Leu	Gln	Cys	Cys	
			305					310						315		
cag	tcg	gag	atc	ctg	gag	ctg	aga	tgc	acg	gtg	aat	gcc	ctg	gag	gtg	1128
Gln	Ser	Glu	Ile	Leu	Glu	Leu	Arg	Cys	Thr	Val	Asn	Ala	Leu	Glu	Val	
			320					325					330			
gag	cgc	caa	gcc	cag	cac	acc	ttg	aag	gac	tgt	ctg	cag	aac	tcc	ctg	1176
Glu	Arg	Gln	Ala	Gln	His	Thr	Leu	Lys	Asp	Cys	Leu	Gln	Asn	Ser	Leu	
		335					340					345				
tgt	gaa	gcg	gag	gac	cgc	tac	ggc	aca	gag	ctg	gcc	cag	atg	cag	agc	1224

```

Cys Glu Ala Glu Asp Arg Tyr Gly Thr Glu Leu Ala Gln Met Gln Ser
 350                               355                               360

ctc att agc aac ttg gaa gag cag ttg tct gag atc cgg gcc gac ctg      1272
Leu Ile Ser Asn Leu Glu Glu Gln Leu Ser Glu Ile Arg Ala Asp Leu
365                               370                               375                               380

gag cgg cag aac cag gag tac cag gtg ctg ctg gac gtg aag gcc cgg      1320
Glu Arg Gln Asn Gln Glu Tyr Gln Val Leu Leu Asp Val Lys Ala Arg
                               385                               390                               395

ttg gag aac gag att gcc aca tac cgg aac ctt act ccc ctg caa tcc      1368
Leu Glu Asn Glu Ile Ala Thr Tyr Arg Asn Leu Thr Pro Leu Gln Ser
                               400                               405                               410

ctg ttc cac gcc tgc ctc ctg tac ttc ttg tcc aag ctg tgg ccc tgt      1416
Leu Phe His Ala Cys Leu Leu Tyr Phe Leu Ser Lys Leu Trp Pro Cys
                               415                               420                               425

cac cgg tgg gtc tcc ctc tgg cca tgg agc cag cat ggg gag atg att      1464
His Arg Trp Val Ser Leu Trp Pro Trp Ser Gln His Gly Glu Met Ile
                               430                               435                               440

ctg aag gcc cga gtt agg aga ttg agg ctg gtt gca ctg ggg tca gga      1512
Leu Lys Ala Arg Val Arg Arg Leu Arg Leu Val Ala Leu Gly Ser Gly
445                               450                               455                               460

gtg ccc tca cct tgc cca gtc ttc ctt caa gac tag actc actgaggcat      1562
Val Pro Ser Pro Cys Pro Val Phe Leu Gln Asp *
                               465                               470

tttcocctaaa tcaaccggta gcagatactt ccaaggagtg gtcacctgcc tatgcctcta      1622

agctgtatatt tttgttggtg ctaaaatggt gtaattatct tccatgaaag caattatttt      1682

tcctggtgtc tcttcttggt acttttagtt ctattccagt gtttcagaat ctccaaaaat      1742

gtaactgggt tccctgcatt aaatggtcaa taaacctcct t      1783

```

```

<210> 707
<211> 422
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (47)..(403)

```

```

<220>
<221> misc_feature
<222> (1)..(422)
<223> n = a,t,c or g

```

```

<400> 707
tgatctgctg cagtgcctga accagcttta ttcagcttct acagag atg tcc tgc      55
Met Ser Cys
1

cag cag agc cag cag cag tgc cag cct cct ccc aaa tgt acc cct aaa      103
Gln Gln Ser Gln Gln Gln Cys Gln Pro Pro Pro Lys Cys Thr Pro Lys
5                               10                               15

```

```

tgc cct ccc aag tgt act cct aag tgt cct ccc aag tgt ccc cca aaa      151
Cys Pro Pro Lys Cys Thr Pro Lys Cys Pro Pro Lys Cys Pro Pro Lys
  20                      25                      30                      35

tgc cct ccc cag tat tca gcc cca tgc cca cct cca gtc tct tcc tgc      199
Cys Pro Pro Gln Tyr Ser Ala Pro Cys Pro Pro Pro Val Ser Ser Cys
                40                      45                      50

tgt ggt tcc agc tct ggg ggc tgc tgc agc tct gag ggt ggt ggc tgc      247
Cys Gly Ser Ser Ser Gly Gly Cys Cys Ser Ser Glu Gly Gly Gly Cys
                55                      60                      65

tgc ctg agc cac cac agg ccc cgc cag tcc ctc cga cgc cga cct cag      295
Cys Leu Ser His His Arg Pro Arg Gln Ser Leu Arg Arg Arg Pro Gln
                70                      75                      80

agt tcc agc tgc tgt ggc agt ggc agt ggc cag cag tct ggg ggc tcc      343
Ser Ser Ser Cys Cys Gly Ser Gly Ser Gly Gln Gln Ser Gly Gly Ser
  85                      90                      95

agc tgc tgc cac agc tct ggg ggc tct ggc tgc tgc cac agc tct gga      391
Ser Cys Cys His Ser Ser Gly Gly Ser Gly Cys Cys His Ser Ser Gly
100                      105                      110                      115

ggc tgc tgc tga cctgggccat gaggagcan      422
Gly Cys Cys *
```

<210> 708
 <211> 1304
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (181)..(723)

```

<400> 708
atttggccct cgaggccaag aattcggcac gagggcggcg cggacagcgt tcggggctgt      60

gtgccggcgc ctctggcagg gattggggaa tttttctgta aacacttcta agggcaatac      120

agccaaaaat ggtggcttgc ttctgtttct ctttttttcc ccacacatag cagtaccaat      180

atg aag tgg gta cag ttt tca aac cta cac gtt gat gtt cca aag gat      228
Met Lys Trp Val Gln Phe Ser Asn Leu His Val Asp Val Pro Lys Asp
  1                      5                      10                      15

ttg acc aaa cct gtg gta aca atc tct gat gaa cca gac ata tta tat      276
Leu Thr Lys Pro Val Val Thr Ile Ser Asp Glu Pro Asp Ile Leu Tyr
                20                      25                      30

aag cgc ctc tcg gtt ttg gtg aaa ggt cac gat aag gct gta ttg gac      324
Lys Arg Leu Ser Val Leu Val Lys Gly His Asp Lys Ala Val Leu Asp
  35                      40                      45

agt tat gaa tat ttt gct gtg ctt gct gct aaa gaa ctt ggt atc tct      372
Ser Tyr Glu Tyr Phe Ala Val Leu Ala Ala Lys Glu Leu Gly Ile Ser
  50                      55                      60
```



```

att aaa gta cat gaa cct cca agg aaa ata gag cga ttt act ctt ctc      420
Ile Lys Val His Glu Pro Pro Arg Lys Ile Glu Arg Phe Thr Leu Leu
 65                               70                               75                               80

caa tca gtg cat att tac aag aag cac aga gtt cag tat gaa atg aga      468
Gln Ser Val His Ile Tyr Lys Lys His Arg Val Gln Tyr Glu Met Arg
                               85                               90                               95

aca ctt tac aga tgt tta gag tta gaa cat cta act gga agc aca gca      516
Thr Leu Tyr Arg Cys Leu Glu Leu Glu His Leu Thr Gly Ser Thr Ala
                               100                              105                              110

gat gtc tac ttg gaa tat att cag cga aac tta cct gaa ggg gtt gcc      564
Asp Val Tyr Leu Glu Tyr Ile Gln Arg Asn Leu Pro Glu Gly Val Ala
                               115                              120                              125

atg gaa gta aca aag ttt tgt ttc ttt att ttt tta gac aca att aga      612
Met Glu Val Thr Lys Phe Cys Phe Phe Ile Phe Leu Asp Thr Ile Arg
                               130                              135                              140

aca gtt acc aga aca cat caa gga gcc aat ctg gga aac act atc aga      660
Thr Val Thr Arg Thr His Gln Gly Ala Asn Leu Gly Asn Thr Ile Arg
                               145                              150                              155                              160

aga aaa aga aga aag caa gtc ata aag cct cag gga ggc cat ttt tgc      708
Arg Lys Arg Arg Lys Gln Val Ile Lys Pro Gln Gly Gly His Phe Cys
                               165                              170                              175

cta aat ttg aaa tga ggggtgggcca gatgagtatg tttaagtgga gagtgcctcc      763
Leu Asn Leu Lys *
                               180

agctgagatg atttgagtct gtcctaactg ctccattgag ttctcgtgcc ctcacagct      823

gagggcaggg aatggaactt taatggaaga accactttta tctattcttt ttattcattg      883

tttcagttct gatttcagca aacatgagca aaccactttg actgaaagca gaaagagtga      943

aaattctatt ttgttacgct actggtgttc aattattagt ttgtaccatt tttaatttat      1003

gtcagttgat gcatctgaaa ataagtgctt ggagtgttcg tacccttatt tttttttaag      1063

attcctagaa ggaatctttg gttaattcag attgagcagt taaagttttt gctattttacc      1123

tttgtgcagg ctggcatatg ctaatttggg ggtggttaacc aaccgatttt atctcatgta      1183

agcattacat tttgaagact gaatatactt cacagcagat caaacacatt tatggcatgc      1243

actgacctct tcttggagcc cagactttat agagttgcct accagggggtt actgtaatgg      1303

a                                                                 1304

```

<210> 709
 <211> 414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (53) .. (370)

<220>

<221> misc_feature

<222> (1)...(414)

<223> n = a,t,c or g

<400> 709

```

ggacgtatct gttgctgcgt ctgaaccac tgtttatcga aatcccacca ag      atg      55
                                   Met      1

tcc tgc cag cag aac caa cag cag tgc cag ccc cct ccc aag tgt cct      103
Ser Cys Gln Gln Asn Gln Gln Cys Gln Pro Pro Pro Lys Cys Pro
              5                      10                      15

atc ccc aag tat ccc cca aaa tgt ccc tca aag tgt gca tcc tca tgc      151
Ile Pro Lys Tyr Pro Pro Lys Cys Pro Ser Lys Cys Ala Ser Ser Cys
              20                      25                      30

cca cct cca atc tct tcc tgc tgt ggc tcc agc tct ggg ggc tgc tgt      199
Pro Pro Pro Ile Ser Ser Cys Cys Gly Ser Ser Ser Gly Gly Cys Cys
              35                      40                      45

agc tct ggg ggc tgt ggt tgc tgc agc tct gag gga ggt ggc tgc tgc      247
Ser Ser Gly Gly Cys Gly Cys Cys Ser Ser Glu Gly Gly Gly Cys Cys
              50                      55                      60                      65

ctg agc cac cac aga cac cat agg tcc cac tgc cac aga ccc aag agc      295
Leu Ser His His Arg His His Arg Ser His Cys His Arg Pro Lys Ser
              70                      75                      80

tcc aat tgc tat ggc agt ggc agt ggc cag cag tct ggg ggt tct ggc      343
Ser Asn Cys Tyr Gly Ser Gly Ser Gly Gln Gln Ser Gly Gly Ser Gly
              85                      90                      95

tgc tgc tct gga ggg ggc tgt tgc tga cctgg accaggagca gcaccaaagg      395
Cys Cys Ser Gly Gly Gly Cys Cys *
              100                      105

aattagtggg cgaaggacn      414

```

<210> 710

<211> 2254

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (238)..(1278)

<400> 710

```

aattccgggt cgacctacgc gtccgaagct ataggctacc cattcagctc ccctgtcaga      60

gactcaagct ttgagaaagg ctagcaaaga gcaaggaaag agagaaaaca acaaagtggc      120

gaggccctca gagtgaaagc gtaaggttca gtcagcctgc tgcagctttg cagacctcag      180

ctgggcatct ccagactccc ctgaaggaag agccttctc acccaaacc acaaaag      237
atg ctg aaa aag cct ctc tca gct gtg acc tgg ctc tgc att ttc atc      285
Met Leu Lys Lys Pro Leu Ser Ala Val Thr Trp Leu Cys Ile Phe Ile
  1              5                      10                      15

```

gtg gcc ttt gtc agc cac cca gcg tgg ctg cag aag ctc tct aag cac	333
Val Ala Phe Val Ser His Pro Ala Trp Leu Gln Lys Leu Ser Lys His	
20 25 30	
aag aca cca gca cag cca cag ctc aaa gcg gcc aac tgc tgt gag gag	381
Lys Thr Pro Ala Gln Pro Gln Leu Lys Ala Ala Asn Cys Cys Glu Glu	
35 40 45	
gtg aag gag ctc aag gcc caa gtt gcc aac ctt agc agc ctg ctg agt	429
Val Lys Glu Leu Lys Ala Gln Val Ala Asn Leu Ser Ser Leu Leu Ser	
50 55 60	
gaa ctg aac aag aag cag gag agg gac tgg gtc agc gtg gtc atg cag	477
Glu Leu Asn Lys Lys Gln Glu Arg Asp Trp Val Ser Val Val Met Gln	
65 70 75 80	
gtg atg gag ctg gag agc aac agc aag cgc atg gag tcg cgg ctc aca	525
Val Met Glu Leu Glu Ser Asn Ser Lys Arg Met Glu Ser Arg Leu Thr	
85 90 95	
gat gct gag agc aag tac tcc gag atg aac aac caa att gac atc atg	573
Asp Ala Glu Ser Lys Tyr Ser Glu Met Asn Asn Gln Ile Asp Ile Met	
100 105 110	
cag ctg cag gca gca cag acg gtc act cag acc tcc gca gat gcc atc	621
Gln Leu Gln Ala Ala Gln Thr Val Thr Gln Thr Ser Ala Asp Ala Ile	
115 120 125	
tac gac tgc tct tcc ctc tac cag aag aac tac cgc atc tct gga gtg	669
Tyr Asp Cys Ser Ser Leu Tyr Gln Lys Asn Tyr Arg Ile Ser Gly Val	
130 135 140	
tat aag ctt cct cct gat gac ttc ctg ggc agc cct gaa ctg gag gtg	717
Tyr Lys Leu Pro Pro Asp Asp Phe Leu Gly Ser Pro Glu Leu Glu Val	
145 150 155 160	
ttc tgt gac atg gag act tca ggc gga ggc tgg acc atc atc cag aga	765
Phe Cys Asp Met Glu Thr Ser Gly Gly Trp Thr Ile Ile Gln Arg	
165 170 175	
cga aaa agt ggc ctt gtc tcc ttc tac cgg gac tgg aag cag tac aag	813
Arg Lys Ser Gly Leu Val Ser Phe Tyr Arg Asp Trp Lys Gln Tyr Lys	
180 185 190	
cag ggc ttt ggc agc atc cgt ggg gac ttc tgg ctg ggg aac gaa cac	861
Gln Gly Phe Gly Ser Ile Arg Gly Asp Phe Trp Leu Gly Asn Glu His	
195 200 205	
atc cac cgg ctc tcc aga cag cca acc cgg ctg cgt gta gag atg gag	909
Ile His Arg Leu Ser Arg Gln Pro Thr Arg Leu Arg Val Glu Met Glu	
210 215 220	
gac tgg gag ggc aac ctg cgc tac gct gag tat agc cac ttt gtt ttg	957
Asp Trp Glu Gly Asn Leu Arg Tyr Ala Glu Tyr Ser His Phe Val Leu	
225 230 235 240	
ggc aat gaa ctc aac agc tat cgc ctc ttc ctg ggg aac tac act ggc	1005
Gly Asn Glu Leu Asn Ser Tyr Arg Leu Phe Leu Gly Asn Tyr Thr Gly	
245 250 255	
aat gtg ggg aac gac gcc ctc cag tat cat aac aac aca gcc ttc agc	1053
Asn Val Gly Asn Asp Ala Leu Gln Tyr His Asn Asn Thr Ala Phe Ser	
260 265 270	

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acc aag gac aag gac aat gac aac tgc ttg gac aag tgt gca cag ctc      1101
Thr Lys Asp Lys Asp Asn Asp Asn Cys Leu Asp Lys Cys Ala Gln Leu
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cgc aaa ggt ggc tac tgg tac aac tgc tgc aca gac tcc aac ctc aat      1149
Arg Lys Gly Gly Tyr Trp Tyr Asn Cys Cys Thr Asp Ser Asn Leu Asn
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gga gtg tac tac cgc ctg ggt gag cac aat aag cac ctg gat ggc atc      1197
Gly Val Tyr Tyr Arg Leu Gly Glu His Asn Lys His Leu Asp Gly Ile
      305                      310                      315                      320

acc tgg tat ggc tgg cat gga tct acc tac tcc ctc aaa cgg gtg gag      1245
Thr Trp Tyr Gly Trp His Gly Ser Thr Tyr Ser Leu Lys Arg Val Glu
      325                      330                      335

atg aaa atc cgc cca gaa gac ttc aag cct taa aaggaggc tgccgtggag      1296
Met Lys Ile Arg Pro Glu Asp Phe Lys Pro *
      340                      345

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taattttgag atcggtttat ctattttctc tacggcttag gctatgtgag ggcaaaacac      1656

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Asn Thr Val Trp Asn Met Glu Asp Leu Asp Leu Glu Tyr Ala Lys Thr
5 10 15

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Asp Ile Asn Cys Gly Thr Asp Leu Met Phe Tyr Ile Glu Met Asp Pro
20 25 30

cca gca ctg cct cct aaa cca cca aaa cct act act gta gcc aac aac 199
Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Thr Thr Val Ala Asn Asn
35 40 45 50

ggt atg aat aac aat atg tcc tta caa gat gct gaa tgg tac tgg gga 247
Gly Met Asn Asn Asn Met Ser Leu Gln Asp Ala Glu Trp Tyr Trp Gly
55 60 65

gat atc tcg agg gaa gaa gtg aat gaa aaa ctt cga gat aca gca gac 295
Asp Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg Asp Thr Ala Asp
70 75 80

ggg acc ttt ttg gta cga gat gcg tct act aaa atg cat ggt gat tat 343
Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met His Gly Asp Tyr
85 90 95

act ctt aca cta agg aaa ggg gga aat aac aaa tta atc aaa ata ttt 391
Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu Ile Lys Ile Phe
100 105 110

cat cga gat ggg aaa tat ggc ttc tct gac cca tta acc ttc agt tct 439
His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu Thr Phe Ser Ser
115 120 125 130

gtg gtt gaa tta ata aac cac tac cgg aat gaa tct cta gct cag tat 487
Val Val Glu Leu Ile Asn His Tyr Arg Asn Glu Ser Leu Ala Gln Tyr
135 140 145

aat ccc aaa ttg gat gtg aaa tta ctt tat cca gta tcc aaa tac caa 535
Asn Pro Lys Leu Asp Val Lys Leu Leu Tyr Pro Val Ser Lys Tyr Gln
150 155 160

cag gat caa gtt gtc aaa gaa gat aat att gaa gct gta ggg aaa aaa 583
Gln Asp Gln Val Val Lys Glu Asp Asn Ile Glu Ala Val Gly Lys Lys
165 170 175

tta cat gaa tat aac act cag ttt caa gaa aaa agt cga gaa tat gat 631
Leu His Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser Arg Glu Tyr Asp
180 185 190

aga tta tat gaa gaa tat acc cgc aca tcc cag gaa atc caa atg aaa 679
Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu Ile Gln Met Lys
195 200 205 210

agg aca gct att gaa gca ttt aat gaa acc ata aaa ata ttt gaa gaa 727
Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu Glu
215 220 225

cag tgc cag acc caa gag cgg tac agc aaa gaa tac ata gaa aag ttt 775
Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr Ile Glu Lys Phe

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agc tct ctg aaa gaa ctg gtg cta cat tac caa cac acc tcc ctt gtg Ser Ser Leu Lys Glu Leu Val Leu His Tyr Gln His Thr Ser Leu Val 420 425 430			1351
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<221> CDS

<222> (329) .. (1429)

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tcagtcaggc agatgtttgt cgactgga   atg gcg cca aat ctt aaa ggc aga      352
                               Met Ala Pro Asn Leu Lys Gly Arg
                               1                               5

cca cgc aaa aag aaa cca tgc cca caa aga aga gat tca ttc agt ggt      400
Pro Arg Lys Lys Lys Pro Cys Pro Gln Arg Arg Asp Ser Phe Ser Gly
   10                               15                               20

ggt aag gat tcc aac aac aat tcc gat ggc aaa gcc gtt gcc aag gtg      448
Val Lys Asp Ser Asn Asn Asn Ser Asp Gly Lys Ala Val Ala Lys Val
   25                               30                               35                               40

aaa tgt gag gcc agg tca gcc ttg acc aag ccg aag aat aac cat aac      496
Lys Cys Glu Ala Arg Ser Ala Leu Thr Lys Pro Lys Asn Asn His Asn
                               45                               50                               55

tgt aaa aaa gtc tca aat gaa gaa aaa cca aag gtt gcc att ggt gaa      544
Cys Lys Lys Val Ser Asn Glu Glu Lys Pro Lys Val Ala Ile Gly Glu
                               60                               65                               70

gag tgc agg gca gat gaa caa gcc ttc ttg gtg gca ctt tat aaa tac      592
Glu Cys Arg Ala Asp Glu Gln Ala Phe Leu Val Ala Leu Tyr Lys Tyr
   75                               80                               85

atg aaa gaa agg aaa acg ccg ata gaa cga ata ccc tat tta ggt ttt      640
Met Lys Glu Arg Lys Thr Pro Ile Glu Arg Ile Pro Tyr Leu Gly Phe
   90                               95                               100

aaa cag att aac ctt tgg act atg ttt caa gct gct caa aaa ctg gga      688
Lys Gln Ile Asn Leu Trp Thr Met Phe Gln Ala Ala Gln Lys Leu Gly
  105                               110                               115                               120

gga tat gaa aca ata aca gcc cgc cgt cag tgg aaa cat att tat gat      736
Gly Tyr Glu Thr Ile Thr Ala Arg Arg Gln Trp Lys His Ile Tyr Asp
                               125                               130                               135

gaa tta ggc ggt aat cct ggg agc acc agc gct gcc act tgt acc cgc      784
Glu Leu Gly Gly Asn Pro Gly Ser Thr Ser Ala Ala Thr Cys Thr Arg
                               140                               145                               150

aga cat tat gaa aga tta atc cta cca tat gaa aga ttt att aaa gga      832
Arg His Tyr Glu Arg Leu Ile Leu Pro Tyr Glu Arg Phe Ile Lys Gly
                               155                               160                               165

gaa gaa gat aag ccc ctg cct cca atc aaa cct cgg aaa cag gag aac      880
Glu Glu Asp Lys Pro Leu Pro Pro Ile Lys Pro Arg Lys Gln Glu Asn
  170                               175                               180

agt tca cag gaa aat gag aac aaa aca aaa gta tct gga acc aaa cgc      928
Ser Ser Gln Glu Asn Glu Asn Lys Thr Lys Val Ser Gly Thr Lys Arg

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185	190	195	200	
atc aaa cat gaa ata cct aaa agc aag aaa gaa aaa gaa aat gcc cca Ile Lys His Glu Ile Pro Lys Ser Lys Lys Glu Lys Glu Asn Ala Pro	205	210	215	976
aag ccc cag gat gca gca gag gtt tca tca gag caa gaa aaa gaa caa Lys Pro Gln Asp Ala Ala Glu Val Ser Ser Glu Gln Glu Lys Glu Gln	220	225	230	1024
gag act tta ata agc cag aaa agc atc cct gag cct ctc cca gca gca Glu Thr Leu Ile Ser Gln Lys Ser Ile Pro Glu Pro Leu Pro Ala Ala	235	240	245	1072
gac atg aag aaa aaa ata gaa ggg tat cag gaa ttt tca gcg aag ccc Asp Met Lys Lys Lys Ile Glu Gly Tyr Gln Glu Phe Ser Ala Lys Pro	250	255	260	1120
ctg gca tcc aga gta gac cca gag aag gac aac gaa aca gac caa ggt Leu Ala Ser Arg Val Asp Pro Glu Lys Asp Asn Glu Thr Asp Gln Gly	265	270	275	1168
tcc aac agt gag aag gtg gca gag gag gcg gga gag aag ggg ccc aca Ser Asn Ser Glu Lys Val Ala Glu Glu Ala Gly Glu Lys Gly Pro Thr	285	290	295	1216
cct cca ctc cca agt gct cct ctg gcc cca gaa aaa gat tca gcc ttg Pro Pro Leu Pro Ser Ala Pro Leu Ala Pro Glu Lys Asp Ser Ala Leu	300	305	310	1264
gtc cct ggg gcc agc aaa cag cca ctc acc tct cct agt gcc ctg gtg Val Pro Gly Ala Ser Lys Gln Pro Leu Thr Ser Pro Ser Ala Leu Val	315	320	325	1312
gac tca aaa caa gaa tcc aaa ctg tgc tgt ttt aca gag agc cct gaa Asp Ser Lys Gln Glu Ser Lys Leu Cys Cys Phe Thr Glu Ser Pro Glu	330	335	340	1360
agt gaa ccc caa gaa gca tcc ttc ccc agc ttc ccc acc aca cag gcc Ser Glu Pro Gln Glu Ala Ser Phe Pro Ser Phe Pro Thr Thr Gln Ala	345	350	355	1408
acc gct ggc aaa cca gaa tga ga cggaggatga caaactgccc gccatggcag Thr Ala Gly Lys Pro Glu *	365			1461
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<211> 1925

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (130)..(1497)

<400> 714

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ctgcaggag   atg tgt aca aag aca atc cca gtc ctc tgg gga tgt ttc      168
             Met Cys Thr Lys Thr Ile Pro Val Leu Trp Gly Cys Phe
             1             5             10
ctc ctg tgg aat ctc tat gtc tca tcc tct cag acc att tac cct gga      216
Leu Leu Trp Asn Leu Tyr Val Ser Ser Ser Gln Thr Ile Tyr Pro Gly
             15             20             25
atc aag gca agg att act cag agg gca ctt gac tat ggt gtt caa gct      264
Ile Lys Ala Arg Ile Thr Gln Arg Ala Leu Asp Tyr Gly Val Gln Ala
             30             35             40             45
gga atg aag atg att gag caa atg cta aaa gaa aag aaa ctc cca gat      312
Gly Met Lys Met Ile Glu Gln Met Leu Lys Glu Lys Lys Leu Pro Asp
             50             55             60
tta agc ggt tct gag tct ctt gaa ttt cta aaa gtt gat tat gta aac      360
Leu Ser Gly Ser Glu Ser Leu Glu Phe Leu Lys Val Asp Tyr Val Asn
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Tyr Asn Phe Ser Asn Ile Lys Ile Ser Ala Phe Ser Phe Pro Asn Thr
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Ser Leu Ala Phe Val Pro Gly Val Gly Ile Lys Ala Leu Thr Asn His
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ggc act gcc aac atc agc aca gac tgg ggg ttc gag tct cca ctt ttt      504
Gly Thr Ala Asn Ile Ser Thr Asp Trp Gly Phe Glu Ser Pro Leu Phe
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Asn Leu Asn Glu Met Leu Cys Pro Ile Ile Ala Ser Glu Val Lys Ala
             145             150             155
cta aat gcc aac ctc agc aca ctg gag gtt tta acc aag att gac aac      648
Leu Asn Ala Asn Leu Ser Thr Leu Glu Val Leu Thr Lys Ile Asp Asn
             160             165             170
tac act ctg ctg gat tac tcc cta atc agt tct cca gaa att act gag      696
Tyr Thr Leu Leu Asp Tyr Ser Leu Ile Ser Ser Pro Glu Ile Thr Glu
             175             180             185
aac tac ctt gac ctg aac ttg aag ggt gta ttc tac cca ctg gaa aac      744
Asn Tyr Leu Asp Leu Asn Leu Lys Gly Val Phe Tyr Pro Leu Glu Asn
             190             195             200             205
ctc acc gac ccc ccc ttc tca cca gtt cct ttt gtg ctc cca gaa cgc      792

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Leu Thr Asp	Pro	Pro	Phe	Ser	Pro	Val	Pro	Phe	Val	Leu	Pro	Glu	Arg	
		210					215					220		
agc aac tcc atg ctc tac att gga atc gcc gag tat ttc ttt aaa tct														840
Ser Asn Ser Met Leu Tyr Ile Gly Ile Ala Glu Tyr Phe Phe Lys Ser		225				230					235			
gcg tcc ttt gct cat ttc aca gct ggg gtt ttc aat gtc act ctc tcc														888
Ala Ser Phe Ala His Phe Thr Ala Gly Val Phe Asn Val Thr Leu Ser		240				245					250			
acc gaa gag att tcc aac cat ttt gtt caa aac tct caa ggc ctt ggc														936
Thr Glu Glu Ile Ser Asn His Phe Val Gln Asn Ser Gln Gly Leu Gly		255				260					265			
aac gtg ctc tcc cgg att gca gag atc tac atc ttg tcc cag ccc ttc														984
Asn Val Leu Ser Arg Ile Ala Glu Ile Tyr Ile Leu Ser Gln Pro Phe		270				275				280				285
atg gtg agg atc atg gcc aca gag cct ccc ata atc aat cta caa cca														1032
Met Val Arg Ile Met Ala Thr Glu Pro Pro Ile Ile Asn Leu Gln Pro						290				295				300
ggc aat ttc acc ctg gac atc cct gcc tcc atc atg atg ctc acc caa														1080
Gly Asn Phe Thr Leu Asp Ile Pro Ala Ser Ile Met Met Leu Thr Gln		305												315
ccc aag aac tcc aca gtt gaa acc atc gtt tcc atg gac ttc gtt gct														1128
Pro Lys Asn Ser Thr Val Glu Thr Ile Val Ser Met Asp Phe Val Ala		320												330
agt acc agt gtt ggc ctg gtt att ttg gga caa aga ctg gtc tgc tcc														1176
Ser Thr Ser Val Gly Leu Val Ile Leu Gly Gln Arg Leu Val Cys Ser		335				340								345
ttg tct ctg aac aga ttc cgc ctt gct ttg cca gag tcc aat cgc agc														1224
Leu Ser Leu Asn Arg Phe Arg Leu Ala Leu Pro Glu Ser Asn Arg Ser		350				355								365
aac att gag gtc ttg agg ttt gaa aat att cta tcg tcc att ctt cac														1272
Asn Ile Glu Val Leu Arg Phe Glu Asn Ile Leu Ser Ser Ile Leu His						370								380
ttt gga gtc ctc cca ctg gcc aat gca aaa ttg cag caa gga ttt cct														1320
Phe Gly Val Leu Pro Leu Ala Asn Ala Lys Leu Gln Gln Gly Phe Pro		385												395
ctg ccc aat cca cac aaa ttc tta ttc gtc aat tca gat att gaa gtt														1368
Leu Pro Asn Pro His Lys Phe Leu Phe Val Asn Ser Asp Ile Glu Val		400												410
ctt gag ggt ttc ctt ttg att tcc acc gac ctg aag tat gaa aca tcc														1416
Leu Glu Gly Phe Leu Leu Ile Ser Thr Asp Leu Lys Tyr Glu Thr Ser		415												425
tca aag cag cag cca agt ttc cac gta tgg gaa ggt ctg aac ctg ata														1464
Ser Lys Gln Gln Pro Ser Phe His Val Trp Glu Gly Leu Asn Leu Ile		430				435								445
agc aga cag tgg agg ggg aag tca gcc cct tga ttgccggt ttgcaattca														1515
Ser Arg Gln Trp Arg Gly Lys Ser Ala Pro *						450								455
ccccaggaag taaatggtcc ttaatcctac aactactgta aaccagaag ggaaagacag														1575

tacacactgg aattgtaaag cccttgtgaa ttgcttaggc agaaagtttt ctttcttaag 1635
 ccttcaggaa cccagaataa ggcagactct gttaaaggga taaatagagg tgtctgaatg 1695
 tgagtgtatg catgctgcgt gtgtctgtgt ttatgtttgt ttgtttgttt ggggcaagaa 1755
 agattctagg acaagagcta ggcattgtact tctgaccagg tgggtaagca actctaagtc 1815
 tgtatttgta ttggtcattc tcagtggaaa tcccttaggc cctctagtgg ttttccccta 1875
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 <213> Homo sapiens

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 gagaccagcc tgggcaacat agcgagcacc ccatctccag aaaaaattta aaaattggct 180
 ggacgcagtg gctcatgcct gtaatcccag cactttggga ggccgagggg gatggatcat 240
 ttgagggtcag gagtttgaga ccagcctggc caacatgggtg aaaccccatc tctactaaaa 300
 atacaaaaat tagccgggca tgggtggtggg cacctgtaat cctagctact tgggaggctg 360
 aggcaggaga atcgcttgaa cccaggaggc ggtggttgta gtgagctagg atcatgccat 420
 tgcagtccag cctggacagc aaagctagac tccatctcaa aaaaaaaaaa aaaaagtcga 480
 ccggccgcga atttagtagt agtagggcgc cgctctagag gatccaagct tacgtacgcg 540
 tgcatgcgac gtcatagctc ttctatagtg tcacctaaat tcaattcact ggtcgtaggt 600
 ctacaacatc atg act ggc aaa aca acc aag gta ccc aat gcc tgt tta 649
 Met Thr Gly Lys Thr Thr Lys Val Pro Asn Ala Cys Leu
 1 5 10
 ttc acc atc aac aaa gaa gac cac aca ctg gga aac atc att aaa tca 697
 Phe Thr Ile Asn Lys Glu Asp His Thr Leu Gly Asn Ile Ile Lys Ser
 15 20 25
 caa ctc cta aaa gac ccg caa gtg cta ttt gct ggc tac aaa gtc ccc 745
 Gln Leu Leu Lys Asp Pro Gln Val Leu Phe Ala Gly Tyr Lys Val Pro
 30 35 40 45
 cac ccc ttg gag cac aag atc atc atc cga gtg cag acc acg ccg gac 793
 His Pro Leu Glu His Lys Ile Ile Ile Arg Val Gln Thr Thr Pro Asp
 50 55 60
 tac agc ccc cag gaa gcc ttt acc aac gcc atc acc gac ctc atc agc 841
 Tyr Ser Pro Gln Glu Ala Phe Thr Asn Ala Ile Thr Asp Leu Ile Ser

65	70	75	
gag ctg tcc ctg ctg gag gag cgc ttc cgg acg tgc ctg ctt ccc ctt			889
Glu Leu Ser Leu Leu Glu Glu Arg Phe Arg Thr Cys Leu Leu Pro Leu			
80	85	90	
cgc ctt ctg ccg tga ttgtcagttt cctgaggcct cccagccac gcttcctgta			944
Arg Leu Leu Pro *			
95			
cagcctgcag aactgccgga catggtggct cacacctgga atcccagaac ttcaggagggc			1004
tgaggtggga ggatcacttg agcccaggag tttgagacca gcctgggcaa cacgctgccc			1064
cagagcacat cagctatgtg cccagctct caaacgacac cttggcgggg aggctcacc			1124
tgtccacctt cacgctggag cagcctttag gccagttcag cagccacaac atctctgact			1184
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gagccacaca tggacacgta agtatcttgt gtgtggacct gtataggcag gtgaatctcc			180
gaactgcaag gccggcgaag gctctctga cattcttctt ttctaactct tcagctctcc			240
ttcctccact aagagcggaa a atg aac aaa tcc cag gaa caa gtg tca ttc			291
Met Asn Lys Ser Gln Glu Gln Val Ser Phe			
1	5	10	
aag gat gta tgt gtg gac ttc act cag gaa gag tgg tat ctg ctg gac			339
Lys Asp Val Cys Val Asp Phe Thr Gln Glu Glu Trp Tyr Leu Leu Asp			
15	20	25	
cct gct cag aag att cta tac aga gat gtg atc ctg gaa aat tat agc			387
Pro Ala Gln Lys Ile Leu Tyr Arg Asp Val Ile Leu Glu Asn Tyr Ser			
30	35	40	
aat ctt gtc tca gta ggg tat tgc att act aaa cca gaa gtg atc ttt			435
Asn Leu Val Ser Val Gly Tyr Cys Ile Thr Lys Pro Glu Val Ile Phe			
45	50	55	
aag atc gag caa gga gaa gag ccc tgg ata tta gaa aaa gga ttc cca			483
Lys Ile Glu Gln Gly Glu Pro Trp Ile Leu Glu Lys Gly Phe Pro			
60	65	70	
agc cag tgc caa cca gaa agg gaa tgg gaa gtt gat gac gtg tta gag			531

Ser Gln Cys Gln Pro Glu Arg Glu Trp Glu Val Asp Asp Val Leu Glu
 75 80 85 90

agc agc cag gaa cat gaa gat gac cca ttt tgg gag ctt cta ttc ccc 579
 Ser Ser Gln Glu His Glu Asp Asp Pro Phe Trp Glu Leu Leu Phe Pro
 95 100 105

aac aac aaa cag taa gtgtagaaaa tggggataga ggaagcaaac tttcaatttg 634
 Asn Asn Lys Gln *

110

gggcaagacc ctgttcttta agaattaccc tataaatttg tgcccatgtg aatgatttgg 694

gaattttggg gttaattttt gtaaagactt tccgaaagtc ctggtggttt atgttta 751

<210> 717
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (981)..(1880)

<400> 717

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taagggcaaa gtgagttaat gtgtagacaa aggcgaggga caagagagag ttaacatcta 120

gacagtggaa aaagccatgg tgtgtggttt ctgggaacca ccaacacttg caggtttagc 180

tttttccag ggttgactac aagaaagaaa accatgtttt tgcaagatta aaatgtggtt 240

gagtgtgcct aaattaacca tccccatttt tatcatattt ccaccatcac ttcagggttt 300

taagagtcag tgctcacctg ggcgagctg gtagtacatt ttgcttctta gaaagctaag 360

tcctgggttc cgtctgattt taggttccag gaacttctg agaacacccg atcgagagg 420

gtaattttct ggagtttgtt ttgcagggat agctgggagt atggccaccc tgctccacga 480

tgcggtaatg aatccagcag aagtggtgaa gcagcgcttg cagatgtaca actcgagca 540

ccggtcagca atcagctgca tccggacggt gtggaggacc gaggggttgg gggccttcta 600

ccggagctac accacgcagc tgaccatgaa catcccttc cagtccatcc acttcatcac 660

ctatgagttc ctgcaggagc aggtcaaccc ccaccggacc tacaacccgc attcccat 720

catctcaggc gggctggccg gggccctcgc cgcggccgcc acgacccccc tggacgtctg 780

taaaaccctt ctgaacactc aggagaacgt ggccctctcg ctggccaaca tcagcggccg 840

gctggtggtg cctatgggcc ctctgctccc caatgcctta gagagaggag gggacggcac 900

ggccgctcac cggaaggctg tgtgcgggga catccgagag gtctgggagc tggaccggt 960

gctgccttgt gacatccggg atg gcg cct tca tta cta tgc cct ttc act 1010
 Met Ala Pro Ser Leu Leu Cys Pro Phe Thr
 1 5 10

gct atg cac aaa acc gtg ggg agg gcc tcc tgc gcc ccg ccg agc tgg	1058
Ala Met His Lys Thr Val Gly Arg Ala Ser Cys Ala Pro Pro Ser Trp	
15 20 25	
cgg atg gag ctg cgc agc ggg agc gtg ggc agc cag gcg gtg gcg cgg	1106
Arg Met Glu Leu Arg Ser Gly Ser Val Gly Ser Gln Ala Val Ala Arg	
30 35 40	
agg atg gat ggg gac agc cga gat ggc ggc ggc ggc aag gac gcc acc	1154
Arg Met Asp Gly Asp Ser Arg Asp Gly Gly Gly Lys Asp Ala Thr	
45 50 55	
ggg tcg gag gac tac gag aac ctg ccg act agc gcc tcc gtg tcc acc	1202
Gly Ser Glu Asp Tyr Glu Asn Leu Pro Thr Ser Ala Ser Val Ser Thr	
60 65 70	
cac atg aca gca gga gcg atg gcc ggg atc ctg gag cac tcg gtc atg	1250
His Met Thr Ala Gly Ala Met Ala Gly Ile Leu Glu His Ser Val Met	
75 80 85 90	
tac ccg gtg gac tcg gtg aag aca cga atg cag agt ttg agt cca gat	1298
Tyr Pro Val Asp Ser Val Lys Thr Arg Met Gln Ser Leu Ser Pro Asp	
95 100 105	
ccc aaa gcc cag tac aca agt gtc tac gga gcc ctc aag aaa atc atg	1346
Pro Lys Ala Gln Tyr Thr Ser Val Tyr Gly Ala Leu Lys Lys Ile Met	
110 115 120	
cgg acc gaa ggc ttc tgg agg ccc ttg cga ggc gtc aac gtc atg atc	1394
Arg Thr Glu Gly Phe Trp Arg Pro Leu Arg Gly Val Asn Val Met Ile	
125 130 135	
atg ggt gca ggg cca gcc cat gcc atg tat ttt gcc tgc tat gaa aac	1442
Met Gly Ala Gly Pro Ala His Ala Met Tyr Phe Ala Cys Tyr Glu Asn	
140 145 150	
atg aaa agg act tta aat gac gtt ttc cac cac caa gga aac agc cac	1490
Met Lys Arg Thr Leu Asn Asp Val Phe His His Gln Gly Asn Ser His	
155 160 165 170	
cta gcc aac ggg ata gct ggg agt atg gcc acc ctg ctc cac gat gcg	1538
Leu Ala Asn Gly Ile Ala Gly Ser Met Ala Thr Leu Leu His Asp Ala	
175 180 185	
gta atg aat cca gca gaa gtg gtg aag cag cgc ttg cag atg tac aac	1586
Val Met Asn Pro Ala Glu Val Val Lys Gln Arg Leu Gln Met Tyr Asn	
190 195 200	
tcg cag cac cgg tca gca atc agc tgc atc cgg acg gtg tgg agg acc	1634
Ser Gln His Arg Ser Ala Ile Ser Cys Ile Arg Thr Val Trp Arg Thr	
205 210 215	
gag ggg ttg ggg gcc ttc tac cgg agc tac acc acg cag ctg acc atg	1682
Glu Gly Leu Gly Ala Phe Tyr Arg Ser Tyr Thr Thr Gln Leu Thr Met	
220 225 230	
aac atc ccc ttc cag tcc atc cac ttc atc acc tat gag ttc ctg cag	1730
Asn Ile Pro Phe Gln Ser Ile His Phe Ile Thr Tyr Glu Phe Leu Gln	
235 240 245 250	
gag cag gtc aac ccc cac cgg acc tac aac ccg cag tcc cac atc atc	1778
Glu Gln Val Asn Pro His Arg Thr Tyr Asn Pro Gln Ser His Ile Ile	
255 260 265	

tca ggc ggg ctg gcc ggg gcc ctc gcc gcg gcc gcg aat tcg gat cct	1826
Ser Gly Gly Leu Ala Gly Ala Leu Ala Ala Ala Ala Asn Ser Asp Pro	
270 275 280	
cga gag atc tct ttt ttt ggg ttt ggt ggg gta tct tca tca tcg aat	1874
Arg Glu Ile Ser Phe Phe Gly Phe Gly Gly Val Ser Ser Ser Ser Asn	
285 290 295	
aga tag ttatatgcac agccattcta tg	1902
Arg *	
300	

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<210> 718
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<212> DNA
<213> Homo sapiens
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<222> (217) .. (330)
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[illegible]

<210> 719
<211> 608
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49) .. (468)

<400> 719

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                                     Met Ser Ser
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tta ccc gtg cca tac aaa ctg cct gtg tct ttg tct gtt ggt tcc tgc      105
Leu Pro Val Pro Tyr Lys Leu Pro Val Ser Leu Ser Val Gly Ser Cys
   5                10                15

gtg ata atc aaa ggg aca cca atc cac tct ttt atc aat gac cca cag      153
Val Ile Ile Lys Gly Thr Pro Ile His Ser Phe Ile Asn Asp Pro Gln
  20                25                30                35

ctg cag gtg gat ttc tac act gac atg gat gag gat tca gat att gcc      201
Leu Gln Val Asp Phe Tyr Thr Asp Met Asp Glu Asp Ser Asp Ile Ala
                40                45                50

ttc cgt ttc cga gtg cac ttt ggc aat cat gtg gtc atg aac agg cgt      249
Phe Arg Phe Arg Val His Phe Gly Asn His Val Val Met Asn Arg Arg
                55                60                65

gag ttt ggg ata tgg atg ttg gag gag aca aca gac tac gtg ccc ttt      297
Glu Phe Gly Ile Trp Met Leu Glu Glu Thr Thr Asp Tyr Val Pro Phe
   70                75                80

gag gat ggc aaa caa ttt gag ctg tgc atc tac gta cat tac aat gag      345
Glu Asp Gly Lys Gln Phe Glu Leu Cys Ile Tyr Val His Tyr Asn Glu
   85                90                95

tat gag ata aag gtc aat ggc ata cgc att tac ggc ttt gtc cat cga      393
Tyr Glu Ile Lys Val Asn Gly Ile Arg Ile Tyr Gly Phe Val His Arg
 100                105                110                115

atc ccg cca tca ttt gtg aag atg gtg caa gtg tgc aga gat atc tcc      441
Ile Pro Pro Ser Phe Val Lys Met Val Gln Val Ser Arg Asp Ile Ser
                120                125                130

ctg acc tca gtg tgt gtc tgc aat tga gggag atgatcacac tctcattgt      493
Leu Thr Ser Val Cys Val Cys Asn *
                135                140

tgaggaatcc ctctttctac ctgaccatgg gattcccaga acctgctaac agaataatcc      553

ctgctcacat tttcccctac actttgtcat taaaacagca cgaaaactca aaaaa      608

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<210> 720

<211> 1625

<212> DNA

<213> Homo sapiens

<220>

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<222> (40) .. (1179)

<400> 720

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	Met Ser Ser Pro Ser	
	1 5	
ctc agt gac ctg ggc aag aga gag ccg gcc gcc gcc gcg gac gag cgg		102
Leu Ser Asp Leu Gly Lys Arg Glu Pro Ala Ala Ala Asp Glu Arg		
10 15 20		
ggc acg cag cag cgc cgg gcc tgc gcc aac gcc acc tgg aac agc atc		150
Gly Thr Gln Gln Arg Arg Ala Cys Ala Asn Ala Thr Trp Asn Ser Ile		
25 30 35		
cac aac ggg gtg atc gcc gtc ttc cag cgc aag ggg ctg ccc gac cag		198
His Asn Gly Val Ile Ala Val Phe Gln Arg Lys Gly Leu Pro Asp Gln		
40 45 50		
gag ctc ttc agc ctc aac gag ggc gtc cgg cag ctg ttg aag aca gag		246
Glu Leu Phe Ser Leu Asn Glu Gly Val Arg Gln Leu Leu Lys Thr Glu		
55 60 65		
ctg ggg tcc ttc ttc acg gag tac ctg cag aac cag ctg ctg aca aaa		294
Leu Gly Ser Phe Phe Thr Glu Tyr Leu Gln Asn Gln Leu Leu Thr Lys		
70 75 80 85		
ggc atg gtg atc ctt cgg gac aag att cgc ttc tat gag gga cag aag		342
Gly Met Val Ile Leu Arg Asp Lys Ile Arg Phe Tyr Glu Gly Gln Lys		
90 95 100		
ctg ctg gac tca ctg gca gag acc tgg gac ttc ttc ttc agt gac gtg		390
Leu Leu Asp Ser Leu Ala Glu Thr Trp Asp Phe Phe Phe Ser Asp Val		
105 110 115		
ctg ccc atg ctg cag gcc atc ttc tac ccg gtg cag ggc aag gag cca		438
Leu Pro Met Leu Gln Ala Ile Phe Tyr Pro Val Gln Gly Lys Glu Pro		
120 125 130		
tcg gtg cgc cag ctg gcc ctg ctg cac ttc cgg aat gcc atc acc ctc		486
Ser Val Arg Gln Leu Ala Leu Leu His Phe Arg Asn Ala Ile Thr Leu		
135 140 145		
agt gtg aag cta gag gat gcg ctg gcc cgg gcc cat gcc cgt gtg ccc		534
Ser Val Lys Leu Glu Asp Ala Leu Ala Arg Ala His Ala Arg Val Pro		
150 155 160 165		
cct gcc atc gtg cag atg ctg ctg gtg ctg cag ggg gta cat gag tcc		582
Pro Ala Ile Val Gln Met Leu Leu Val Leu Gln Gly Val His Glu Ser		
170 175 180		
agg ggc gtg act gag gac tac ctg cgc ctg gag acg ctg gtc cag aag		630
Arg Gly Val Thr Glu Asp Tyr Leu Arg Leu Glu Thr Leu Val Gln Lys		
185 190 195		
gtg gtg tcg cca tac ctg ggc acc tac ggc ctc cac tcc agc gag ggg		678
Val Val Ser Pro Tyr Leu Gly Thr Tyr Gly Leu His Ser Ser Glu Gly		
200 205 210		
ccc ttc acc cat tcc tgc atc ctg gaa aag cgc ctc ctc cgc cgc tcc		726
Pro Phe Thr His Ser Cys Ile Leu Glu Lys Arg Leu Leu Arg Arg Ser		
215 220 225		
cgc tcg ggg gac gtg ctg gcc aag aac cct gtg gtg cgc tcc aag agc		774
Arg Ser Gly Asp Val Leu Ala Lys Asn Pro Val Val Arg Ser Lys Ser		
230 235 240 245		

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tac aac acg cct ctg ctg aac ccc gtg cag gag cac gag gcg gag ggc      822
Tyr Asn Thr Pro Leu Leu Asn Pro Val Gln Glu His Glu Ala Glu Gly
                250                255                260

gcg gcg gcc ggc ggt acc agc atc cgc agg cac tct gtg tcg gag atg      870
Ala Ala Ala Gly Gly Thr Ser Ile Arg Arg His Ser Val Ser Glu Met
                265                270                275

acg tcc tgc ccc gag cct cag ggc ttc tcc gac ccg ccc ggc cag ggc      918
Thr Ser Cys Pro Glu Pro Gln Gly Phe Ser Asp Pro Pro Gly Gln Gly
                280                285                290

ccc acc ggg acc ttc agg tcc tcc ccg gcg ccc cac tca ggg ccc tgc      966
Pro Thr Gly Thr Phe Arg Ser Ser Pro Ala Pro His Ser Gly Pro Cys
                295                300                305

ccc agc aga ctg tac ccc acg acc cag ccc cct gag cag ggc ttg gat      1014
Pro Ser Arg Leu Tyr Pro Thr Thr Gln Pro Pro Glu Gln Gly Leu Asp
                310                315                320                325

ccc acc cgc agc tcc ctg ccc cgc tcc agc ccg gag aac ctg gtg gac      1062
Pro Thr Arg Ser Ser Leu Pro Arg Ser Ser Pro Glu Asn Leu Val Asp
                330                335                340

cag atc ctg gag tcc gtg gac tcg gat tct gaa ggg att ttc att gac      1110
Gln Ile Leu Glu Ser Val Asp Ser Asp Ser Glu Gly Ile Phe Ile Asp
                345                350                355

ttt ggc cgg ggc cgg ggc tct ggc atg tcc gac ttg gag ggc tct ggg      1158
Phe Gly Arg Gly Arg Gly Ser Gly Met Ser Asp Leu Glu Gly Ser Gly
                360                365                370

ggc cgg cag agt gtc gtg tga gg cctcacagct ggccttgagt ttttactgac      1211
Gly Arg Gln Ser Val Val *
                375                380

acgtccctgt gtgcgggggt gtccatgtgg cgtgtgtgtg agtgagaactt ttttactgcg      1271

tcccgtcctcg ccagccctat cggcctcgtc actggccttg gtcactttgt atttctgtct      1331

tggttggaag taccatcagc cttccttgct cggcccaggt ctgtttcagg catctgagtc      1391

ggcgtttacc caggggcccgg gccagagacg ggggtcggcc gtcgctccc acgctcctcc      1451

tgccccagcc ctctggtgtc cacacctgcc cacagagaat gtaaaccag tgggctctgc      1511

ccacgcccgg ccccaaagt accagactcc agcacacctg tctcctcctg cctgggggtgg      1571

ccatggggat ggaaggggggt ggaataaaac ctgtcaacct ggaaaaaaaaa aaaa      1625

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<210> 721
 <211> 1116
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (163) .. (789)

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1972

taaaatagtt gaacttgaca gcatataact taaagtgaat atgtttttgc cagaacatgt 1039
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 ctctgaaaaa aaaaaaa 1116

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 gctgctgctc cgcggtggag tcaccgcacc gctcccgga tc atg gtg ttc tac 174
 Met Val Phe Tyr
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 ttc acc agc agc agc gtt aat tca tct gcc tac act att tac atg gga 222
 Phe Thr Ser Ser Ser Val Asn Ser Ser Ala Tyr Thr Ile Tyr Met Gly
 5 10 15 20
 aaa gat aaa tat gaa aat gaa gat ctg atc aag cat ggc tgg cct gaa 270
 Lys Asp Lys Tyr Glu Asn Glu Asp Leu Ile Lys His Gly Trp Pro Glu
 25 30 35
 gat atc tgg ttt cat gtg gac aaa ctc tct tcg gct cat gta tac ctt 318
 Asp Ile Trp Phe His Val Asp Lys Leu Ser Ser Ala His Val Tyr Leu
 40 45 50
 cga tta cat aag gga gag aat ata gaa gac atc cca aag gaa gtg ctg 366
 Arg Leu His Lys Gly Glu Asn Ile Glu Asp Ile Pro Lys Glu Val Leu
 55 60 65
 atg gac tgt gcc cac ctt gtg aag gcc aat agc att caa gga gct att 414
 Met Asp Cys Ala His Leu Val Lys Ala Asn Ser Ile Gln Gly Ala Ile
 70 75 80
 cat cac taa tgaaagt tgaaaatatg tcttcaaatac aggatggcca tgattcatat 470
 His His *
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Met Arg Val	His Ile Ser	Ser Cys Leu	Lys Val Gln	Glu Gln Met	Ala	
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Asn Cys Pro	Lys Phe Val	Pro Val Val	Pro Thr Ser	Gln Pro Ile	Pro	
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Ser Asn Ile	Pro Asn Arg	Ser Thr Phe	Ala Cys Pro	Tyr Cys Gly	Ala	
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Arg Asn Leu	Asp Gln Gln	Glu Leu Val	Lys His Cys	Val Glu Ser	His	
	50	55	60			
cgc agc gac	ccc aac cgc	gtg gtg tgc	ccc atc tgc	tcg gca atg	ccc	1198
Arg Ser Asp	Pro Asn Arg	Val Val Cys	Pro Ile Cys	Ser Ala Met	Pro	
	65	70	75	80		
tgg ggg gac	ccc agc tac	aag agc gcc	aac ttc ctg	cag cac ctg	ctt	1246
Trp Gly Asp	Pro Ser Tyr	Lys Ser Ala	Asn Phe Leu	Gln His Leu	Leu	
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cac cga cac	aag ttc tcc	tac gac acc	ttt gtg gac	tac agt att	gac	1294
His Arg His	Lys Phe Ser	Tyr Asp Thr	Phe Val Asp	Tyr Ser Ile	Asp	
	100	105	110			
gag gag gcc	gcc ttc cag	gct gct ctg	gcc ctg tct	ctc tct gag	aac	1342
Glu Glu Ala	Ala Phe Gln	Ala Ala Leu	Ala Leu Ser	Leu Ser Glu	Asn	

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	Met Ile Ser
	1
aga tac act	cgg aag gcg gtg cca cag agc ttg gag ctg aaa gga ata 164
Arg Tyr Thr	Arg Lys Ala Val Pro Gln Ser Leu Glu Leu Lys Gly Ile
5	10 15
aca aaa cat	gct ctt aac cat cat ccc cct cca gag aag ctg gag gaa 212

Thr Lys His Ala Leu Asn His His Pro Pro Pro Glu Lys Leu Glu Glu	
20 25 30 35	
att tcc ccc acc agt gac agt cat gag aaa gac aca agt tcc caa agc	260
Ile Ser Pro Thr Ser Asp Ser His Glu Lys Asp Thr Ser Ser Gln Ser	
40 45 50	
aag tct gac atc aca aga gaa tca tct ttt aca tca gcc gac act ggg	308
Lys Ser Asp Ile Thr Arg Glu Ser Ser Phe Thr Ser Ala Asp Thr Gly	
55 60 65	
aat tca ctg tct gct ttt cca agt tat aca ggc gca ggg ata tct act	356
Asn Ser Leu Ser Ala Phe Pro Ser Tyr Thr Gly Ala Gly Ile Ser Thr	
70 75 80	
gaa gga agc tcg gac ttc tcc tgg gga tat ggt gaa ctc gat caa aat	404
Glu Gly Ser Ser Asp Phe Ser Trp Gly Tyr Gly Glu Leu Asp Gln Asn	
85 90 95	
gcc act gaa aaa gtc cag aca atg ttc aca gcc att gat gaa ctc ttg	452
Ala Thr Glu Lys Val Gln Thr Met Phe Thr Ala Ile Asp Glu Leu Leu	
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tat gag cag aag ttg agt gtg cat acc aag agt cta caa gaa gag tgc	500
Tyr Glu Gln Lys Leu Ser Val His Thr Lys Ser Leu Gln Glu Glu Cys	
120 125 130	
caa cag tgg aca gct agc ttt cct cac ctc agg att cta ggt agg cag	548
Gln Gln Trp Thr Ala Ser Phe Pro His Leu Arg Ile Leu Gly Arg Gln	
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Ile Ile Thr Pro Ser Glu Gly Tyr Arg Leu Tyr Pro Arg Ser Pro Ser	
150 155 160	
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Ala Val Ser Ala Ser Tyr Glu Thr Thr Leu Ser Gln Glu Arg Asp Ser	
165 170 175	
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Thr Ile Phe Gly Ile Arg Gly Lys Lys Leu His Phe Ser Ser Ser Tyr	
180 185 190 195	
gct cat aaa gca tct tcc att gcc aaa tcc tcc agc ttt tgt tct atg	740
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Glu Tyr Leu Ala Phe Asp His Ile Asp Ile Glu Glu Gly Phe His Gly	
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Lys Lys Ser Glu Ala Ala Thr Glu Lys Gln Lys Leu Gly Tyr Pro Pro	
245 250 255	
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Ile Ala Pro Phe Tyr Cys Met Lys Glu Asp Val Leu Ala Tyr Val Phe	
260 265 270 275	
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Asp Ser Val Trp Cys Lys Val Val Ser Cys Met Glu Gln Leu Thr Arg	
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Ser His Trp Glu Gly Phe Ala Ser Asp Asp Glu Ser Asn Val Ala Val	
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acc aga ccc gat tca gaa agt tcc tgt gtg ctg agt gaa cta cat cct	1076
Thr Arg Pro Asp Ser Glu Ser Cys Val Leu Ser Glu Leu His Pro	
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Leu Val Leu Pro Arg Val Pro Gln Ser Lys Val Leu Tyr Ile Thr Ser	
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Asn Pro Met Ser Leu Cys Gln Ala Ser Arg His Gln Pro Asn Val Asn	
340 345 350 355	
gat ctc ttg gtt cat gga atg cct cta cag cca aga aat ctc tcc cta	1220
Asp Leu Leu Val His Gly Met Pro Leu Gln Pro Arg Asn Leu Ser Leu	
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Met Asp Lys Leu Leu Asp Leu Asp Asp Lys Leu Leu Met Arg Pro Gly	
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Phe Ser Thr Ser Ser Leu Ser Tyr Thr Val Gln Ser Thr Arg Arg Arg	
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Asn Pro Pro Pro Arg Thr Leu His Pro Ile Ser Thr Ser His Ser Cys	
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Ala Glu Thr Pro Arg Ser Val Glu Glu Ile Leu Arg Gly Ala Arg Val	
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Pro Val Ala Pro Asp Ser Leu Ser Pro Ser Pro Thr Pro Leu Ser	
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Gln Gly Pro *	
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1981

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gtc cac cgg gtg gct aag aag ctg cag tct ggc ttg gtc tgg acc aac Val His Arg Val Ala Lys Lys Leu Gln Ser Gly Leu Val Trp Thr Asn 330 335 340	1302
tgc tgg ctc atc agg gag ctg aac ctt cct ttc ggg ggg atg aag agt Cys Trp Leu Ile Arg Glu Leu Asn Leu Pro Phe Gly Gly Met Lys Ser 345 350 355	1350
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375 380	

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 Ala Ser Ser Thr Pro Lys Asp His Ser Ala Ser Pro Ala Thr Glu Gln
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 Ser Trp Met Gly Asn Asp Phe Asp Glu Leu Thr Glu Leu Gly Phe Arg
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 Lys Ser Val Met Thr Asn Phe Ser Gln Leu Lys Glu Asp Val Arg Thr
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 His His Lys Glu Ala Lys Asn Leu Glu Lys Arg Leu Asp Lys Trp Leu
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 Thr Arg Ile Asn Ser Ile Glu Glu Thr Leu Asn Asp Leu Met Glu Leu
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 aaa acc atg gca cga gaa cta cgt gac aca tgc aca agc ttc agt agc 336
 Lys Thr Met Ala Arg Glu Leu Arg Asp Thr Cys Thr Ser Phe Ser Ser
 100 105 110
 cga ttc gat caa gtg gaa gaa ggg gaa ata caa act acc atc aga gaa 384
 Arg Phe Asp Gln Val Glu Glu Gly Glu Ile Gln Thr Thr Ile Arg Glu
 115 120 125
 tat tat gaa cac ctc tac gca aat aaa cta gaa aat cta gaa gaa atg 432
 Tyr Tyr Glu His Leu Tyr Ala Asn Lys Leu Glu Asn Leu Glu Glu Met
 130 135 140
 gat aaa ttc ctg gac aca tac act ctc cca aga cta aac cag gaa gaa 480
 Asp Lys Phe Leu Asp Thr Tyr Thr Leu Pro Arg Leu Asn Gln Glu Glu
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Ile Asn Ser Leu Pro Thr Lys Lys Ile Pro Gly Pro Asp Arg Phe Thr	
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gcc aaa ttc tac cag agg tac aaa gag gag ctg agt aac ctg atc cac	624
Ala Lys Phe Tyr Gln Arg Tyr Lys Glu Glu Leu Ser Asn Leu Ile His	
195 200 205	
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Tyr Leu Gly Leu Ser His His Leu Leu Ala Leu Asn Phe Ile Ile Val	
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tct ttt ggc aaa aaa agc gcg tgg tct tct gcc caa gtg aag gtg acc	720
Ser Phe Gly Lys Lys Ser Ala Trp Ser Ser Ala Gln Val Lys Val Thr	
225 230 235 240	
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Asp Thr Asp Phe Asp Gly Val Glu Val Arg Val Phe Glu Gly Pro Pro	
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Lys Pro Glu Glu Pro Leu Lys Arg Ser Val Val Tyr Ile His Gly Gly	
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Gly Trp Ala Leu Ala Ser Ala Lys Ile Arg Tyr Tyr Asp Glu Leu Cys	
275 280 285	
aca gca atg gct gag gaa ttg aat gct gtc att gtt tcc att gaa tac	912
Thr Ala Met Ala Glu Glu Leu Asn Ala Val Ile Val Ser Ile Glu Tyr	
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Arg Leu Val Pro Lys Val Tyr Phe Pro Glu Gln Ile His Asp Val Val	
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Val Asp Pro Gly Arg Ile Cys Ile Ser Gly Asp Ser Ala Gly Gly Asn	
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Asn Lys Leu Lys Leu Gln Ala Leu Ile Tyr Pro Val Leu Gln Ala Leu	
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ccc cgc tat gtc atg gtg aag tat tgg gtg gac tac ttc aaa ggc aac	1248
Pro Arg Tyr Val Met Val Lys Tyr Trp Val Asp Tyr Phe Lys Gly Asn	
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Leu Pro Ala Ser Phe Thr Lys Asn Tyr Lys Pro Val Val Gln Thr Thr
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tcc gcc cca ctc att gca gac cag gca gtg ctg cag ctc ctc cca aag      1488
Ser Ala Pro Leu Ile Ala Asp Gln Ala Val Leu Gln Leu Leu Pro Lys
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acc tac att ctg acg tgt gag cat gat gtc ctc aga gac gat ggc atc      1536
Thr Tyr Ile Leu Thr Cys Glu His Asp Val Leu Arg Asp Asp Gly Ile
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atg tat gcc aag cgt ttg gag agt gcc ggt gtg gag gtg acc ctg gat      1584
Met Tyr Ala Lys Arg Leu Glu Ser Ala Gly Val Glu Val Thr Leu Asp
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cac ttt gag gat ggc ttt cac gga tgt atg att ttc act agc tgg ccc      1632
His Phe Glu Asp Gly Phe His Gly Cys Met Ile Phe Thr Ser Trp Pro
      530                      535                      540

acc aac ttc tca gtg gga atc cgg act agg aat agt tac atc aag tgg      1680
Thr Asn Phe Ser Val Gly Ile Arg Thr Arg Asn Ser Tyr Ile Lys Trp
      545                      550                      555                      560

cta gat caa aac ctg taa aggagc aaaacttcca gaagcctcga gccctcttg      1734
Leu Asp Gln Asn Leu *
      565

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ctccttaatt ctgctagagt taaccttgag ttcagagcag tattaaatgc gtgcactttc      2154

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tgccaggatg aaagagttgg agtaacctag gtgattctga gtgaatcagt caggaggcct      240
tcctggaggg ggctgaggcc ccagcttggtg gccaccacaa cgtatcaagc tatctccagg      300
gttgggctca ggactcagag ctgacgcagc tgggggtgccc cttggttctg gagg  atg      357
                                     Met
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agg ctc ctc cgc aga cgc cac atg ccc ctg cgc ctg gcc atg gtg ggc      405
Arg Leu Leu Arg Arg Arg His Met Pro Leu Arg Leu Ala Met Val Gly
          5                      10                      15

tgc gcc ttt gtg ctc ttc ctc ttc ctc ctg cat agg gat gtg agc agc      453
Cys Ala Phe Val Leu Phe Leu Phe Leu Leu His Arg Asp Val Ser Ser
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aga gag gag gcc aca gag aag ccg tgg ctg aag tcc ctg gtg agc cgg      501
Arg Glu Glu Ala Thr Glu Lys Pro Trp Leu Lys Ser Leu Val Ser Arg
          35                      40                      45

aag gat cac gtc ctg gac ctc atg ctg gag gcc atg aac aac ctt aga      549
Lys Asp His Val Leu Asp Leu Met Leu Glu Ala Met Asn Asn Leu Arg
          50                      55                      60                      65

gat tca atg ccc aag ctc caa atc agg gct cca gaa gcc cag cag act      597
Asp Ser Met Pro Lys Leu Gln Ile Arg Ala Pro Glu Ala Gln Gln Thr
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ctg ttc tcc ata aat cag tcc tgc ctc cct ggg ttc tat acc cca gct      645
Leu Phe Ser Ile Asn Gln Ser Cys Leu Pro Gly Phe Tyr Thr Pro Ala
          85                      90                      95

gaa ctg aag ccc ttc tgg gaa cgg cca cca cag gac ccc aat gcc cct      693
Glu Leu Lys Pro Phe Trp Glu Arg Pro Pro Gln Asp Pro Asn Ala Pro
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ggg gca gat gga aaa gca ttt cag aag agc aag tgg acc ccc ctg gag      741
Gly Ala Asp Gly Lys Ala Phe Gln Lys Ser Lys Trp Thr Pro Leu Glu
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acc cag gaa aag gaa gaa ggc tat aag aag cac tgt ttc aat gcc ttt      789
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Pro Pro Glu Cys Val Asp Gln Lys Phe Arg Arg Cys Pro Pro Leu Ala
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Ser Val Ala Gln Ala Glu Val Leu Thr Phe Leu Asp Ala His Cys Glu	
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Cys Phe His Gly Trp Leu Glu Pro Leu Leu Ala Arg Ile Ala Glu Asp	
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Phe Glu Phe Ala Lys Pro Val Gln Arg Gly Arg Val His Ser Arg Gly	
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Asn Phe Asp Trp Ser Leu Thr Phe Gly Trp Glu Thr Leu Pro Pro His	
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Phe Ala Gly Gly Leu Phe Ser Ile Ser Lys Ser Tyr Phe Glu His Ile	
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Gly Thr Tyr Asp Asn Gln Met Glu Ile Trp Gly Gly Glu Asn Val Glu	
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Cys Ser Val Val Gly His Val Phe Arg Thr Lys Ser Pro His Thr Phe	
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420 425 430	
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Val Trp Met Asp Ser Tyr Lys Lys Ile Phe Tyr Arg Arg Asn Leu Gln	
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cac aat gtc tac cca gag atg ttt gtt cct gac ctg acg ccc acc ttc	1845
His Asn Val Tyr Pro Glu Met Phe Val Pro Asp Leu Thr Pro Thr Phe	
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Tyr Gly Ala Ile Lys Asn Leu Gly Thr Asn Gln Cys Leu Asp Val Gly	
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2844

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 95 100 105
 aaa gag atg gaa gaa aaa ata agc aat ctt aag gaa cac ctt gca agc 864
 Lys Glu Met Glu Glu Lys Ile Ser Asn Leu Lys Glu His Leu Ala Ser
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<222> (399) .. (1313)

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cagctggaag gcagctggca ctggcagccc ccttcattgc acctatctcc cccatctcat	300
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atg gcc cat ctt gga	
Met Ala His Leu Gly	
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aac tgc ctc ctg tcc atc aag ccc cag gag aag tca gag gga ctt cag	461
Asn Cys Leu Leu Ser Ile Lys Pro Gln Glu Lys Ser Glu Gly Leu Gln	
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Phe Glu Tyr Thr Pro Glu Cys Ser Val Phe Asp Leu Leu Gly Ile Pro	
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Leu Tyr His Gly Trp Leu Val Asp Pro Gln Gln Ser Pro Glu Ala Ala	
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Arg Ala Val Gly Lys Leu Ser Tyr Asn Gln Leu Val Glu Arg Ile Ile	
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Phe Arg Asn Asn His Phe Ser Thr Met Thr Lys His Lys Ser His Leu	
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Asp	Phe	His	Leu	Ser	His	Ser	Leu	Gly	Lys	Gly	Pro	Gly	Ala	Glu	Gly		
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Gly	Ser	Gly	Ser	Pro	Glu	Lys	Gln	Leu	Gln	Val	Asp	Gln	Asp	Tyr	Leu		
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Thr	Asp	Leu	Glu	Leu	Ala	Gln	Gln	Leu	Gln	Gln	Glu	Glu	Tyr	Gln	Gln		
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agg	ccg	aag	cac	gag	tca	gac	tgc	att	ctg	ctg	tag	ctct	gccccagtgc			1327	
Arg	Pro	Lys	His	Glu	Ser	Asp	Cys	Ile	Leu	Leu	*						
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Val Arg Asp Leu Ala Gly Ala Glu Glu Phe Gly Gly Gly Glu Glu Gly	
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Thr Gly Leu Thr Gly Ile Lys Glu Ile Gly Asp Gly Glu Glu Gly Ser	
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gga caa agg cca gag gaa ata ccg atg gac cta acg gta gtg aag cag	240
Gly Gln Arg Pro Glu Glu Ile Pro Met Asp Leu Thr Val Val Lys Gln	
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gaa att ata gac tgg cca ggt aca gaa ggc agg ttg gct ggc cag tgg	288
Glu Ile Ile Asp Trp Pro Gly Thr Glu Gly Arg Leu Ala Gly Gln Trp	
85 90 95	
gta gaa cag gag gtg gag gat agg cct gag gtg aag gat gag aac gca	336
Val Glu Gln Glu Val Glu Asp Arg Pro Glu Val Lys Asp Glu Asn Ala	
100 105 110	
ggc gta ttg gag gtg aag cag gag acg gat agt agt tta gtg gta aaa	384
Gly Val Leu Glu Val Lys Gln Glu Thr Asp Ser Ser Leu Val Val Lys	
115 120 125	
gaa gcg aag gtg ggt gaa cca gag gta aag gaa gag aag gta aag gaa	432
Glu Ala Lys Val Gly Glu Pro Glu Val Lys Glu Glu Lys Val Lys Glu	
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Glu Val Met Asp Trp Ser Glu Val Lys Glu Glu Lys Asp Asn Leu Glu	
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Ile Lys Gln Glu Glu Lys Phe Val Gly Gln Cys Ile Lys Glu Glu Leu	
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Met His Gly Glu Cys Val Lys Glu Glu Lys Asp Phe Leu Lys Lys Glu	
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Ile Val Asp Asp Thr Lys Val Lys Glu Glu Pro Pro Ile Asn His Pro	
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260 265 270	

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Asn Leu Leu Ser Asp Tyr Arg Phe Leu Glu Asp Val Ala Arg Thr Ala	
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Asp His Ile Ser Arg Asp Ala Phe Leu Lys Arg Pro Ile Ser Asn Lys	
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Tyr Met Tyr Phe Met Lys Asn Arg Ala Arg Arg Gln Gly Ile Asn Leu	
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Lys Leu Leu Pro Asn Gly Phe Thr Lys Arg Lys Glu Asn Ser Thr Phe	
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Pro Gln Ser Gln Ala Glu Tyr Ile Glu Lys Arg Val Pro Asp Asp Lys	
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370 375 380	
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Pro Val Ile Arg Gln Arg Leu Lys Ala Tyr Ile Arg Ser Gln Thr Gly	
385 390 395 400	
gtt cag att tta atg aag att gaa tat atg cag caa aat tta gta aga	1248
Val Gln Ile Leu Met Lys Ile Glu Tyr Met Gln Gln Asn Leu Val Arg	
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tat tat gaa cta gat cct tat aaa agt ctc cta gac aat ttg agg aac	1296
Tyr Tyr Glu Leu Asp Pro Tyr Lys Ser Leu Leu Asp Asn Leu Arg Asn	
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Lys Val Ile Ile Glu Tyr Pro Thr Leu His Val Val Leu Lys Gly Ser	
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Asn Asn Asp Met Lys Val Leu His Gln Val Lys Ser Glu Ser Thr Lys	
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Asn Val Gly Asn Glu Asn *	
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<213> Homo sapiens

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<222> (319)..(2253)
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Arg Gly Val Leu Gln Lys Leu Ile His His Arg Lys Glu Thr Leu Ser	15	20 25
cgc aga ggc cct tca gcc tcc agt gtt gca gtt atg acc tca tca acc 447		
Arg Arg Gly Pro Ser Ala Ser Ser Val Ala Val Met Thr Ser Ser Thr	30	35 40
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Ser Asp His His Leu Asp Ala Ala Ala Arg Gln Pro Asn Gly Val	45	50 55
tgt cga gct ggg ttc gag cgg cag cac agc cta ccc agt tct gag cat 543		
Cys Arg Ala Gly Phe Glu Arg Gln His Ser Leu Pro Ser Ser Glu His	60	65 70 75
ctt ggg gca gat gga ggc ctc tac cag atc cca ctt cca tct tcc cag 591		
Leu Gly Ala Asp Gly Gly Leu Tyr Gln Ile Pro Leu Pro Ser Ser Gln	80	85 90
atc cca cca cag cct cgc cga gca gca ccc acc aca ccg ccc cca cca 639		
Ile Pro Pro Gln Pro Arg Arg Ala Ala Pro Thr Thr Pro Pro Pro	95	100 105
gtg aag cgc cga gac cgc gag gcc ctg atg gcc tct ggg agt ggt ggc 687		
Val Lys Arg Arg Asp Arg Glu Ala Leu Met Ala Ser Gly Ser Gly Gly	110	115 120
cac aac acc atg ccc tcc ggg ggt aac tct gtg tcc agc ggc tcc tca 735		
His Asn Thr Met Pro Ser Gly Gly Asn Ser Val Ser Ser Gly Ser Ser	125	130 135

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ggc acc cac acc acc gtg tcc caa gtc cag ccc cct ccc tcc aag gca Gly Thr His Thr Thr Val Ser Gln Val Gln Pro Pro Pro Ser Lys Ala 175 180 185	879
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Met Leu Lys Ser Met
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gtt ctg tgg tta gga gaa cag gta caa agc ttg cag ttg cag cag caa 163
Val Leu Trp Leu Gly Glu Gln Val Gln Ser Leu Gln Leu Gln Gln Gln
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Leu Arg His His Phe Asn His Ile His Ile Cys Val Thr Asn Ser Glu
25 30 35

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Tyr Asn Gln Ser Glu Tyr Pro Trp Asp Leu Val Lys Ala His Leu Gln
40 45 50

gga gct ttc aca tcc aac atc acc ttt gat att agt gaa tta caa aac 307
Gly Ala Phe Thr Ser Asn Ile Thr Phe Asp Ile Ser Glu Leu Gln Asn
55 60 65

aaa att ctt gat tta aat agg cac act caa gaa ttt cag cct tct tta 355
Lys Ile Leu Asp Leu Asn Arg His Thr Gln Glu Phe Gln Pro Ser Leu
70 75 80 85

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gaa gac tgg act gaa ttc cag gaa ggc ctg gag agc ctc aac cct tgg 403
 Glu Asp Trp Thr Glu Phe Gln Glu Gly Leu Glu Ser Leu Asn Pro Trp
 90 95 100

 acc tat cta aag tac cac agt aac atc tta tat gta gtt ctt gga gta 451
 Thr Tyr Leu Lys Tyr His Ser Asn Ile Leu Tyr Val Val Leu Gly Val
 105 110 115

 atg ttg ttt tgt ctc tgt ctt ctg ttt ata gtc tgt aaa atc gga tgg 499
 Met Leu Phe Cys Leu Cys Leu Leu Phe Ile Val Cys Lys Ile Gly Trp
 120 125 130

 acc gcc aat cgg aga atg aga gct gcc cag cct ggt ctt aca ttc ttt 547
 Thr Ala Asn Arg Arg Met Arg Ala Ala Gln Pro Gly Leu Thr Phe Phe
 135 140 145

 caa tta att cat aaa cag ggg gat atg cag gga gcc gaa ggc cca tgg 595
 Gln Leu Ile His Lys Gln Gly Asp Met Gln Gly Ala Glu Gly Pro Trp
 150 155 160 165

 gac gtg acc aac tca gca ttc cac tgg agg cta tat gat caa aca gca 643
 Asp Val Thr Asn Ser Ala Phe His Trp Arg Leu Tyr Asp Gln Thr Ala
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 Asn Cys Leu Ser *
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 cggcagcagc ggcagcggct atggtgtggt cgctcgattc tcccagtgcc tggctgagtt 180
 tcggacgtgg ttaagaacca actggttgag gttcaatgca gacaagacgg atgtgatgct 240
 gtagaaaatg tgcattcag atg ttt atg ttt aat tgg ttt aca gac tgt ctg 291
 Met Phe Met Phe Asn Trp Phe Thr Asp Cys Leu
 1 5 10

 tgg act ctt ttc ctg tca aat tac cag cca tct gtt gaa tct tca agt 339
 Trp Thr Leu Phe Leu Ser Asn Tyr Gln Pro Ser Val Glu Ser Ser Ser
 15 20 25

 cca gga ggt tca gca aca tca gat gac cat gaa ttt gat cca tca gct 387
 Pro Gly Gly Ser Ala Thr Ser Asp Asp His Glu Phe Asp Pro Ser Ala
 30 35 40

 gac atg ctg gtt cat gat ttt gat gat gaa cga aca tta gaa gag gaa 435
 Asp Met Leu Val His Asp Phe Asp Asp Glu Arg Thr Leu Glu Glu Glu

45	50	55	
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gca agg gaa ggc gac atg cca att cat gaa ctt ctc agc ctt tat ggt Ala Arg Glu Gly Asp Met Pro Ile His Glu Leu Leu Ser Leu Tyr Gly 80 85 90			531
tat ggt agt act gtt cga cta cct gaa gaa gat gag gaa gag gaa gaa Tyr Gly Ser Thr Val Arg Leu Pro Glu Glu Asp Glu Glu Glu Glu Glu 95 100 105			579
gag gaa gaa gaa ggt gaa gat gat gaa gat gct gat aat gat gac aac Glu Glu Glu Glu Gly Glu Asp Asp Glu Asp Ala Asp Asn Asp Asp Asn 110 115 120			627
agt ggc tgt agt ggg gaa aat aaa gag gag aat ata aag gat tca tca Ser Gly Cys Ser Gly Glu Asn Lys Glu Glu Asn Ile Lys Asp Ser Ser 125 130 135			675
ggt cag gag gat gaa act cag tct tcc aat gat gat cca tca caa tct Gly Gln Glu Asp Glu Thr Gln Ser Ser Asn Asp Asp Pro Ser Gln Ser 140 145 150 155			723
ggt gct tct caa gat gcc cag gaa ata atc cgc cca cgt cga tgt aaa Val Ala Ser Gln Asp Ala Gln Glu Ile Ile Arg Pro Arg Arg Cys Lys 160 165 170			771
tat ttt gat aca aat agt gaa gta gaa gaa gaa tct gaa gaa gat gaa Tyr Phe Asp Thr Asn Ser Glu Val Glu Glu Glu Ser Glu Glu Asp Glu 175 180 185			819
gat tat att cca tca gaa gac tgg aaa aag gag att atg gtg ggc tcc Asp Tyr Ile Pro Ser Glu Asp Trp Lys Lys Glu Ile Met Val Gly Ser 190 195 200			867
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gaa aaa gta tat gaa aat gat gat cag ctc ctg tgg gac cct gag tac Glu Lys Val Tyr Glu Asn Asp Asp Gln Leu Leu Trp Asp Pro Glu Tyr 220 225 230 235			963
tta cca gaa gat aaa gtg att ata ttt ctt aaa gat gca tct aga aga Leu Pro Glu Asp Lys Val Ile Ile Phe Leu Lys Asp Ala Ser Arg Arg 240 245 250			1011
aca ggt gat gag aag ggt gta gaa gca att cct gaa gga tct cac ata Thr Gly Asp Glu Lys Gly Val Glu Ala Ile Pro Glu Gly Ser His Ile 255 260 265			1059
aaa gac aat gaa cag gct tta tat gaa ttg gtt aaa tgc aat ttt gat Lys Asp Asn Glu Gln Ala Leu Tyr Glu Leu Val Lys Cys Asn Phe Asp 270 275 280			1107
aca gaa gaa gca ttg aga aga tta aga ttt aat gta aaa gca gct aga Thr Glu Glu Ala Leu Arg Arg Leu Arg Phe Asn Val Lys Ala Ala Arg 285 290 295			1155
gag gaa tta tct gtt tgg aca gag gaa gag tgt aga aat ttt gaa caa Glu Glu Leu Ser Val Trp Thr Glu Glu Glu Cys Arg Asn Phe Glu Gln			1203

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ggg ctg aag gcc tat gga aag gat ttt cat ttg att cag gct aat aaa				1251
Gly Leu Lys Ala Tyr Gly Lys Asp Phe His Leu Ile Gln Ala Asn Lys				
	320	325	330	
gtc cga aca agg tca gtt ggt gaa tgt gta gca ttc tat tac atg tgg				1299
Val Arg Thr Arg Ser Val Gly Glu Cys Val Ala Phe Tyr Tyr Met Trp				
	335	340	345	
aaa aaa tct gaa cgt tat gat ttc ttt gct cag caa aca cga ttt gga				1347
Lys Lys Ser Glu Arg Tyr Asp Phe Phe Ala Gln Gln Thr Arg Phe Gly				
	350	355	360	
aag aag aaa tat aat ctt cat cct ggt gta acg gat tac atg gat cgt				1395
Lys Lys Lys Tyr Asn Leu His Pro Gly Val Thr Asp Tyr Met Asp Arg				
	365	370	375	
ctt cta gac gaa agt gaa agt gct gca tct agt cga gca caa tcc cct				1443
Leu Leu Asp Glu Ser Glu Ser Ala Ala Ser Ser Arg Ala Gln Ser Pro				
	380	385	390	395
ccc cca act gca tca aac agt agt aac agc cag tct gag aaa gaa gat				1491
Pro Pro Thr Ala Ser Asn Ser Ser Asn Ser Gln Ser Glu Lys Glu Asp				
	400	405	410	
ggc act gta agc act gct aat caa aat ggt aag caa cca gag aaa cat				1539
Gly Thr Val Ser Thr Ala Asn Gln Asn Gly Lys Gln Pro Glu Lys His				
	415	420	425	
ttc tct ttc ttc ata ata agg gac act ttc ttg cag tga cttgggaaat				1588
Phe Ser Phe Phe Ile Ile Arg Asp Thr Phe Leu Gln *				
	430	435	440	
tccgtttggtg tttctattaa acttccagag cagaaagtaa aaaatgataa cacatgagac				1648
aaacataaca tcagcataca tatatactaa cagaatacaa agtgattgga catcactaaa				1708
aagtaatttt aataaagcct actgtcaaca gtgactattt cttgtaagaa atttgttctt				1768
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cctgctaggc tgcggggca tggcccgcg gccggcgcg acctctgcgg attgcatcgg	180
tgtgtggcgg cggggcatgc ccagagcacc gggcacggcc ttca atg ggc gag gac	236
Met Gly Glu Asp	

acg gac acg cgg aaa att aac cac agc ttc ctg cgg gac cac agc tat	284
Thr Asp Thr Arg Lys Ile Asn His Ser Phe Leu Arg Asp His Ser Tyr	
5 10 15 20	
gtg act gaa gct gac atc atc tct acc gtt gag ttc aac cac acg gga	332
Val Thr Glu Ala Asp Ile Ile Ser Thr Val Glu Phe Asn His Thr Gly	
25 30 35	
gag ctg ctg gcc aca ggt gac aag ggc ggc cgg gtc gtc atc ttc cag	380
Glu Leu Leu Ala Thr Gly Asp Lys Gly Gly Arg Val Val Ile Phe Gln	
40 45 50	
cgg gaa cca gag agt aaa aat gcg ccc cac agc cag ggc gaa tac gac	428
Arg Glu Pro Glu Ser Lys Asn Ala Pro His Ser Gln Gly Glu Tyr Asp	
55 60 65	
gtg tac agc act ttc cag agc cac gag ccg gag ttt gac tat ctc aag	476
Val Tyr Ser Thr Phe Gln Ser His Glu Pro Glu Phe Asp Tyr Leu Lys	
70 75 80	
agc ctg gag ata gag gag aag atc aac aag atc aag tgg ctc cca cag	524
Ser Leu Glu Ile Glu Glu Lys Ile Asn Lys Ile Lys Trp Leu Pro Gln	
85 90 95 100	
cag aac gcc gcc cac tca ctc ctg tcc acc aac gat aaa act atc aaa	572
Gln Asn Ala Ala His Ser Leu Leu Ser Thr Asn Asp Lys Thr Ile Lys	
105 110 115	
tta tgg aag att acc gaa cga gat aaa agg ccc gaa gga tac aac ctg	620
Leu Trp Lys Ile Thr Glu Arg Asp Lys Arg Pro Glu Gly Tyr Asn Leu	
120 125 130	
aag gat gaa gag ggg aaa ctt aag gac ctg tcc acg gtg acg tca ctg	668
Lys Asp Glu Glu Gly Lys Leu Lys Asp Leu Ser Thr Val Thr Ser Leu	
135 140 145	
cag gtg cca gtg ctg aag ccc atg gat ctg atg gtg gag gtg agc cct	716
Gln Val Pro Val Leu Lys Pro Met Asp Leu Met Val Glu Val Ser Pro	
150 155 160	
cgg agg atc ttt gcc aat ggc cac acc tac cac atc aac tcc atc tcc	764
Arg Arg Ile Phe Ala Asn Gly His Thr Tyr His Ile Asn Ser Ile Ser	
165 170 175 180	
gtc aac agt gac tgc gag acc tac atg tcg gcg gat gac ctg cgc atc	812
Val Asn Ser Asp Cys Glu Thr Tyr Met Ser Ala Asp Asp Leu Arg Ile	
185 190 195	
aac ctc tgg cac ctg gcc atc acc gac agg agc ttc aac atc gtg gac	860
Asn Leu Trp His Leu Ala Ile Thr Asp Arg Ser Phe Asn Ile Val Asp	
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atc aag ccg gcc aac atg gag gac ctt acg gag gtg atc aca gca tct	908
Ile Lys Pro Ala Asn Met Glu Asp Leu Thr Glu Val Ile Thr Ala Ser	
215 220 225	
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Glu Phe His Pro His His Cys Asn Leu Phe Val Tyr Ser Ser Ser Lys	
230 235 240	
ggc tcc ctg cgg ctc tgc gac atg cgg gca gct gcc ctg tgt gac aag	1004
Gly Ser Leu Arg Leu Cys Asp Met Arg Ala Ala Leu Cys Asp Lys	
245 250 255 260	

cat tcc aag ctc ttt gaa gag cct gag gac ccc agt aac cgc tca ttc	1052
His Ser Lys Leu Phe Glu Glu Pro Glu Asp Pro Ser Asn Arg Ser Phe	
265 270 275	
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Phe Ser Glu Ile Ile Ser Ser Val Ser Asp Val Lys Phe Ser His Ser	
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Gly Arg Tyr Met Leu Thr Arg Asp Tyr Leu Thr Val Lys Val Trp Asp	
295 300 305	
ctg aac atg gag gca aga ccc ata gag acc tac cag gtc cat gac tac	1196
Leu Asn Met Glu Ala Arg Pro Ile Glu Thr Tyr Gln Val His Asp Tyr	
310 315 320	
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Leu Arg Ser Lys Leu Cys Ser Leu Tyr Glu Asn Asp Cys Ile Phe Asp	
325 330 335 340	
aag ttt gaa tgt gcc tgg aac ggg agc gac agc gtc atc atg acc ggg	1292
Lys Phe Glu Cys Ala Trp Asn Gly Ser Asp Ser Val Ile Met Thr Gly	
345 350 355	
acc tac aac aac ttc ttc cgc atg ttc gat cgg aac acc aag cgg gac	1340
Thr Tyr Asn Asn Phe Phe Arg Met Phe Asp Arg Asn Thr Lys Arg Asp	
360 365 370	
gtg acc ctg gag gcc tcg agg gaa agc agc aag ccc cgg gct gtg ctc	1388
Val Thr Leu Glu Ala Ser Arg Glu Ser Ser Lys Pro Arg Ala Val Leu	
375 380 385	
aag cca cgg cgc gtg tgc gtg ggg ggc aag cgc cgg cgt gat gac atc	1436
Lys Pro Arg Arg Val Cys Val Gly Gly Lys Arg Arg Arg Asp Asp Ile	
390 395 400	
agt gtg gac agc ttg gac ttc acc aag aag atc ctg cac acg gcc tgg	1484
Ser Val Asp Ser Leu Asp Phe Thr Lys Lys Ile Leu His Thr Ala Trp	
405 410 415 420	
cac ccg gct gag aac atc att gcc att gcc gcc acc aac aac ctg tac	1532
His Pro Ala Glu Asn Ile Ile Ala Ile Ala Thr Asn Asn Leu Tyr	
425 430 435	
atc ttc cag gac aag gta aac tct gac atg cac tag gtat gtgcagatcc	1582
Ile Phe Gln Asp Lys Val Asn Ser Asp Met His *	
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 gactgtcaga a atg agt ttt tca ctg aac ttc acc ctg ccg gcg aac aca 170
 Met Ser Phe Ser Leu Asn Phe Thr Leu Pro Ala Asn Thr
 1 5 10
 acg tcc tct cct gtc aca ggt ggg aaa gaa acg gac tgt ggg ccc tct 218
 Thr Ser Ser Pro Val Thr Gly Gly Lys Glu Thr Asp Cys Gly Pro Ser
 15 20 25
 ctt gga tta gcg gcg ggc ata cca ttg ctg gtg gcc aca gcc ctg ctg 266
 Leu Gly Leu Ala Ala Gly Ile Pro Leu Leu Val Ala Thr Ala Leu Leu
 30 35 40 45
 gtg gct tta cta ttt act ttg att cac cga aga aga agc agc att gag 314
 Val Ala Leu Leu Phe Thr Leu Ile His Arg Arg Arg Ser Ser Ile Glu
 50 55 60
 gcc atg gag gaa agt gac aga cca tgt gaa att tca gaa att gat gac 362
 Ala Met Glu Glu Ser Asp Arg Pro Cys Glu Ile Ser Glu Ile Asp Asp
 65 70 75
 aat ccc aag ata tct gag aat cct agg aga tca ccc aca cat gag aag 410
 Asn Pro Lys Ile Ser Glu Asn Pro Arg Arg Ser Pro Thr His Glu Lys
 80 85 90
 aat acg atg gga gca caa gag gcc cac ata tat gtg aag act gta gca 458
 Asn Thr Met Gly Ala Gln Glu Ala His Ile Tyr Val Lys Thr Val Ala
 95 100 105
 gga agc gag gaa cct gtg cat gac cgt tac cgt cct act ata gaa atg 506
 Gly Ser Glu Glu Pro Val His Asp Arg Tyr Arg Pro Thr Ile Glu Met

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                               1               5

cag gac ctc cgg agg ccc aag atc cat ggg gca gtc cag gca tct ccc      523
Gln Asp Leu Arg Arg Pro Lys Ile His Gly Ala Val Gln Ala Ser Pro
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Tyr Gln Pro Pro Thr Leu Ala Ser Leu Gln Arg Leu Leu Trp Val Arg
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cag gct gcc aca ctg aac cat atc gat gag gtc tgg ccc agc ctc ttc      619
Gln Ala Ala Thr Leu Asn His Ile Asp Glu Val Trp Pro Ser Leu Phe
              40              45              50

ctg gga gat gcg tac gca gcc cgg gac aag agc aag ctg atc cag ctg      667
Leu Gly Asp Ala Tyr Ala Ala Arg Asp Lys Ser Lys Leu Ile Gln Leu
              55              60              65              70

gga atc acc cac gtt gtg aat gcc gct gca ggc cgc gtg ctg gta cac      715
Gly Ile Thr His Val Val Asn Ala Ala Gly Arg Val Leu Val His
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tgt gcc atg ggg gta agc cgc tct gcc aca ctt gtc ctg gcc ttc ctc      763
Cys Ala Met Gly Val Ser Arg Ser Ala Thr Leu Val Leu Ala Phe Leu
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atg atc tat gag aac atg acg ctg gta gag gcc atc cag acg gtg cag      811
Met Ile Tyr Glu Asn Met Thr Leu Val Glu Ala Ile Gln Thr Val Gln
              105              110              115

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Ala His Arg Asn Ile Cys Pro Asn Ser Gly Phe Leu Arg Gln Leu Gln
              120              125              130

gtt ctg gac aac cga ctg ggg cgg gag acg ggg cgg ttc tga tctggca      908
Val Leu Asp Asn Arg Leu Gly Arg Glu Thr Gly Arg Phe *
              135              140              145

ggcagccagg atccctgacc cttggcccaa cccacccag cctggccctg ggaacagcag      968
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 Met Gly Ala His
 1
 ctg gtc cgg cgc tac ctg ggc gat gcc tcg gtg gag ccc gac ccc ctg 164
 Leu Val Arg Arg Tyr Leu Gly Asp Ala Ser Val Glu Pro Asp Pro Leu
 5 10 15 20
 cag atg cca acc ttc ccg cca gac tac ggc ttc ccc gaa cgc aag gag 212
 Gln Met Pro Thr Phe Pro Pro Asp Tyr Gly Phe Pro Glu Arg Lys Glu
 25 30 35
 cgc gag atg gtg gcc aca cag cag gag atg atg gac gcg cag ctg agg 260
 Arg Glu Met Val Ala Thr Gln Gln Glu Met Met Asp Ala Gln Leu Arg
 40 45 50
 ctc cag ctg cgg gac tac tgc gcc cac cac ctc atc cgg ctg ctc aag 308
 Leu Gln Leu Arg Asp Tyr Cys Ala His His Leu Ile Arg Leu Leu Lys
 55 60 65
 tgc aag cgt gac agc ttc ccc aac ttc ctg gcc tgc aag cag gag cgg 356
 Cys Lys Arg Asp Ser Phe Pro Asn Phe Leu Ala Cys Lys Gln Glu Arg
 70 75 80
 cac gac tgg gac tac tgc gag cac cgc gac tat gtg atg cgc atg aag 404
 His Asp Trp Asp Tyr Cys Glu His Arg Asp Tyr Val Met Arg Met Lys
 85 90 95 100
 gag ttt gag cgg gag cgg agg ctg ctc cag cgg aag aag cgg cgg gag 452
 Glu Phe Glu Arg Glu Arg Arg Leu Leu Gln Arg Lys Lys Arg Arg Glu
 105 110 115
 aag aag gcg gca gag ttg gcc aaa ggc cag gga ccc ggg gaa gtg gac 500
 Lys Lys Ala Ala Glu Leu Ala Lys Gly Gln Gly Pro Gly Glu Val Asp
 120 125 130
 ccc aag gtg gcc ctg tag ggggtg cccccccac cctatggacc agtcaaataa 554
 Pro Lys Val Ala Leu *
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 aagccttcag gccctcaaa aaaaaaaaaa 583

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<213> Homo sapiens

<220>

<221> CDS

<222> (105) .. (470)

<400> 739

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                                   Met Gly Ala His
                                   1
ctg gtc cgg cgc tac ctg ggc gat gcc tcg gtg gag ccc gac ccc ctg      164
Leu Val Arg Arg Tyr Leu Gly Asp Ala Ser Val Glu Pro Asp Pro Leu
  5                10                15                20
cag atg cca acc ttc ccg cca gac tac ggc ttc ccc gaa cgc aag gag      212
Gln Met Pro Thr Phe Pro Pro Asp Tyr Gly Phe Pro Glu Arg Lys Glu
                25                30                35
cgc gag atg gtg gcc aca cag cag gag atg atg gac gcg ctg ctc aag      260
Arg Glu Met Val Ala Thr Gln Gln Glu Met Met Asp Ala Leu Leu Lys
                40                45                50
tgc aag cgt gac agc ttc ccc aac ttc ctg gcc tgc aag cag gag cgg      308
Cys Lys Arg Asp Ser Phe Pro Asn Phe Leu Ala Cys Lys Gln Glu Arg
                55                60                65
cac gac tgg gac tac tgc gag cac cgc gac tat gtg atg cgc atg aag      356
His Asp Trp Asp Tyr Cys Glu His Arg Asp Tyr Val Met Arg Met Lys
                70                75                80
gag ttt gag cgg gag cgg agg ctg ctc cag cgg aag aag cgg cgg gag      404
Glu Phe Glu Arg Glu Arg Arg Leu Leu Gln Arg Lys Lys Arg Arg Glu
                85                90                95                100
aag aag gcg gca gag ttg gcc aaa ggc cag gga ccc ggg gaa gtg gac      452
Lys Lys Ala Ala Glu Leu Ala Lys Gly Gln Gly Pro Gly Glu Val Asp
                105                110                115
ccc aag gtg gcc ctg tag ggggtg cccccccac cctatggacc agtcaaataa      506
Pro Lys Val Ala Leu *
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aagccttcag gccctcaaa aaaaaaaaaa      535

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<210> 740

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<222> (75) .. (3800)

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taagggaagc cgtg atg agg gcc gtg ttg acg tgg aga gat aaa gcc gag      110
                                   Met Arg Ala Val Leu Thr Trp Arg Asp Lys Ala Glu

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cac tgt ata aat gac atc gca ttt aag cct gat gga act caa ctg att				158
His Cys Ile Asn Asp Ile Ala Phe Lys Pro Asp Gly Thr Gln Leu Ile	15	20	25	
ttg gct gcc gga agc aga tta ctg gtt tat gac acc tct gat ggc acc				206
Leu Ala Ala Gly Ser Arg Leu Leu Val Tyr Asp Thr Ser Asp Gly Thr	30	35	40	
tta ctt cag ccc ctc aag gga cac aaa gac act gtg tac tgt gtg gca				254
Leu Leu Gln Pro Leu Lys Gly His Lys Asp Thr Val Tyr Cys Val Ala	45	50	55	60
tat gcg aag gat ggc aag cgc ttt gct tct gga tca gct gac aaa agc				302
Tyr Ala Lys Asp Gly Lys Arg Phe Ala Ser Gly Ser Ala Asp Lys Ser	65	70	75	
gtt att atc tgg aca tca aaa ctg gaa ggc att ctg aag tac acg cac				350
Val Ile Ile Trp Thr Ser Lys Leu Glu Gly Ile Leu Lys Tyr Thr His	80	85	90	
aat gat gct ata caa tgt gtc tcc tac aat cct att act cat caa ctg				398
Asn Asp Ala Ile Gln Cys Val Ser Tyr Asn Pro Ile Thr His Gln Leu	95	100	105	
gca tct tgt tcc tcc agt gac ttt ggg ttg tgg tct cct gaa cag aag				446
Ala Ser Cys Ser Ser Ser Asp Phe Gly Leu Trp Ser Pro Glu Gln Lys	110	115	120	
tct gtc tcc aaa cac aaa tca agc agc aag atc atc tgc tgc agc tgg				494
Ser Val Ser Lys His Lys Ser Ser Ser Lys Ile Ile Cys Cys Ser Trp	125	130	135	140
aca aat gat ggt cag tac ctg gcg ctg ggg atg ttc aat ggg atc atc				542
Thr Asn Asp Gly Gln Tyr Leu Ala Leu Gly Met Phe Asn Gly Ile Ile	145	150	155	
agc ata cgg aac aaa aat ggc gag gag aaa gta aag atc gag cgg ccg				590
Ser Ile Arg Asn Lys Asn Gly Glu Glu Lys Val Lys Ile Glu Arg Pro	160	165	170	
ggg ggc tcc ctc tcg cca ata tgg tcc atc tgc tgg aac cct tca agc				638
Gly Gly Ser Leu Ser Pro Ile Trp Ser Ile Cys Trp Asn Pro Ser Ser	175	180	185	
cga tgg gag agt ttc tgg atg aac aga gag aat gag gat gcc gag gat				686
Arg Trp Glu Ser Phe Trp Met Asn Arg Glu Asn Glu Asp Ala Glu Asp	190	195	200	
gtc att gtc aac aga tat att cag gaa atc cct tcc act ctg aag tca				734
Val Ile Val Asn Arg Tyr Ile Gln Glu Ile Pro Ser Thr Leu Lys Ser	205	210	215	220
gca gtg tac agt agt cag ggt agt gag gca gag gag gaa gaa cca gag				782
Ala Val Tyr Ser Ser Gln Gly Ser Glu Ala Glu Glu Glu Glu Pro Glu	225	230	235	
gaa gag gac gac agt ccc agg gac gac aac tta gag gaa cgt aat gac				830
Glu Glu Asp Asp Ser Pro Arg Asp Asp Asn Leu Glu Glu Arg Asn Asp	240	245	250	
atc ctg gct gtg gct gac tgg gga cag aaa gtt tcc ttc tac cag ctg				878
Ile Leu Ala Val Ala Asp Trp Gly Gln Lys Val Ser Phe Tyr Gln Leu				

255	260	265	
agt gga aaa cag att gga aag gat cgg gca ctg aac ttt gac ccc tgc Ser Gly Lys Gln Ile Gly Lys Asp Arg Ala Leu Asn Phe Asp Pro Cys 270 275 280			926
tgc atc agc tac ttt act aaa ggc gag tac att ttg ctg ggg ggt tca Cys Ile Ser Tyr Phe Thr Lys Gly Glu Tyr Ile Leu Leu Gly Gly Ser 285 290 295 300			974
gac aag caa gta tct ctt ttc acc aag gat gga gtg cgg ctt ggg act Asp Lys Gln Val Ser Leu Phe Thr Lys Asp Gly Val Arg Leu Gly Thr 305 310 315			1022
gtt ggg gag cag aac tcc tgg gtg tgg acg tgt caa gcg aaa ccg gat Val Gly Glu Gln Asn Ser Trp Val Trp Cys Gln Ala Lys Pro Asp 320 325 330			1070
tcc aac tat gtg gtg gtc ggc tgc cag gac ggc acc att tcc ttc tac Ser Asn Tyr Val Val Val Gly Cys Gln Asp Gly Thr Ile Ser Phe Tyr 335 340 345			1118
cag ctt att ttc agc aca gtc cat ggg ctt tac aag gac cgc tat gcc Gln Leu Ile Phe Ser Thr Val His Gly Leu Tyr Lys Asp Arg Tyr Ala 350 355 360			1166
tac agg gat agc atg act gac gtc att gtg cag cac ctg atc act gag Tyr Arg Asp Ser Met Thr Asp Val Ile Val Gln His Leu Ile Thr Glu 365 370 375 380			1214
cag aaa gtt cgg att aaa tgc aaa gag ctt gtc aag aag att gcc atc Gln Lys Val Arg Ile Lys Cys Lys Glu Leu Val Lys Lys Ile Ala Ile 385 390 395			1262
tac aga aat cga ttg gct atc caa ctg cca gag aaa atc ctc atc tat Tyr Arg Asn Arg Leu Ala Ile Gln Leu Pro Glu Lys Ile Leu Ile Tyr 400 405 410			1310
gag ttg tat tca gag gac tta tca gac atg cat tac cgg gta aag gag Glu Leu Tyr Ser Glu Asp Leu Ser Asp Met His Tyr Arg Val Lys Glu 415 420 425			1358
aag att atc aag aag ttt gag tgc aac ctc ctg gtg gtg tgt gcc aat Lys Ile Ile Lys Lys Phe Glu Cys Asn Leu Leu Val Val Cys Ala Asn 430 435 440			1406
cac atc atc ctg tgc cag gag aaa cgg ctg cag tgc ctg tcc ttc agc His Ile Ile Leu Cys Gln Glu Lys Arg Leu Gln Cys Leu Ser Phe Ser 445 450 455 460			1454
gga gtg aag gag cgg gag tgg cag atg gag tct ctc att cgt tac atc Gly Val Lys Glu Arg Glu Trp Gln Met Glu Ser Leu Ile Arg Tyr Ile 465 470 475			1502
aag gtg atc ggt ggc cct cct gga aga gaa ggc ctc tta gtg ggg ctg Lys Val Ile Gly Gly Pro Pro Gly Arg Glu Gly Leu Leu Val Gly Leu 480 485 490			1550
aag aat gga cag atc ctg aag atc ttc gtg gac aat ctc ttt gct atc Lys Asn Gly Gln Ile Leu Lys Ile Phe Val Asp Asn Leu Phe Ala Ile 495 500 505			1598
gtc ctg ctg aag cag gcc aca gct gtg cgc tgc ttg gac atg agt gcc Val Leu Leu Lys Gln Ala Thr Ala Val Arg Cys Leu Asp Met Ser Ala 1646			

510	515	520	
tcc cgt aag aag ctg gcc gtg gta gat gaa aat gac act tgc ctg gtg Ser Arg Lys Lys Leu Ala Val Val Asp Glu Asn Asp Thr Cys Leu Val 525 530 535 540			1694
tat gac atc gac acc aag gag ctg ctt ttt cag gaa cca aac gcc aac Tyr Asp Ile Asp Thr Lys Glu Leu Leu Phe Gln Glu Pro Asn Ala Asn 545 550 555			1742
agt gta gct tgg aac acc cag tgt gag gac atg ctc tgc ttc tcg gga Ser Val Ala Trp Asn Thr Gln Cys Glu Asp Met Leu Cys Phe Ser Gly 560 565 570			1790
gga ggc tac ctc aac atc aaa gcc agc acc ttc cct gtg cac cgg cag Gly Gly Tyr Leu Asn Ile Lys Ala Ser Thr Phe Pro Val His Arg Gln 575 580 585			1838
aag ctg cag ggc ttt gtg gtc ggc tac aat ggc tcc aag atc ttc tgc Lys Leu Gln Gly Phe Val Val Gly Tyr Asn Gly Ser Lys Ile Phe Cys 590 595 600			1886
ctc cat gtc ttc tcc att tct gcc gtg gag gtg ccg cag tcc gct ccc Leu His Val Phe Ser Ile Ser Ala Val Glu Val Pro Gln Ser Ala Pro 605 610 615 620			1934
atg tac cag tac ctg gat agg aaa ctg ttc aag gaa gcc tac cag att Met Tyr Gln Tyr Leu Asp Arg Lys Leu Phe Lys Glu Ala Tyr Gln Ile 625 630 635			1982
gct tgc ttg ggt gtc aca gac act gat tgg cgt gaa ctg gcc atg gaa Ala Cys Leu Gly Val Thr Asp Thr Asp Trp Arg Glu Leu Ala Met Glu 640 645 650			2030
gcg cta gaa ggt tta gat ttt gaa aca gca aag aag gcc ttc atc aga Ala Leu Glu Gly Leu Asp Phe Glu Thr Ala Lys Lys Ala Phe Ile Arg 655 660 665			2078
gta caa gac ctc cga tat tta gag ctc atc agc agc att gag gag agg Val Gln Asp Leu Arg Tyr Leu Glu Leu Ile Ser Ser Ile Glu Glu Arg 670 675 680			2126
aag aag cgg gga gag acc aac aat gac ctg ttt ctg gca gat gtg ttt Lys Lys Arg Gly Glu Thr Asn Asn Asp Leu Phe Leu Ala Asp Val Phe 685 690 695 700			2174
tcc tac cag ggg aag ttc cat gag gcc gcc aaa ctg tac aag agg agt Ser Tyr Gln Gly Lys Phe His Glu Ala Ala Lys Leu Tyr Lys Arg Ser 705 710 715			2222
ggg cac gag aac ctc gcg ctt gaa atg tac acc gac ctc tgc atg ttt Gly His Glu Asn Leu Ala Leu Glu Met Tyr Thr Asp Leu Cys Met Phe 720 725 730			2270
gag tat gcc aag gat ttc ctt gga tct gga gac ccc aaa gaa aca aag Glu Tyr Ala Lys Asp Phe Leu Gly Ser Gly Asp Pro Lys Glu Thr Lys 735 740 745			2318
atg cta atc acc aaa cag gct gac tgg gcc aga aat atc aag gag ccc Met Leu Ile Thr Lys Gln Ala Asp Trp Ala Arg Asn Ile Lys Glu Pro 750 755 760			2366
aaa gcc gcc gtg gag atg tac atc tca gca gga gag cac gtc aag gcc Lys Ala Ala Val Glu Met Tyr Ile Ser Ala Gly Glu His Val Lys Ala			2414

765	770	775	780	
atc gag atc tgt ggt gac cat ggc tgg gtt gac atg ttg atc gac atc Ile Glu Ile Cys Gly Asp His Gly Trp Val Asp Met Leu Ile Asp Ile	785	790	795	2462
gcc cgc aaa ctg gac aag gct gag cgc gag ccc ctg ctg ctg tgc gct Ala Arg Lys Leu Asp Lys Ala Glu Arg Glu Pro Leu Leu Leu Cys Ala	800	805	810	2510
acc tac ctc aag aag ctg gac agc cct ggc tat gct gct gag acc tac Thr Tyr Leu Lys Lys Leu Asp Ser Pro Gly Tyr Ala Ala Glu Thr Tyr	815	820	825	2558
ctg aag atg ggt gac ctc aag tcc ctg gtg cag ctg cac gtg gag acc Leu Lys Met Gly Asp Leu Lys Ser Leu Val Gln Leu His Val Glu Thr	830	835	840	2606
cag cgc tgg gat gag gcc ttt gct ttg ggt gag aag cat cct gag ttt Gln Arg Trp Asp Glu Ala Phe Ala Leu Gly Glu Lys His Pro Glu Phe	845	850	855	2654
aag gat gac atc tac atg ccg tat gct cag tgg cta gca gag aac gat Lys Asp Asp Ile Tyr Met Pro Tyr Ala Gln Trp Leu Ala Glu Asn Asp	865	870	875	2702
cgc ttt gag gaa gcc cag aaa gcg ttc cac aag gct ggg cga cag aga Arg Phe Glu Glu Ala Gln Lys Ala Phe His Lys Ala Gly Arg Gln Arg	880	885	890	2750
gaa gcg gtc cag gtg ctg gag cag ctc aca aac aat gcc gtg gcg gag Glu Ala Val Gln Val Leu Glu Gln Leu Thr Asn Asn Ala Val Ala Glu	895	900	905	2798
agc agg ttt aat gat gct gcc tat tat tac tgg atg ctg tcc atg cag Ser Arg Phe Asn Asp Ala Tyr Tyr Tyr Trp Met Leu Ser Met Gln	910	915	920	2846
tgc ctc gat ata gct caa gat cct gcc cag aag gac aca atg ctt gcc Cys Leu Asp Ile Ala Gln Asp Pro Ala Gln Lys Asp Thr Met Leu Gly	925	930	935	2894
aag ttc tac cac ttc cag cgt ttg gca gag ctg tac cat ggt tac cat Lys Phe Tyr His Phe Gln Arg Leu Ala Glu Leu Tyr His Gly Tyr His	945	950	955	2942
gcc atc cat cgc cac acg gaa gat ccg ttc agt gtc cat cgt cct gaa Ala Ile His Arg His Thr Glu Asp Pro Phe Ser Val His Arg Pro Glu	960	965	970	2990
act ctt ttc aac atc tcc agg ttc ctg ctg cac agc ctg ccc aag gac Thr Leu Phe Asn Ile Ser Arg Phe Leu Leu His Ser Leu Pro Lys Asp	975	980	985	3038
acc ccc tcg ggc atc tct aaa gtg aaa ata ctc ttc acc ttg gcc aag Thr Pro Ser Gly Ile Ser Lys Val Lys Ile Leu Phe Thr Leu Ala Lys	990	995	1000	3086
cag agc aag gcc ctc ggt gcc tac agg ctg gcc cgg cac gcc tat gac Gln Ser Lys Ala Leu Gly Ala Tyr Arg Leu Ala Arg His Ala Tyr Asp	1005	1010	1015	3134
aag ctg cgt ggc ctg tac atc cct gcc aga ttc caa aag tcc att gag Lys Leu Arg Gly Leu Tyr Ile Pro Ala Arg Phe Gln Lys Ser Ile Glu				3182

1025	1030	1035	
ctg ggt acc ctg acc atc cgc gcc aag ccc ttc cac gac agt gag gag			3230
Leu Gly Thr Leu Thr Ile Arg Ala Lys Pro Phe His Asp Ser Glu Glu			
1040	1045	1050	
ttg gtg ccc ttg tgc tac cgc tgc tcc acc aac aac ccg ctg ctc aac			3278
Leu Val Pro Leu Cys Tyr Arg Cys Ser Thr Asn Asn Pro Leu Leu Asn			
1055	1060	1065	
aac ctg ggc aac gtc tgc atc aac tgc cgc cag ccc ttc atc ttc tcc			3326
Asn Leu Gly Asn Val Cys Ile Asn Cys Arg Gln Pro Phe Ile Phe Ser			
1070	1075	1080	
gcc tct tcc tac gac gtg cta cac ctg gtt gag ttc tac ctg gag gaa			3374
Ala Ser Ser Tyr Asp Val Leu His Leu Val Glu Phe Tyr Leu Glu Glu			
1085	1090	1095	1100
ggg atc act gat gaa gaa gcc atc tcc ctc atc gac ctg gag gtg ctg			3422
Gly Ile Thr Asp Glu Glu Ala Ile Ser Leu Ile Asp Leu Glu Val Leu			
1105	1110	1115	
aga ccc aag cgg gat gac aga cag cta gag att gca aac aac agc tcc			3470
Arg Pro Lys Arg Asp Asp Arg Gln Leu Glu Ile Ala Asn Asn Ser Ser			
1120	1125	1130	
cag att ctg cgg cta gtg gag acc aag gac tcc atc gga gat gag gac			3518
Gln Ile Leu Arg Leu Val Glu Thr Lys Asp Ser Ile Gly Asp Glu Asp			
1135	1140	1145	
ccg ttc aca gct aag ctg agc ttt gag caa ggt ggc tca gag ttc gtg			3566
Pro Phe Thr Ala Lys Leu Ser Phe Glu Gln Gly Gly Ser Glu Phe Val			
1150	1155	1160	
cca gtg gtg gtg agc cgg ctg gtg ctg cgc tcc atg agc cgc cgg gat			3614
Pro Val Val Val Ser Arg Leu Val Leu Arg Ser Met Ser Arg Arg Asp			
1165	1170	1175	1180
gtc ctc atc aag cga tgg ccc cca ccc ctg agg tgg caa tac ttc cgc			3662
Val Leu Ile Lys Arg Trp Pro Pro Pro Leu Arg Trp Gln Tyr Phe Arg			
1185	1190	1195	
tca ctg ctg cct gac gcc tcc att acc atg tgc ccc tcc tgc ttc cag			3710
Ser Leu Leu Pro Asp Ala Ser Ile Thr Met Cys Pro Ser Cys Phe Gln			
1200	1205	1210	
atg ttc cat tct gag gac tat gag ttg ctg gtg ctt cag cat ggc tgc			3758
Met Phe His Ser Glu Asp Tyr Glu Leu Leu Val Leu Gln His Gly Cys			
1215	1220	1225	
tgc ccc tac tgc cgc agg tgc aag gat gac cct ggc cca tga ccagcat			3807
Cys Pro Tyr Cys Arg Arg Cys Lys Asp Asp Pro Gly Pro *			
1230	1235	1240	
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<210> 741

<211> 1802

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<220>

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<400> 741

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                        Met Asn Pro Arg Gly Leu Phe Gln Asp
                        1                      5

ttc aac ccc agt aag gtt ctc atc tac acc tgc ctg ctg ctc ttc tcg      161
Phe Asn Pro Ser Lys Val Leu Ile Tyr Thr Cys Leu Leu Leu Phe Ser
10                      15                      20                      25

ggg ctg ctg ccc ctc cgc ctg gac ggc atc atc caa tgg agc tac tgg      209
Gly Leu Leu Pro Leu Arg Leu Asp Gly Ile Ile Gln Trp Ser Tyr Trp
                      30                      35                      40

gcc gtc ttt gcc ccc ata tgg ctg agg aag ctt cta gtc gtc gca ggc      257
Ala Val Phe Ala Pro Ile Trp Leu Arg Lys Leu Leu Val Val Ala Gly
                      45                      50                      55

gcc tcc gtg ggc gcg ggc gtt tgg gcc cgc aac cct cgc tac cgc acc      305
Ala Ser Val Gly Ala Gly Val Trp Ala Arg Asn Pro Arg Tyr Arg Thr
                      60                      65                      70

gag gga gag gcc tgt gtg gag atc aaa gcc atg ctg atc gct gtg ggc      353
Glu Gly Glu Ala Cys Val Glu Ile Lys Ala Met Leu Ile Ala Val Gly
                      75                      80                      85

atc cac ctg ctg ctg ctc atg ttc gaa gtc ctg gtc tgc gac agg gtg      401
Ile His Leu Leu Leu Leu Met Phe Glu Val Leu Val Cys Asp Arg Val
90                      95                      100                      105

gag agg ggc acc cac ttc tgg ctg ctg gtc ttc atg cct ctc ttc ttc      449
Glu Arg Gly Thr His Phe Trp Leu Leu Val Phe Met Pro Leu Phe Phe
                      110                      115                      120

gtg tcc ccc gtg tcc gtg gct gcc tgc gtc tgg ggc ttt cga cac gat      497
Val Ser Pro Val Ser Val Ala Ala Cys Val Trp Gly Phe Arg His Asp
                      125                      130                      135

agg tcg ctg gag ctg gag atc ctg tgc tcg gtc aac atc ctg cag ttc      545
Arg Ser Leu Glu Leu Glu Ile Leu Cys Ser Val Asn Ile Leu Gln Phe
                      140                      145                      150

atc ttc atc gcc cta aag ctg gac agg att att cac tgg ccg tgg ctg      593
Ile Phe Ile Ala Leu Lys Leu Asp Arg Ile Ile His Trp Pro Trp Leu
155                      160                      165

gtg gtg ttt gtg ccc ctg tgg atc ctc atg tcg ttc ctt tgc ctg gtc      641
Val Val Phe Val Pro Leu Trp Ile Leu Met Ser Phe Leu Cys Leu Val
170                      175                      180                      185

gtc ctc tat tac atc gtc tgg tcc ctc ctg ttc ctg cgg tcc ctg gat      689
Val Leu Tyr Tyr Ile Val Trp Ser Leu Leu Phe Leu Arg Ser Leu Asp
                      190                      195                      200

gtg gtt gcc gag cag cgg aga aca cac gtg acc atg gct atc agt tgg      737
Val Val Ala Glu Gln Arg Arg Thr His Val Thr Met Ala Ile Ser Trp
205                      210                      215

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aga ttg gat ggc cac aat aca ttc tcc tac gtc tcc ata ttt gtc ccc Arg Leu Asp Gly His Asn Thr Phe Ser Tyr Val Ser Ile Phe Val Pro 235 240 245	833
ctt tgg ctt tcc tta cta act tta atg gcc aca aca ttt agg cga aag Leu Trp Leu Ser Leu Leu Thr Leu Met Ala Thr Thr Phe Arg Arg Lys 250 255 260 265	881
ggg ggc aat cat tgg tgg ttt ggc att cgc aga gac ttc tgt cag ttt Gly Gly Asn His Trp Trp Phe Gly Ile Arg Arg Asp Phe Cys Gln Phe 270 275 280	929
ctg ctt gaa att ttc cca ttt tta aga gaa tat ggg aac att tca tat Leu Leu Glu Ile Phe Pro Phe Leu Arg Glu Tyr Gly Asn Ile Ser Tyr 285 290 295	977
gat ctc cat cac gaa gat agt gaa gat gct gaa gaa aca tca gtt cca Asp Leu His His Glu Asp Ser Glu Asp Ala Glu Glu Thr Ser Val Pro 300 305 310	1025
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ata acc cag agc cct ggg aaa tac gtt ccc ccc cct ccc aag tta aat Ile Thr Gln Ser Pro Gly Lys Tyr Val Pro Pro Pro Pro Lys Leu Asn 330 335 340 345	1121
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ctttcaggtg tagctggggg cagtaagtcg aattgtttta gtaggtcctc aaaaggaata	1415
accacacagc tgtttgttta aatgctactg tacctatcaa aactattggt taaaaagtat	1475
ttttatacac tgctaatacta aaattgtatt tcagattgtg cctgtcataa caatagcaaa	1535
tgtaaaaagt tctctttccc accacttggt tataaacctc atagttgata tttttagtgt	1595
tcctactggt aaaataactct ctccctgggc ttgtctgata ctggtcttta atattctgat	1655
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cagtgaata tgttgaattc tagttctctg cattaccatt attacgttaa agtatttttt	1775
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<211> 1413

<212> DNA
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<220>
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<222> (21) .. (740)

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Met Thr Cys Phe Gly Pro Tyr Pro Ile Gly
1 5 10

act gga ctt cag gga ata acc ttg tgt tat agt tgt ttt ccc tcc ttc 98
Thr Gly Leu Gln Gly Ile Thr Leu Cys Tyr Ser Cys Phe Pro Ser Phe
15 20 25

tgc aag atg aaa agc agg atg tgc atg gct atc agc att tgt cag acg 146
Cys Lys Met Lys Ser Arg Met Cys Met Ala Ile Ser Ile Cys Gln Thr
30 35 40

ctt tcc atg ttg agt ttt gtg gtc tgt gct ttc agg tac agg cat atg 194
Leu Ser Met Leu Ser Phe Val Val Cys Ala Phe Arg Tyr Arg His Met
45 50 55

ttc aaa agg ggt tgg cca atg ggt aca tgt tgt ttg ttt ctg ccc aca 242
Phe Lys Arg Gly Trp Pro Met Gly Thr Cys Cys Leu Phe Leu Pro Thr
60 65 70

gct gcc cca gtg ctc agc tgt gaa gct gca aca cag act gaa agg aga 290
Ala Ala Pro Val Leu Ser Cys Glu Ala Ala Thr Gln Thr Glu Arg Arg
75 80 85 90

ctg gat ctg gct gca gtg act ctg agg aga ggc ttg aga tct aga gct 338
Leu Asp Leu Ala Ala Val Thr Leu Arg Arg Gly Leu Arg Ser Arg Ala
95 100 105

tcg cga tgc aga ccg cgg tct ttg ata gat tac aaa tcc tac atg gac 386
Ser Arg Cys Arg Pro Arg Ser Leu Ile Asp Tyr Lys Ser Tyr Met Asp
110 115 120

acc aag ctg ctg gtg gcg agg ttc ctg gag cag tcc tct tgt acc atg 434
Thr Lys Leu Leu Val Ala Arg Phe Leu Glu Gln Ser Ser Cys Thr Met
125 130 135

acc cca gac atc cat gaa ctt gta gaa aac att aaa tct gtt ttg aaa 482
Thr Pro Asp Ile His Glu Leu Val Glu Asn Ile Lys Ser Val Leu Lys
140 145 150

tct gat gag gag cac atg gag gaa gcc atc aca agt gcc agt ttt cta 530
Ser Asp Glu Glu His Met Glu Glu Ala Ile Thr Ser Ala Ser Phe Leu
155 160 165 170

gaa cag ata atg gcc cca ttg cag ccc agc aca tcc agg gcc cac aag 578
Glu Gln Ile Met Ala Pro Leu Gln Pro Ser Thr Ser Arg Ala His Lys
175 180 185

ctg ccc ttg cgg aga cag cct ggc ctg ctg cac ctc cag agc tgc ggc 626
Leu Pro Leu Arg Arg Gln Pro Gly Leu Leu His Leu Gln Ser Cys Gly
190 195 200

gac ctt cac acc atc aca cca gcg ggg agg ccc cga gcc gag agg agg 674
Asp Leu His Thr Ile Thr Pro Ala Gly Arg Pro Arg Ala Glu Arg Arg
205 210 215

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ccc cgg cga gtg gag gct gag cgg tca cac agc ctc att ggg gtc atc      722
Pro Arg Arg Val Glu Ala Glu Arg Ser His Ser Leu Ile Gly Val Ile
    220                      225                      230

cga gag act gtc ctg tga accctg gaagacagaa ggtcactcca aggggaagga      776
Arg Glu Thr Val Leu *
235                      240

tcctctctct ctctgtcatg tcttggatgg gagctgtggc ccacctcaaa aaaaaaggag      836

cactctggac acgtgttccc acctgttggg tcccggtgtct gctgactgag ggcattcagg      896

agtaaatgca caggtcgggc caggcccgctc tgggtttggg atgcactgag ttggagggtta      956

tgaaagcttt gatcctcttc ttcctctgct gggcctcgca gcattcccaa gggtcacatg     1016

ccctggcatg ggcagaaact gggctaata tcttttgccc acttcacccc tcgtgtctct      1076

ctttgttgct aagttctttc cctcttgga ggacagatct gccgggctgc tatttatagt      1136

tgcccttggc ctttcactgc tctgcgattt ggcaggaaat aaggcgatta accctatgtg      1196

tcacaaagcc tcaagccttg ttccaggtca cctcaaata acactctctt taggcaaaac      1256

aggaaacttc ttaagtgaca aattttaatg ccagacattt aaggagagga ttattgttga      1316

ttccatttac tcatgcttgc aaaactagag acccctaagg cagaactgag aataaacatg      1376

tttactttgg gccactgggc ttgatgtgta aaaaaaa                                1413

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<210> 743
 <211> 1711
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (338)..(1051)

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<400> 743
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tgaggacgtt tgggacaaag gtatagtcaa agtgatcaga gcattacatt catctgacaa      120

gtcttgtctc tcttcagccc ctctctctct taattgacta cttcatcctc gtccttggga      180

acatcctttc attggtcagc cacatttttc ctgcttggcc catccatccc catctatttg      240

tcatacccca tgaaacttaa cctcattatg gtttgcattc tggattctcc tctccaccat      300

ctggcctttac cttgggggtg gtgtcgtaca tgacaca atg acg tgt ttc ggg cca      355
                      Met Thr Cys Phe Gly Pro
                      1                      5

tat cct att gga act gga ctt cag gga ata acc ttg tgt tgt ttt ccc      403
Tyr Pro Ile Gly Thr Gly Leu Gln Gly Ile Thr Leu Cys Cys Phe Pro
    10                      15                      20

tcc ttc tgc aag atg aaa agc agg atg tgc atg gct atc agc att tgt      451
Ser Phe Cys Lys Met Lys Ser Arg Met Cys Met Ala Ile Ser Ile Cys
    25                      30                      35

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cag atg ctt tcc atg ttg agt ttt gtg gtc tgt gct ttc agg tac agg 499
 Gln Met Leu Ser Met Leu Ser Phe Val Val Cys Ala Phe Arg Tyr Arg
 40 45 50

cat atg ttc aaa agg ggc tgg cca atg ggt aca tgt tgt ttg ttt ctg 547
 His Met Phe Lys Arg Gly Trp Pro Met Gly Thr Cys Cys Leu Phe Leu
 55 60 65 70

ccc aca gct gcc cca gtg ctc agc tgt gaa gct gca aca cag act gaa 595
 Pro Thr Ala Ala Pro Val Leu Ser Cys Glu Ala Ala Thr Gln Thr Glu
 75 80 85

agg aga ctg gat ctg gct gca gtg act ctg agg aga ggc ttg aga tct 643
 Arg Arg Leu Asp Leu Ala Ala Val Thr Leu Arg Arg Gly Leu Arg Ser
 90 95 100

aga gct tcg cga tgc aga ccg cgg tct ttg ata gat tac aaa tcc tac 691
 Arg Ala Ser Arg Cys Arg Pro Arg Ser Leu Ile Asp Tyr Lys Ser Tyr
 105 110 115

atg gac acc aag ctg ctg gtg gcg agg ttc ctg gag cag tcc tct tgt 739
 Met Asp Thr Lys Leu Leu Val Ala Arg Phe Leu Glu Gln Ser Ser Cys
 120 125 130

acc atg acc cca gac atc cat gaa ctt gta gaa aac att aaa tct gtt 787
 Thr Met Thr Pro Asp Ile His Glu Leu Val Glu Asn Ile Lys Ser Val
 135 140 145 150

ttg aaa tct gat gag gag cac atg gag gaa gcc atc aca agt gcc agt 835
 Leu Lys Ser Asp Glu Glu His Met Glu Glu Ala Ile Thr Ser Ala Ser
 155 160 165

ttt cta gaa cag ata atg gcc cca ttg cag ccc agc aca tcc agg gcc 883
 Phe Leu Glu Gln Ile Met Ala Pro Leu Gln Pro Ser Thr Ser Arg Ala
 170 175 180

cac aag ctg ccc tcg cgg aga cag cct ggc ctg ctg cac ctc cag agc 931
 His Lys Leu Pro Ser Arg Arg Gln Pro Gly Leu Leu His Leu Gln Ser
 185 190 195

tgc ggc gac ctt cac acc ttc aca cca gcg ggg agg ccc cga gcc gag 979
 Cys Gly Asp Leu His Thr Phe Thr Pro Ala Gly Arg Pro Arg Ala Glu
 200 205 210

agg agg ccc cgg cga gtg gag gct gag cgg cca cac agc ctc att ggg 1027
 Arg Arg Pro Arg Arg Val Glu Ala Glu Arg Pro His Ser Leu Ile Gly
 215 220 225 230

gtc atc cga gag act gtc ctg tga accctggaag acagaaggcc actccaagg 1081
 Val Ile Arg Glu Thr Val Leu *
 235

gaaggatccc tctcctctct gccatttctt ggctgggagc tgtgttccac ctcaaaaaa 1141

aggagcactc tggaggacac gttttccac ctgttggtc cgtgtctgc tgactgagg 1201

cattcaggag taaatgcaca ggtcgtcca ggccgtctg ggtttgggat gcaactgagtt 1261

ggaggttatg aaagctttga tctcttctt cctctgctgg gctcgcagc attcccaagg 1321

gtcacatgcc ctggcatggg cagaaactgg gctaattgatt ctttgccac ttcaccctc 1381

gtgtctctct ttgttctaa gttctttccc tcttgaagg acagatctgc cgggctgcta 1441

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tttatagttg cctttggcct ttcactgctc tgcgatttgg caggaaataa ggcgattaac 1501
cctatgtgtc cacaagcctc aagccttggt tcaggtcacc ctcaaatac actctcttta 1561
ggcaaaacag gaaacttctt aagtgacaaa ttttaatgcc agacatttaa ggagaggatt 1621
attgttgatt ccatttactc atgcttgcaa aactagagac ccctaaggca gaactgagaa 1681
taaacatggt tactttgggc caaaaaaaaaa 1711

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<210> 744
 <211> 453
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (90)..(407)

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<400> 744
ccaatgatga ccattagtcc atgcggtgga attcggagga agcgagaggc atctaagcag 60
gcagtgtttt gccttcaccc caagtgacc atg aga ggt gcc acg cga gtc tca 113
Met Arg Gly Ala Thr Arg Val Ser
1 5
atc atg ctc ctc cta gta act gtg tct gac tgt gct gtg atc aca ggg 161
Ile Met Leu Leu Leu Val Thr Val Ser Asp Cys Ala Val Ile Thr Gly
10 15 20
gcc tgt gag cgg gat gtc cag tgt ggg gca ggc acc tgc tgt gcc atc 209
Ala Cys Glu Arg Asp Val Gln Cys Gly Ala Gly Thr Cys Cys Ala Ile
25 30 35 40
agc ctg tgg ctt cga ggg ctg cgg atg tgc acc ccg ctg ggg cgg gaa 257
Ser Leu Trp Leu Arg Gly Leu Arg Met Cys Thr Pro Leu Gly Arg Glu
45 50 55
ggc gag gag tgc cac ccc ggc agc cac aag atc ccc ttc ttc agg aaa 305
Gly Glu Glu Cys His Pro Gly Ser His Lys Ile Pro Phe Phe Arg Lys
60 65 70
cgc aag cac cac acc tgt cct tgc ttg ccc aac ctg ctg tgc tcc agg 353
Arg Lys His His Thr Cys Pro Cys Leu Pro Asn Leu Leu Cys Ser Arg
75 80 85
ttc ccg gac ggc agg tac cgc tgc tcc atg gac ttg aag aac atc aat 401
Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu Lys Asn Ile Asn
90 95 100
ttt tag gcgcttgctt ggtctcagga taccacccat tcttttctg agcaca 453
Phe *
105

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<210> 745
 <211> 1735

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (473) .. (1201)

<400> 745

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ccccgggtcga cccacgcgtc cggcggcgct cggctcggct cgggcatttc cgctctttg      60
ttttaaactc cggacgggct tttttctcct cctcttgggg gggacccaga gggagcggcg      120
ccccctcccc cctccggcgc ggaccccgcg tgcgccttgc tcgcccgcag ccccagagacc      180
gcaggcggtca caatgtagca gggacccag gcgctgtgct cagaaaatgg aaaaagagcc      240
agggccggaa ggagggtgca gaagcgagtc cgcgtgcgga gccaggaggc agcgtcgcgt      300
gggagtgtctg gcctgaagcc tccatgcccc ggcagagggg cggacacgcg gacgtctagc      360
ggaggctccc gtgtcctcag tatgcatcag gtctcccgaa cctcacagcc cgcagggag      420
gaggagaagg ggaggatttg actttggaag tctctgtgac cagaagccaa ag      atg      475
                                     Met
                                     1

ttg acc agg aag atc aag ctg tgg gac atc aac gcc cac atc acc tgc      523
Leu Thr Arg Lys Ile Lys Leu Trp Asp Ile Asn Ala His Ile Thr Cys
                    5                      10                      15

cgc ctg tgc agc ggg tac ctc atc gac gcc acc acg gtg acc gag tgt      571
Arg Leu Cys Ser Gly Tyr Leu Ile Asp Ala Thr Thr Val Thr Glu Cys
                    20                      25                      30

ctg cac acc ttc tgc agg agc tgc ctg gtg aag tac ctg gag gag aac      619
Leu His Thr Phe Cys Arg Ser Cys Leu Val Lys Tyr Leu Glu Glu Asn
                    35                      40                      45

atc acc tgc ccc acc tgc agg att gtg atc cac cag agc cac ccc ctg      667
Ile Thr Cys Pro Thr Cys Arg Ile Val Ile His Gln Ser His Pro Leu
                    50                      55                      60                      65

cag tac atc ggt cat gac aga acc atg caa gat att gtt tac aaa ttg      715
Gln Tyr Ile Gly His Asp Arg Thr Met Gln Asp Ile Val Tyr Lys Leu
                    70                      75                      80

gta cca ggc ctc caa gaa gcg gaa atg aga aag cag agg gag ttc tat      763
Val Pro Gly Leu Gln Glu Ala Glu Met Arg Lys Gln Arg Glu Phe Tyr
                    85                      90                      95

cac aaa ttg ggc atg gag gtg ccg gga gac atc aag ggg gag acc tgc      811
His Lys Leu Gly Met Glu Val Pro Gly Asp Ile Lys Gly Glu Thr Cys
                    100                     105                     110

tct gca aaa cag cac tta gat tcc cat cgg aat ggt gaa acc aaa gca      859
Ser Ala Lys Gln His Leu Asp Ser His Arg Asn Gly Glu Thr Lys Ala
                    115                     120                     125

gac gac agt tca aac aaa gag gcc gcg gag gag aag ccg gag gag gac      907
Asp Asp Ser Ser Asn Lys Glu Ala Ala Glu Glu Lys Pro Glu Glu Asp
                    130                     135                     140                     145

aac gac tac cac cgc agc gac gag cag gtg agc atc tgc ctg gag tgt      955
Asn Asp Tyr His Arg Ser Asp Glu Gln Val Ser Ile Cys Leu Glu Cys

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	150	155	160	
aac agc agc aaa ctg cgc ggg ctg aag cgg aag tgg atc cgc tgc tca				1003
Asn Ser Ser Lys Leu Arg Gly Leu Lys Arg Lys Trp Ile Arg Cys Ser				
	165	170	175	
gcc cag gcg acc gtc ttg cat ctg aag aag ttc atc gcc aaa aaa ctc				1051
Ala Gln Ala Thr Val Leu His Leu Lys Lys Phe Ile Ala Lys Lys Leu				
	180	185	190	
aac ctt tca tcc ttt aac gag ctg gac att tta tgc aac gag gag atc				1099
Asn Leu Ser Ser Phe Asn Glu Leu Asp Ile Leu Cys Asn Glu Glu Ile				
	195	200	205	
ctg ggc aag gac cac aca ctc aag ttc gtg gtt gtc act agg tgg aga				1147
Leu Gly Lys Asp His Thr Leu Lys Phe Val Val Val Thr Arg Trp Arg				
	210	215	220	225
ttc aag aag gcg ccg ctc ctg ctg cac tac aga ccc aag atg gac ttg				1195
Phe Lys Lys Ala Pro Leu Leu Leu His Tyr Arg Pro Lys Met Asp Leu				
	230	235	240	
ctg tga atggtgccac acagcgccca cagactgggc cctcgacccc ttgggtgctc				1251
Leu *				
ccggccgccc cgcttaagaa cattgcctct ggggtgcatg tggaccagac ttctgaatag				1311
agaatattta taacttttgt atgagagaga attcacactc aacaagacac taccagcacc				1371
acgtttacag aggatgaaaa cacttcacag tctcccagag ccgacgtccc tctccccgc				1431
cccaccccggt gcttcagcct tgcagggaga gtgatgctcc aggcaacacg gttctgagtc				1491
accttctgac acgagctccc tctgcttgct ttccagggtct tgaaaatctg aattcacttc				1551
agtttagttt atgaatttta ggtttcatga taagcctcaa ttgtagtgg acttttattg				1611
aatccttcct aagttattga aaaaatgtct tttcatgggtg aatgacaata tttatgttgc				1671
cttttagcttc ttgaagattt agaagttata taaaaaatta atttaaaagc aaaaaaaaaa				1731
aaaa				1735

<210> 746
 <211> 1185
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (6) .. (1139)

<400> 746	
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Met Pro His Glu Val Val Arg Asp Glu Asn Ser Ser Val Tyr	
1 5 10	
gcc gag gtc tcc cgg ctg ctc ctc gcc acc ggc cac tgg aag agg ctg	95
Ala Glu Val Ser Arg Leu Leu Leu Ala Thr Gly His Trp Lys Arg Leu	
15 20 25 30	

cgg cga gac aac ccc aga ttc aac ctg atg ctg gga gag agg aat cgg	143
Arg Arg Asp Asn Pro Arg Phe Asn Leu Met Leu Gly Glu Arg Asn Arg	
35 40 45	
ctg ccc ttc ggg aga ctg ggt cac gag ccc ggg ctg gta cag ttg gtg	191
Leu Pro Phe Gly Arg Leu Gly His Glu Pro Gly Leu Val Gln Leu Val	
50 55 60	
aat tac tac agg ggt gct gac aaa ctg tgt cgc aaa gct tct tta gtg	239
Asn Tyr Tyr Arg Gly Ala Asp Lys Leu Cys Arg Lys Ala Ser Leu Val	
65 70 75	
aag cta atc aag aca agc cct gaa ctg gct gag tcc tgc aca tgg ttc	287
Lys Leu Ile Lys Thr Ser Pro Glu Leu Ala Glu Ser Cys Thr Trp Phe	
80 85 90	
cct gaa tct tat gtg att tat cca acc aat ctc aag act cca gtt gct	335
Pro Glu Ser Tyr Val Ile Tyr Pro Thr Asn Leu Lys Thr Pro Val Ala	
95 100 105 110	
cca gca cag aat gga att cag cca cca atc agt aac tca agg aca gat	383
Pro Ala Gln Asn Gly Ile Gln Pro Pro Ile Ser Asn Ser Arg Thr Asp	
115 120 125	
gaa aga gaa ttc ttt ctc gcc tct tat aac aga aag aaa gag gat gga	431
Glu Arg Glu Phe Phe Leu Ala Ser Tyr Asn Arg Lys Lys Glu Asp Gly	
130 135 140	
gag ggc aac gtt tgg att gca aag tca tca gcc ggt gcc aaa ggt gaa	479
Glu Gly Asn Val Trp Ile Ala Lys Ser Ser Ala Gly Ala Lys Gly Glu	
145 150 155	
ggc att ctc atc tcc tca gag gct tca gag ctt ctc gat ttc ata gac	527
Gly Ile Leu Ile Ser Ser Glu Ala Ser Glu Leu Leu Asp Phe Ile Asp	
160 165 170	
aac cag ggc caa gtg cac gtg atc cag aaa tat ctt gag cac cct ctg	575
Asn Gln Gly Gln Val His Val Ile Gln Lys Tyr Leu Glu His Pro Leu	
175 180 185 190	
ctg ctt gag cca ggt cat cgc aag ttt gac atc cga agc tgg gtc ttg	623
Leu Leu Glu Pro Gly His Arg Lys Phe Asp Ile Arg Ser Trp Val Leu	
195 200 205	
gtg gat cat cag tat aat atc tac ctc tat aga gag ggt gtg ctt cgg	671
Val Asp His Gln Tyr Asn Ile Tyr Leu Tyr Arg Glu Gly Val Leu Arg	
210 215 220	
act gct tca gaa cca tat cat gtt gat aat ttc caa gac aaa acc tgc	719
Thr Ala Ser Glu Pro Tyr His Val Asp Asn Phe Gln Asp Lys Thr Cys	
225 230 235	
cat ttg acc aat cac tgc att caa aaa gag tat tca aag aac tac ggg	767
His Leu Thr Asn His Cys Ile Gln Lys Glu Tyr Ser Lys Asn Tyr Gly	
240 245 250	
aag tat gaa gaa gga aat gaa atg ttc ttc aag gag ttc aat cag tac	815
Lys Tyr Glu Glu Gly Asn Glu Met Phe Phe Lys Glu Phe Asn Gln Tyr	
255 260 265 270	
cta aca agt gct ttg aac att acc cta gaa agt agt atc tta cta caa	863
Leu Thr Ser Ala Leu Asn Ile Thr Leu Glu Ser Ser Ile Leu Leu Gln	
275 280 285	

atc aaa cat ata ata agg aac tgc ctc ctg agc gtg gag cct gcc att 911
 Ile Lys His Ile Ile Arg Asn Cys Leu Leu Ser Val Glu Pro Ala Ile
 290 295 300
 agc acc aag cac ctc cct tac cag agc ttc cag ctc ttc ggc ttt gac 959
 Ser Thr Lys His Leu Pro Tyr Gln Ser Phe Gln Leu Phe Gly Phe Asp
 305 310 315
 ttc atg gtc gac gag gag ctg aag gtg tgg ctc att gag gtc aac ggt 1007
 Phe Met Val Asp Glu Glu Leu Lys Val Trp Leu Ile Glu Val Asn Gly
 320 325 330
 gcc cct gca tgt gct cag aag ctc tat gca gaa ctg tgc caa ggc atc 1055
 Ala Pro Ala Cys Ala Gln Lys Leu Tyr Ala Glu Leu Cys Gln Gly Ile
 335 340 345 350
 gtg gac ata gcc att tcc agt gtc ttc cca ccc cca gat gtg gag caa 1103
 Val Asp Ile Ala Ile Ser Ser Val Phe Pro Pro Pro Asp Val Glu Gln
 355 360 365
 cct cag acc cag cca gct gcc ttc atc aag ctg tga caga gggcactccc 1153
 Pro Gln Thr Gln Pro Ala Ala Phe Ile Lys Leu *
 370 375
 tgctgccttg gaaaaagcac ggtgtactgc tc 1185

<210> 747
 <211> 1986
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (251)..(913)

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 gageggcggc ggccatcgag acccacccaa ggcgcgctcc cctcggcctc ccagegctcc 180
 caagccgtag cggccgcgcc ccttcagcta gctcgctcgc tcgctctgct tccctgctgc 240
 cggctgcgcc atg gcg ttg gcg ttg gcg gcg ctg gcg gcg gtc gag ccg 289
 Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro
 1 5 10
 gcc tgc ggc agc cgg tac cag cag ttg cag aat gaa gaa gag tct gga 337
 Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly
 15 20 25
 gaa cct gaa cag gct gca ggt gat gct cct cca cct tac agc agc att 385
 Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile
 30 35 40 45
 tct gca gag agc gca gca tat ttt gac tac aag gat gag tct ggg ttt 433
 Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe
 50 55 60

cca aag ccc cca tct tac aat gta gct aca aca ctg ccc agt tat gat 481
 Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp
 65 70 75

gaa gcg gag agg acc aag gct gaa gct act atc cct ttg gtt cct ggg 529
 Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly
 80 85 90

aga gat gag gat ttt gtg ggt cgg gat gat ttt gat gat gct gac cag 577
 Arg Asp Glu Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln
 95 100 105

ctg agg ata gga aat gat ggg att ttc atg tta act ttt ttc atg gca 625
 Leu Arg Ile Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala
 110 115 120 125

ttc ctc ttt aac tgg att ggg ttt ttc ctg tct ttt tgc ctg acc act 673
 Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr
 130 135 140

tca gct gca gga agg tat ggg gcc att tca gga ttt ggt ctc tct cta 721
 Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu
 145 150 155

att aaa tgg atc ctg att gtc agg ttt tcc acc tat ttc cct gga tat 769
 Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr
 160 165 170

ttt gat ggt cag tac tgg ctc tgg tgg gtg ttc ctt gtt tta ggc ttt 817
 Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe
 175 180 185

ctc ctg ttt ctc aga gga ttt atc aat tat gca aaa gtt cgg aag atg 865
 Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met
 190 195 200 205

cca gaa act ttc tca aat ctc ccc agg acc aga gtt ctc ttt att tat 913
 Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr
 210 215 220

taaagatggt ttctggcaaa ggccttcctg catttatgaa ttctctctca agaagcaaga 973

gaacacctgc aggaagtga tcaagatgca gaacacagag gaataatcac ctgctttaaa 1033

aaaataaagt actgttgaaa agatcatttc tctctatttg ttcttaggtg taaaatttta 1093

atagttaatg cagaattctg taatcattga atcattagtg gttaatgttt gaaaaagctc 1153

ttgcaatcaa gtctgtgatg tattaataat gccttatata ttgtttgtag tcattttaag 1213

tagcatgagc catgtccctg tagtcggtag ggggcagtct tgctttattc atcctccatc 1273

tcaaaatgaa cttggaatta aatattgtaa gatatgtata atgctggcca ttttaaaggg 1333

gttttctcaa aagttaaact tttgttatga ctgtgttttt gcacataatc catatttgct 1393

gttcaagtta atctagaaat ttattcaatt ctgtatgaac acctggaagc aaaatcatag 1453

tgcaaaaata catttaagggt gtgggtcaaaa ataagtcttt aattggtaaa taataagcat 1513

taatttttta tagcctgtat tcacaattct gcggtacctt attgtacctt agggattcta 1573

aagggtgtgt cactgtataa aacagaaagc actaggatac aaatgaagct taattactaa 1633

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aatgtaattc ttgacactct ttctataatt agcgttcttc acccccaccc ccacccccac 1693
cccccttatt ttccctttgt ctccctggtga ttaggccaaa gtctgggagt aaggagagga 1753
ttaggtactt aggagcaaag aaagaagtag cttggaactt ttgagatgat ccctaacata 1813
ctgtactact tgctttttaca atgtgttagc agaaaccagt gggttataat gtagaatgat 1873
gtgctttctg cccaagtggg aattcatctt ggtttgctat gttaaaactg taaatacaac 1933
agaacattaa taaatatctc ttgtgtagca ccttttactg taaaaaaaaa aaa 1986

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<210> 748
<211> 1514
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (103)..(1374)

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Met Ala Leu Ala
1

tcc ggg ccc gca agg cgg gcg cta gct ggc tcc ggg cag ctc ggc ctt 162
Ser Gly Pro Ala Arg Arg Ala Leu Ala Gly Ser Gly Gln Leu Gly Leu
5 10 15 20

ggg ggc ttc ggg gcc ccg aga cgc ggg gcg tat gag tgg ggc gtg cgc 210
Gly Gly Phe Gly Ala Pro Arg Arg Gly Ala Tyr Glu Trp Gly Val Arg
25 30 35

tcc acg cgg aag tcg gag cct cct ccc ctg gat agg gtg tac gag atc 258
Ser Thr Arg Lys Ser Glu Pro Pro Pro Leu Asp Arg Val Tyr Glu Ile
40 45 50

cct gga ctg gag ccc atc acc ttt gcg ggg aag atg cac ttc gtg ccc 306
Pro Gly Leu Glu Pro Ile Thr Phe Ala Gly Lys Met His Phe Val Pro
55 60 65

tgg ctg gcg cgg ccg atc ttt ccg ccc tgg gac cgc ggc tac aag gac 354
Trp Leu Ala Arg Pro Ile Phe Pro Pro Trp Asp Arg Gly Tyr Lys Asp
70 75 80

cca agg ttc tac cgc tcg ccc cct ctt cac gag cat ccg ctg tac aaa 402
Pro Arg Phe Tyr Arg Ser Pro Pro Leu His Glu His Pro Leu Tyr Lys
85 90 95 100

gac cag gcc tgc tat atc ttt cac cac cgt tgc cgc ctt ctc gag ggt 450
Asp Gln Ala Cys Tyr Ile Phe His His Arg Cys Arg Leu Leu Glu Gly
105 110 115

gta aag cag gcc ctc tgg ctc acc aag acc aag tta ata gaa ggc ctt 498
Val Lys Gln Ala Leu Trp Leu Thr Lys Thr Lys Leu Ile Glu Gly Leu
120 125 130

ccc gag aaa gtg ctt agc ctt gtt gat gat cca agg aac cac ata gag 546

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Pro	Glu	Lys	Val	Leu	Ser	Leu	Val	Asp	Asp	Pro	Arg	Asn	His	Ile	Glu		
			135				140					145					
aac	caa	gac	gag	tgc	gtt	ctg	aat	gtg	atc	tct	cac	gcc	cgt	ctc	tgg	594	
Asn	Gln	Asp	Glu	Cys	Val	Leu	Asn	Val	Ile	Ser	His	Ala	Arg	Leu	Trp		
		150				155					160						
cag	acc	act	gag	gaa	atc	ccc	aag	aga	gag	acc	tac	tgc	ccg	gtc	atc	642	
Gln	Thr	Thr	Glu	Glu	Ile	Pro	Lys	Arg	Glu	Thr	Tyr	Cys	Pro	Val	Ile		
		165			170				175					180			
gtg	gac	aac	cta	ata	cag	ctg	tgt	aaa	tct	cag	att	ctc	aag	cat	cct	690	
Val	Asp	Asn	Leu	Ile	Gln	Leu	Cys	Lys	Ser	Gln	Ile	Leu	Lys	His	Pro		
			185				190						195				
tct	ctg	gcc	agg	agg	atc	tgt	gtc	caa	aac	tcc	acg	ttt	tct	gct	acc	738	
Ser	Leu	Ala	Arg	Arg	Ile	Cys	Val	Gln	Asn	Ser	Thr	Phe	Ser	Ala	Thr		
			200				205						210				
tgg	aac	cga	gag	tct	ctt	ctc	ctt	caa	gtc	cgt	ggt	tct	ggt	gga	gcc	786	
Trp	Asn	Arg	Glu	Ser	Leu	Leu	Leu	Gln	Val	Arg	Gly	Ser	Gly	Gly	Ala		
		215				220						225					
cga	ctg	agc	act	aag	gat	cct	ctg	ccc	acc	atc	gcc	tcc	aga	gag	gag	834	
Arg	Leu	Ser	Thr	Lys	Asp	Pro	Leu	Pro	Thr	Ile	Ala	Ser	Arg	Glu	Glu		
		230			235					240							
att	gaa	gct	act	aag	aat	cat	gtt	cta	gag	acc	ttc	tac	ccc	ata	tca	882	
Ile	Glu	Ala	Thr	Lys	Asn	His	Val	Leu	Glu	Thr	Phe	Tyr	Pro	Ile	Ser		
	245			250					255					260			
ccc	atc	atc	gat	ctt	cat	gaa	tgc	aat	att	tat	gat	gtg	aaa	aat	gac	930	
Pro	Ile	Ile	Asp	Leu	His	Glu	Cys	Asn	Ile	Tyr	Asp	Val	Lys	Asn	Asp		
			265				270						275				
aca	gga	ttc	cag	gaa	ggc	tat	cct	tac	ccc	tat	ccc	cat	acc	ctg	tac	978	
Thr	Gly	Phe	Gln	Gly	Tyr	Pro	Tyr	Pro	Tyr	Pro	His	Thr	Leu	Tyr			
		280				285						290					
tta	ctg	gac	aaa	gcc	aat	tta	cga	cca	cac	cgc	ctt	caa	cca	gat	cag	1026	
Leu	Leu	Asp	Lys	Ala	Asn	Leu	Arg	Pro	His	Arg	Leu	Gln	Pro	Asp	Gln		
		295				300						305					
ctg	cgg	gcc	aag	atg	atc	ctg	ttt	gct	ttt	ggc	agt	gcc	ctg	gct	cag	1074	
Leu	Arg	Ala	Lys	Met	Ile	Leu	Phe	Ala	Phe	Gly	Ser	Ala	Leu	Ala	Gln		
		310				315				320							
gcc	cgg	ctc	ctc	tat	ggg	aat	gat	gcc	aag	gtc	ttg	gag	cag	ccc	gtg	1122	
Ala	Arg	Leu	Leu	Tyr	Gly	Asn	Asp	Ala	Lys	Val	Leu	Glu	Gln	Pro	Val		
		325			330				335					340			
gtg	gtg	cag	agc	gtg	ggc	acg	gat	gga	cgt	gtc	ttc	cat	ttc	cta	gtg	1170	
Val	Val	Gln	Ser	Val	Gly	Thr	Asp	Gly	Arg	Val	Phe	His	Phe	Leu	Val		
			345				350						355				
ttt	caa	ctg	aat	acc	aca	gac	ctg	gac	tgt	aac	gag	ggt	gtc	aag	aat	1218	
Phe	Gln	Leu	Asn	Thr	Thr	Asp	Leu	Asp	Cys	Asn	Glu	Gly	Val	Lys	Asn		
		360					365					370					
ttg	gcc	tgg	gtg	gac	tca	gac	cag	ctc	ctc	tat	cag	cat	ttt	tgg	tgt	1266	
Leu	Ala	Trp	Val	Asp	Ser	Asp	Gln	Leu	Leu	Tyr	Gln	His	Phe	Trp	Cys		
		375				380					385						
ctc	cca	gtg	atc	aaa	aag	aga	gtg	gtt	gtg	gaa	cct	gtt	ggg	cca	gtt	1314	

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Leu Pro Val Ile Lys Lys Arg Val Val Val Glu Pro Val Gly Pro Val
390                               395                               400

ggt ttc aag cca gag aca ttc aga aag ttt tta gct cta tat ttg cat      1362
Gly Phe Lys Pro Glu Thr Phe Arg Lys Phe Leu Ala Leu Tyr Leu His
405                               410                               415                               420

ggt gct gcg tga gca gaggaccct ctgaatcctg aaaccctct tgcctctctt      1417
Gly Ala Ala *

ccacggaaga gggcctgggc cccgtggagc ctcagtgcc gtttggcctg ctgctctcgc      1477

tgacaataaa gagcccttgc gttgcaaaaa aaaaaaa                               1514

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<210> 749
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<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (147)..(1109)

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ggacattgtg tgggccagag gcaggg atg gtt ggc tat gac ccc aaa cca gat      173
                               Met Val Gly Tyr Asp Pro Lys Pro Asp
                               1                               5

ggc agg aat aac acc aag ttc cag gtg gca gtg gct ggg tct gtg tct      221
Gly Arg Asn Asn Thr Lys Phe Gln Val Ala Val Ala Gly Ser Val Ser
10                               15                               20                               25

gga ctt gtt act cgg gcg ctg atc agt ccc ttc gac gtc atc aag atc      269
Gly Leu Val Thr Arg Ala Leu Ile Ser Pro Phe Asp Val Ile Lys Ile
30                               35                               40

cgt ttc cag ctt cag cat gag cgc ctg tct cgc agt gac ccc agc gca      317
Arg Phe Gln Leu Gln His Glu Arg Leu Ser Arg Ser Asp Pro Ser Ala
45                               50                               55

aag tac cat ggc atc ctc cag gcc tct agg cag att ctg cag gag gag      365
Lys Tyr His Gly Ile Leu Gln Ala Ser Arg Gln Ile Leu Gln Glu Glu
60                               65                               70

ggt ccg aca gct ttc tgg aaa gga cac gtc cca gct cag att ctc tcc      413
Gly Pro Thr Ala Phe Trp Lys Gly His Val Pro Ala Gln Ile Leu Ser
75                               80                               85

ata ggc tat gga gct gtc caa ttc ttg tca ttt gaa atg ctg acg gag      461
Ile Gly Tyr Gly Ala Val Gln Phe Leu Ser Phe Glu Met Leu Thr Glu
90                               95                               100                               105

ctg gtc cac aga ggc agc gtg tac gac gcc cgg gaa ttc tca gtg cac      509
Leu Val His Arg Gly Ser Val Tyr Asp Ala Arg Glu Phe Ser Val His
110                               115                               120

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ttt gta tgt ggt ggc ctg gct gcc tgt atg gcc acc ctc act gtg cac	557
Phe Val Cys Gly Gly Leu Ala Ala Cys Met Ala Thr Leu Thr Val His	
125 130 135	
ccc gtg gat gtt ctg cgc acc cgc ttt gca gct cag ggt gag ccc aag	605
Pro Val Asp Val Leu Arg Thr Arg Phe Ala Ala Gln Gly Glu Pro Lys	
140 145 150	
gtc tat aat acg ctg cgc cac gcc gtg ggg acc atg tat agg agc gaa	653
Val Tyr Asn Thr Leu Arg His Ala Val Gly Thr Met Tyr Arg Ser Glu	
155 160 165	
ggc ccc cag gtt ttc tac aaa ggc ttg gct ccc acc ttg atc gcc atc	701
Gly Pro Gln Val Phe Tyr Lys Gly Leu Ala Pro Thr Leu Ile Ala Ile	
170 175 180 185	
ttc ccc tac gcc ggg ctg cag ttc tct tgc tac agc tcc ttg aag cac	749
Phe Pro Tyr Ala Gly Leu Gln Phe Ser Cys Tyr Ser Ser Leu Lys His	
190 195 200	
ctg tac aag tgg gcc ata cca gcc gaa gga aag aaa aat gag aac ctc	797
Leu Tyr Lys Trp Ala Ile Pro Ala Glu Gly Lys Lys Asn Glu Asn Leu	
205 210 215	
caa aac ctg ctt tgt ggc agt gga gct ggt gtc atc agc aag acc ctg	845
Gln Asn Leu Leu Cys Gly Ser Gly Ala Gly Val Ile Ser Lys Thr Leu	
220 225 230	
aca tat ccg ctg gac ctc ttc aag aag cgg cta cag gtt gga ggg ttt	893
Thr Tyr Pro Leu Asp Leu Phe Lys Lys Arg Leu Gln Val Gly Gly Phe	
235 240 245	
gag cat gcc aga gct gcc ttt ggc cag gta cgg aga tac aag ggc ctc	941
Glu His Ala Arg Ala Phe Gly Gln Val Arg Arg Tyr Lys Gly Leu	
250 255 260 265	
atg gac tgt gcc aag cag gtg cta caa aag gaa ggc gcc ctg ggc ttc	989
Met Asp Cys Ala Lys Gln Val Leu Gln Lys Glu Gly Ala Leu Gly Phe	
270 275 280	
ttc aag ggc ctg tcc ccc agc ttg ctg aag gct gcc ctc tcc aca ggc	1037
Phe Lys Gly Leu Ser Pro Ser Leu Leu Lys Ala Ala Leu Ser Thr Gly	
285 290 295	
ttc atg ttc ttc tcg tat gaa ttc ttc tgt aat gtc ttc cac tgc atg	1085
Phe Met Phe Phe Ser Tyr Glu Phe Phe Cys Asn Val Phe His Cys Met	
300 305 310	
aac agg aca gcc agc cag cgc tga gcgcaggaag gaccccaggt cttccctgga	1139
Asn Arg Thr Ala Ser Gln Arg *	
315 320	
ggcagcctcc tgaaggaagg aagattcagt ctccactgag aggtgccgtc tggcccttcc	1199
ctgcaggcca gctgccccaa gcggggtagc agccttgaac ccaccagct gggacaccac	1259
cagaagggtcc agggctctcc ccatgagaga atcagagggga atgcaggacg tggctctatgg	1319
tgagccaacg acacagttag aaggagcagg aagttgctgt ttctcctctg accagccac	1379
actgcaaagg aaacagacgc catcctacac ctatcagccc tgccctgccag gagaacagaa	1439
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<210> 750
<211> 2187
<212> DNA
<213> Homo sapiens
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<222> (266) .. (1759)
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Gln Leu Ala Lys Glu Gln Ser Met Ser Ser Val Gly Phe Cys Val Ile	
155 160 165	
aat tct gca aaa cgt ggt tat cct tta gag gat gca aca cac ata gca	820
Asn Ser Ala Lys Arg Gly Tyr Pro Leu Glu Asp Ala Thr His Ile Ala	
170 175 180 185	
ctt cgc act gta aga aga ttc cta gag att cat ggg gaa acc att gaa	868
Leu Arg Thr Val Arg Arg Phe Leu Glu Ile His Gly Glu Thr Ile Glu	
190 195 200	
aaa gta gta ttt gct gtc tct gat ctt gaa gag ggt act tac caa aag	916
Lys Val Val Phe Ala Val Ser Asp Leu Glu Glu Gly Thr Tyr Gln Lys	
205 210 215	
ctg cta cct ctc tac ttc cca agg tca tta aaa gag gag aat cga tca	964
Leu Leu Pro Leu Tyr Phe Pro Arg Ser Leu Lys Glu Glu Asn Arg Ser	
220 225 230	
ttg ccc tac cta cct gca gat att gga aat gca gaa ggg gag cct gtg	1012
Leu Pro Tyr Leu Pro Ala Asp Ile Gly Asn Ala Glu Gly Glu Pro Val	
235 240 245	
gta cct gaa cga cag att aga ata agt gag aaa cct ggt gct cca gaa	1060
Val Pro Glu Arg Gln Ile Arg Ile Ser Glu Lys Pro Gly Ala Pro Glu	
250 255 260 265	
gat aac caa gaa gag gag gat gaa ggc ttg gga gtt gat ctc tct ttc	1108
Asp Asn Gln Glu Glu Glu Asp Glu Gly Leu Gly Val Asp Leu Ser Phe	
270 275 280	
att ggc tct cat gct ttt gct cga atg gaa gga gat att gac aag caa	1156
Ile Gly Ser His Ala Phe Ala Arg Met Glu Gly Asp Ile Asp Lys Gln	
285 290 295	
aga aaa ctg atc ctt cag gga caa tta tca gag gca gct ctg cag aag	1204
Arg Lys Leu Ile Leu Gln Gly Gln Leu Ser Glu Ala Ala Leu Gln Lys	
300 305 310	
cag cat caa aga aat tat aat cgc tgg tta tgt caa gca cga gct gag	1252
Gln His Gln Arg Asn Tyr Asn Arg Trp Leu Cys Gln Ala Arg Ala Glu	
315 320 325	
gat ctg tct gat att gct tct cta aaa gcc tta tac caa aca ggt gtt	1300
Asp Leu Ser Asp Ile Ala Ser Leu Lys Ala Leu Tyr Gln Thr Gly Val	
330 335 340 345	
gat aac tgt ggt cga aca gtg atg gtg gta gtt gga aga aac att cct	1348
Asp Asn Cys Gly Arg Thr Val Met Val Val Val Gly Arg Asn Ile Pro	
350 355 360	
gta aca tta ata gat atg gac aag gct ctc tta tat ttc att cat gta	1396
Val Thr Leu Ile Asp Met Asp Lys Ala Leu Leu Tyr Phe Ile His Val	
365 370 375	
atg gat cac att gct gtg aag gag tat gta tta gtg tat ttt cac acc	1444
Met Asp His Ile Ala Val Lys Glu Tyr Val Leu Val Tyr Phe His Thr	
380 385 390	
ctg acc agc gaa tac aat cac ctg gac tcc gac ttc ctg aag aaa ctc	1492
Leu Thr Ser Glu Tyr Asn His Leu Asp Ser Asp Phe Leu Lys Lys Leu	
395 400 405	

tac gat gtt gtt gat gtc aag tac aag agg aat ttg aag gct gtt tat 1540
 Tyr Asp Val Val Asp Val Lys Tyr Lys Arg Asn Leu Lys Ala Val Tyr
 410 415 420 425
 ttt gta cat ccc aca ttt cgt tca aag gtg tca aca tgg ttt ttt acc 1588
 Phe Val His Pro Thr Phe Arg Ser Lys Val Ser Thr Trp Phe Phe Thr
 430 435 440
 acc ttt tct gtc tca gga ctg aag gac aaa atc cac cat gtg gac agc 1636
 Thr Phe Ser Val Ser Gly Leu Lys Asp Lys Ile His His Val Asp Ser
 445 450 455
 ctc cac cag ctg ttt tct gcc ata tca cca gaa cag att gac ttt cct 1684
 Leu His Gln Leu Phe Ser Ala Ile Ser Pro Glu Gln Ile Asp Phe Pro
 460 465 470
 cct ttt gtc ctt gaa tat gat gcc agg gaa aac ggg cct tac tat aca 1732
 Pro Phe Val Leu Glu Tyr Asp Ala Arg Glu Asn Gly Pro Tyr Tyr Thr
 475 480 485
 tca tat ccc cca tca cca gat ttg tga cctgc catctttcag tgcttcttgg 1784
 Ser Tyr Pro Pro Ser Pro Asp Leu *
 490 495
 ttcccaggat gccacttctt ccacgaatag ctacctgttg aagtgatatt cattgttgc 1844
 gtacagatcc agagagcctt ttgtcccccac ctctctggta tttttttatt gactgtatat 1904
 tttctggcac ataagcaatc taaaaatggg aggccattct gaactgcaca cattttaaat 1964
 ttgtatatatt atatgaaatg gaaatgttca ttttttagatt gttaatagaa attggggagc 2024
 aacttttgag tatcttttagt ttcttgaagg acaccgaatt ctccattaga taaaccacca 2084
 agactgttca catcatctct ctaacattgc acgcttctt tgtgtactta agtgattctc 2144
 gaaatataca gaaccaatgt atgctaacca gaaaaaaaaa aaa 2187

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (238) .. (1512)

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 ccttcaggcc tcaggcagag tcacgggtggc agcattgaga gttggacacc cgggtccttg 180
 aagtgatctc taggccccag ccccaaatcc gccaccattc cgtgctgcgg ggacacc 237
 atg gct cca gaa gag gac gct gga ggg gag gcc tta ggg ggc agt ttc 285
 Met Ala Pro Glu Glu Asp Ala Gly Gly Glu Ala Leu Gly Gly Ser Phe
 1 5 10 15
 tgg gag gct ggc aac tac agg cgc acg gta cag cgg gtg gag gac ggg 333

Trp	Glu	Ala	Gly	Asn	Tyr	Arg	Arg	Thr	Val	Gln	Arg	Val	Glu	Asp	Gly	
			20					25					30			
cac	cgg	ctg	tgc	ggg	gac	ctg	gtc	agc	tgc	ttc	cag	gag	cgc	gcc	cgc	381
His	Arg	Leu	Cys	Gly	Asp	Leu	Val	Ser	Cys	Phe	Gln	Glu	Arg	Ala	Arg	
		35					40				45					
atc	gag	aag	gct	tat	gcc	cag	cag	ttg	gct	gac	tgg	gcc	cga	aag	tgg	429
Ile	Glu	Lys	Ala	Tyr	Ala	Gln	Gln	Leu	Ala	Asp	Trp	Ala	Arg	Lys	Trp	
	50					55				60						
agg	ggg	acc	gtg	gag	aag	ggc	ccc	cag	tat	ggc	aca	ctg	gag	aag	gcc	477
Arg	Gly	Thr	Val	Glu	Lys	Gly	Pro	Gln	Tyr	Gly	Thr	Leu	Glu	Lys	Ala	
	65				70				75						80	
tgg	cat	gcc	ttt	ttc	acg	gcg	gct	gag	cgg	ctg	agc	gcg	ctg	cac	ctg	525
Trp	His	Ala	Phe	Phe	Thr	Ala	Ala	Glu	Arg	Leu	Ser	Ala	Leu	His	Leu	
				85					90					95		
gag	gtg	cgg	gag	aag	ctg	caa	ggg	cag	gac	agt	gag	cgg	gtg	cgc	gcc	573
Glu	Val	Arg	Glu	Lys	Leu	Gln	Gly	Gln	Asp	Ser	Glu	Arg	Val	Arg	Ala	
			100					105					110			
tgg	cag	cgg	ggg	gct	ttc	cac	cgg	cct	gtg	ctg	ggc	ggc	ttc	cgc	gag	621
Trp	Gln	Arg	Gly	Ala	Phe	His	Arg	Pro	Val	Leu	Gly	Gly	Phe	Arg	Glu	
		115					120					125				
agc	cgg	gcg	gcc	gag	gac	ggc	ttc	cgc	aag	gcc	cag	aag	ccc	tgg	ctg	669
Ser	Arg	Ala	Ala	Glu	Asp	Phe	Arg	Lys	Ala	Gln	Lys	Pro	Trp	Leu		
	130					135				140						
aag	agg	ctg	aag	gag	gtt	gag	gct	tcc	aag	aaa	agc	tac	cac	gca	gcc	717
Lys	Arg	Leu	Lys	Glu	Val	Glu	Ala	Ser	Lys	Lys	Ser	Tyr	His	Ala	Ala	
	145				150				155						160	
cgg	aag	gat	gag	aag	acc	gcc	cag	acg	agg	gag	agc	cac	gca	aag	gca	765
Arg	Lys	Asp	Glu	Lys	Thr	Ala	Gln	Thr	Arg	Glu	Ser	His	Ala	Lys	Ala	
				165					170					175		
gac	agc	gcc	gtc	tcc	cag	gag	cag	ctg	cgc	aaa	ctg	cag	gaa	cgg	gtg	813
Asp	Ser	Ala	Val	Ser	Gln	Glu	Gln	Leu	Arg	Lys	Leu	Gln	Glu	Arg	Val	
			180					185					190			
gaa	cgc	tgt	gcc	aag	gag	gcc	gag	aag	aca	aaa	gct	cag	tat	gag	cag	861
Glu	Arg	Cys	Ala	Lys	Glu	Ala	Glu	Lys	Thr	Lys	Ala	Gln	Tyr	Glu	Gln	
		195					200					205				
acg	ctg	gca	gag	ctg	cat	cgc	tac	act	cca	cgc	tac	atg	gag	gac	atg	909
Thr	Leu	Ala	Glu	Leu	His	Arg	Tyr	Thr	Pro	Arg	Tyr	Met	Glu	Asp	Met	
	210					215					220					
gaa	cag	gcc	ttt	gag	acc	tgc	cag	gcc	gcc	gag	cgc	cag	cgg	ctt	ctt	957
Glu	Gln	Ala	Phe	Glu	Thr	Cys	Gln	Ala	Ala	Glu	Arg	Gln	Arg	Leu	Leu	
	225				230					235					240	
ttc	ttc	aag	gat	atg	ctg	ctc	acc	tta	cac	cag	cac	ctg	gac	ctt	tcc	1005
Phe	Phe	Lys	Asp	Met	Leu	Leu	Thr	Leu	His	Gln	His	Leu	Asp	Leu	Ser	
				245					250					255		
agc	agt	gag	aag	ttc	cat	gaa	ctc	cac	cgt	gac	ttg	cac	cag	ggc	att	1053
Ser	Ser	Glu	Lys	Phe	His	Glu	Leu	His	Arg	Asp	Leu	His	Gln	Gly	Ile	
			260					265					270			
gag	gca	gcc	agt	gac	gaa	gag	gat	ctg	cgc	tgg	tgg	cgc	agc	acc	cac	1101

PCT/US01/04098

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<210> 752
<211> 4232
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (173)..(1978
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gggaaggagc ctggacacag tgacacattc tcaaaggccc tgcaggacca cc atg	175
	Met
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gct tat gat gac tcc gtg aag aaa gaa gat tgt ttt gat ggt gat cat	223
Ala Tyr Asp Asp Ser Val Lys Lys Glu Asp Cys Phe Asp Gly Asp His	
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acc ttt gag gac ata gga ctt gca gct ggc cga agc caa cga gag aaa	271
Thr Phe Glu Asp Ile Gly Leu Ala Ala Gly Arg Ser Gln Arg Glu Lys	
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aaa cgt tct tac aaa gat ttt tta agg gaa gag gaa gaa att gct gct	319
Lys Arg Ser Tyr Lys Asp Phe Leu Arg Glu Glu Glu Glu Ile Ala Ala	
	35 40 45
cag gtc agg aat tct tcc aag aag aag ttg aag gat agt gaa ctt tac	367
Gln Val Arg Asn Ser Ser Lys Lys Lys Leu Lys Asp Ser Glu Leu Tyr	
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ttc ttg ggg acg gac aca cac aag aag aag agg aag cac tcc tct gat	415
Phe Leu Gly Thr Asp Thr His Lys Lys Lys Arg Lys His Ser Ser Asp	
	70 75 80
gat tac tac tat gga gac att tcg tct ttg gaa tcg tca cag aag aaa	463
Asp Tyr Tyr Tyr Gly Asp Ile Ser Ser Leu Glu Ser Ser Gln Lys Lys	
	85 90 95
aag aaa aag tcc agc cca cag tct act gat aca gct atg gac ctg ttg	511
Lys Lys Lys Ser Ser Pro Gln Ser Thr Asp Thr Ala Met Asp Leu Leu	
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aaa gct atc act tcc cca ctg gca gca ggc tcc aag ccc tcc aaa aag	559
Lys Ala Ile Thr Ser Pro Leu Ala Ala Gly Ser Lys Pro Ser Lys Lys	
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act ggg gag aaa tcc tct ggc tct tca agc cat tcg gag agt aaa aag	607
Thr Gly Glu Lys Ser Ser Gly Ser Ser Ser His Ser Glu Ser Lys Lys	
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gag cac cac agg aag aaa gtc agt gga agc agt ggg gaa cta ccc cta	655
Glu His His Arg Lys Lys Val Ser Gly Ser Ser Gly Glu Leu Pro Leu	
	150 155 160
gag gat ggt ggc tcc cac aaa tcg aaa aaa atg aaa cct ctc tat gtg	703
Glu Asp Gly Gly Ser His Lys Ser Lys Lys Met Lys Pro Leu Tyr Val	
	165 170 175
aac aca gag aca ctg acc ctt cgg gag cct gat ggt tta aaa atg aaa	751
Asn Thr Glu Thr Leu Thr Leu Arg Glu Pro Asp Gly Leu Lys Met Lys	
	180 185 190
ctt att ctg tca cca aag gag aag gga agc agc tct gtt gat gag gag	799
Leu Ile Leu Ser Pro Lys Glu Lys Gly Ser Ser Ser Val Asp Glu Glu	
	195 200 205
tct ttt caa tat ccc tcc caa caa gcg act gtg aaa aaa tcc tca aag	847
Ser Phe Gln Tyr Pro Ser Gln Gln Ala Thr Val Lys Lys Ser Ser Lys	

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Lys Ser Ala Arg Asp Glu Gln Gly Ala Leu Leu Leu Gly His Glu Leu				
	230	235	240	
cag agc ttt ctg aaa aca gcc cgg aaa aag cac aag tca tcc tca gac				943
Gln Ser Phe Leu Lys Thr Ala Arg Lys Lys His Lys Ser Ser Ser Asp				
	245	250	255	
gca cat tca tct cct ggc cct gaa ggc tgt ggg tct gac gcc tcc cag				991
Ala His Ser Ser Pro Gly Pro Glu Gly Cys Gly Ser Asp Ala Ser Gln				
	260	265	270	
ttc gca gag tcc cac agt gct aac ctt gat ctt tca ggg ctt gaa cct				1039
Phe Ala Glu Ser His Ser Ala Asn Leu Asp Leu Ser Gly Leu Glu Pro				
	275	280	285	
att ctg gta gaa tca gac tca tcc tct ggt ggg gaa cta gag gct ggg				1087
Ile Leu Val Glu Ser Asp Ser Ser Ser Gly Gly Glu Leu Glu Ala Gly				
	290	295	300	305
gag tta gtg ata gat gat tct tac cga gaa atc aag aag aaa aag aag				1135
Glu Leu Val Ile Asp Asp Ser Tyr Arg Glu Ile Lys Lys Lys Lys Lys				
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tca aag aag agc aaa aag aag aaa gac aag gag aag cat aaa gag aag				1183
Ser Lys Lys Ser Lys Lys Lys Lys Asp Lys Glu Lys His Lys Glu Lys				
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cga cac tcc aag tcc aag aga agt tta gga ctt tct gcc gtg cca gtg				1231
Arg His Ser Lys Ser Lys Arg Ser Leu Gly Leu Ser Ala Val Pro Val				
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gga gag gtc aca gtg aca tct ggc cct cct ccc agc atc cca tac gct				1279
Gly Glu Val Thr Val Thr Ser Gly Pro Pro Pro Ser Ile Pro Tyr Ala				
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gga gca gca gca cct ccc ctg cca ctt cct ggc ctc cac aca gat ggg				1327
Gly Ala Ala Ala Pro Pro Leu Pro Leu Pro Gly Leu His Thr Asp Gly				
	370	375	380	385
cat agt gaa aaa aaa aaa aaa aaa gag aag gac aaa gag aga gag				1375
His Ser Glu Lys Lys Lys Lys Lys Lys Glu Lys Asp Lys Glu Arg Glu				
	390	395	400	
aga gga gaa aag cca aaa aag aag aac atg tcg gcc tac cag gtg ttc				1423
Arg Gly Glu Lys Pro Lys Lys Lys Asn Met Ser Ala Tyr Gln Val Phe				
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tgt aaa gag tat cgc gtg acc att gtg gct gac cat cca ggt ata gat				1471
Cys Lys Glu Tyr Arg Val Thr Ile Val Ala Asp His Pro Gly Ile Asp				
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ttt ggg gaa ctt agt aaa aaa ctg gct gag gtg tgg aag caa tta cca				1519
Phe Gly Glu Leu Ser Lys Lys Leu Ala Glu Val Trp Lys Gln Leu Pro				
	435	440	445	
gaa aaa gac aaa ctg att tgg aag caa aaa gct cag tat ctg cag cac				1567
Glu Lys Asp Lys Leu Ile Trp Lys Gln Lys Ala Gln Tyr Leu Gln His				
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aaa cag aac aaa gca gaa gcc aca act gtg aaa agg aaa gca tcc agc				1615
Lys Gln Asn Lys Ala Glu Ala Thr Thr Val Lys Arg Lys Ala Ser Ser				

470	475	480	
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Ser Glu Gly Ser Met Lys Val Lys Ala Ser Ser Val Gly Val Leu Ser			
485	490	495	
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Ala Lys Ala Pro Glu Thr Glu Pro Ile Asp Val Ala Ala His Leu Gln			
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Leu Leu Gly Glu Ser Leu Ser Leu Ile Gly His Arg Leu Gln Glu Thr			
530	535	540	545
gag ggt atg gtg gct gtg tct ggc agt ttg tca gtg ctt ctg gat tcc			1855
Glu Gly Met Val Ala Val Ser Gly Ser Leu Ser Val Leu Leu Asp Ser			
550	555	560	
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Ile Ile Cys Ala Leu Gly Pro Leu Ala Cys Leu Thr Thr Gln Leu Pro			
565	570	575	
gaa ttg aat ggc tgt ccc aaa cag gtc ttg tca aac aca tta gac aac			1951
Glu Leu Asn Gly Cys Pro Lys Gln Val Leu Ser Asn Thr Leu Asp Asn			
580	585	590	
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Ile Ala Tyr Thr Thr Pro Gly Leu *			
595	600		
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 tacagctgca gccccagag gtctggctcc ctgacctgt ccaacccat agccatgact 180

2039

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tctctccag tctgcctagc ccagccctgg gactggaatt tgagtagggg atgaggggaa 1160
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aatttctacc tccatagacc ggccagaatt tagcttcaact tgagagagat ctggaatgg 1460
cgccatgatt gaaaccacgc accattacat catcattaca ttaattacat caacataaat 1520
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cttgccctgt cacttgacgc ttctgcctc tgctttgatg gctgaggtga actcatgttc 1820
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ccgcgcccgg agcatctccc tggaggaacg gagacaaagg aggatc atg tcc aaa 176
Met Ser Lys
1

ggg ctc cca gag acc agg acg gac gca gcc atg tca gag ctg gtg cct 224
Gly Leu Pro Glu Thr Arg Thr Asp Ala Ala Met Ser Glu Leu Val Pro
5 10 15

gag ccc agg cct aag cca gcg gtg ccc atg aag ccc atg agc atc aac 272
Glu Pro Arg Pro Lys Pro Ala Val Pro Met Lys Pro Met Ser Ile Asn
20 25 30 35

tcc aac ctg ctg ggc tac atc ggc atc gac acc atc atc gag cag atg 320
Ser Asn Leu Leu Gly Tyr Ile Gly Ile Asp Thr Ile Ile Glu Gln Met
40 45 50

cgc aag aag acc atg aag acc ggt ttc gac ttc aac atc atg gtc gtt 368
Arg Lys Lys Thr Met Lys Thr Gly Phe Asp Phe Asn Ile Met Val Val
55 60 65

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ggc cag agt gga ctg ggc aaa tca acg ctg gtc aac acg ctc ttc aaa	416
Gly Gln Ser Gly Leu Gly Lys Ser Thr Leu Val Asn Thr Leu Phe Lys	
70 75 80	
tcc caa gtg agc cgc aag gcc tcc agc tgg aac cgg gag gag aag atc	464
Ser Gln Val Ser Arg Lys Ala Ser Ser Trp Asn Arg Glu Glu Lys Ile	
85 90 95	
ccc aag aca gtg gag atc aaa gct atc ggg cat gtg ata gag gaa ggc	512
Pro Lys Thr Val Glu Ile Lys Ala Ile Gly His Val Ile Glu Glu Gly	
100 105 110 115	
ggt gtc aaa atg aag ctg acc gtc atc gac acc cca ggc ttt gga gac	560
Gly Val Lys Met Lys Leu Thr Val Ile Asp Thr Pro Gly Phe Gly Asp	
120 125 130	
caa atc aac aat gaa aac tgc tgg gag ccc att gag aag tac atc aat	608
Gln Ile Asn Asn Glu Asn Cys Trp Glu Pro Ile Glu Lys Tyr Ile Asn	
135 140 145	
gag cag tac gag aag ttc ctg aag gag gag gtc aac atc gcc agg aag	656
Glu Gln Tyr Glu Lys Phe Leu Lys Glu Glu Val Asn Ile Ala Arg Lys	
150 155 160	
aaa cgc atc cct gac act cgt gtc cac tgc tgc ctt tac ttc atc tct	704
Lys Arg Ile Pro Asp Thr Arg Val His Cys Cys Leu Tyr Phe Ile Ser	
165 170 175	
ccc aca gga cac tcc ttg cga cct ctg gat ctt gag ttc atg aaa cac	752
Pro Thr Gly His Ser Leu Arg Pro Leu Asp Leu Glu Phe Met Lys His	
180 185 190 195	
ctc agc aag gtt gtg aac atc atc cct gtc att gct aag gct gac acc	800
Leu Ser Lys Val Val Asn Ile Ile Pro Val Ile Ala Lys Ala Asp Thr	
200 205 210	
atg acc ctg gag gag aag tct gaa ttc aag caa agg gtt cgc aag gag	848
Met Thr Leu Glu Glu Lys Ser Glu Phe Lys Gln Arg Val Arg Lys Glu	
215 220 225	
ctt gaa gta aat ggc att gaa ttc tac ccc cag aag gaa ttt gat gag	896
Leu Glu Val Asn Gly Ile Glu Phe Tyr Pro Gln Lys Glu Phe Asp Glu	
230 235 240	
gat ttg gag gat aag acg gag aat gac aaa atc agg cag gag agc atg	944
Asp Leu Glu Asp Lys Thr Glu Asn Asp Lys Ile Arg Gln Glu Ser Met	
245 250 255	
cct ttt gct gtg gtg gga agt gac aag gag tac caa gtg aat ggc aag	992
Pro Phe Ala Val Val Gly Ser Asp Lys Glu Tyr Gln Val Asn Gly Lys	
260 265 270 275	
agg gtc ctc ggc cga aaa act cca tgg ggg atc atc gaa gtg gaa aac	1040
Arg Val Leu Gly Arg Lys Thr Pro Trp Gly Ile Ile Glu Val Glu Asn	
280 285 290	
ctc aac cac tgt gag ttt gcc ctg ctt cga gac ttt gtc atc agg acc	1088
Leu Asn His Cys Glu Phe Ala Leu Leu Arg Asp Phe Val Ile Arg Thr	
295 300 305	
cac ctc cag gac ctc aag gaa gtg aca cac aac atc cac tat gag act	1136
His Leu Gln Asp Leu Lys Glu Val Thr His Asn Ile His Tyr Glu Thr	
310 315 320	

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tac agg gcc aag cgg ctc aat gac aat gga ggc ctc cct ccg gtg agc      1184
Tyr Arg Ala Lys Arg Leu Asn Asp Asn Gly Gly Leu Pro Pro Val Ser
    325                      330                      335

gtg gac aca gag gaa agc cac gac agt aac cca tga cgac cacttctctg      1234
Val Asp Thr Glu Glu Ser His Asp Ser Asn Pro *
    340                      345                      350

tgtcatcaca catacccact tcacacacac acatcccaaa taccaccacc aaccaccttc      1294

ttcctctcaa ctctgtccca caggcctgtc tggatattgt ggagcatctt gtctgtgtgt      1354

gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gacagagaga gagcgagaga gcctgtgtgt      1414

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                                Met
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ttg cgc tgg ctg cgg gac ttc gtg ctg ccc acc gcg gcc tgc cag gac      163
Leu Arg Trp Leu Arg Asp Phe Val Leu Pro Thr Ala Ala Cys Gln Asp
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gcg gag cag ccg atg cgc tac gag acc ctc ttc cag gca ctg gac cgc      211
Ala Glu Gln Pro Met Arg Tyr Glu Thr Leu Phe Gln Ala Leu Asp Arg
    20                      25                      30

aat ggg gac gga gtg gtg gac atc ggc gag ctg cag gag ggg ctc agg      259
Asn Gly Asp Gly Val Val Asp Ile Gly Glu Leu Gln Glu Gly Leu Arg
    35                      40                      45

aac ctg ggc atc cct ctg ggc cag gac gcc gag gag aaa att ttt act      307
Asn Leu Gly Ile Pro Leu Gly Gln Asp Ala Glu Glu Lys Ile Phe Thr
    50                      55                      60                      65

act gga gat gtc aac aaa gat ggg aag ctg gat ttt gaa gaa ttt atg      355
Thr Gly Asp Val Asn Lys Asp Gly Lys Leu Asp Phe Glu Glu Phe Met
    70                      75                      80

aag tac ctt aaa gac cat gag aag aaa atg aaa ttg gca ttt aag agt      403
Lys Tyr Leu Lys Asp His Glu Lys Lys Met Lys Leu Ala Phe Lys Ser
    85                      90                      95

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tta gac aaa aat aat gat gga aaa att gag gct tca gaa att gtc cag	451
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tct ctc cag aca ctg ggt ctg act att tct gaa caa caa gca gag ttg	499
Ser Leu Gln Thr Leu Gly Leu Thr Ile Ser Glu Gln Gln Ala Glu Leu	
115 120 125	
att ctt caa agc att gat gtt gat ggg aca atg aca gtg gac tgg aat	547
Ile Leu Gln Ser Ile Asp Val Asp Gly Thr Met Thr Val Asp Trp Asn	
130 135 140 145	
gaa tgg aga gac tac ttc tta ttt aat cct gtt aca gac att gag gaa	595
Glu Trp Arg Asp Phe Leu Phe Asn Pro Val Thr Asp Ile Glu Glu	
150 155 160	
att atc cgt ttc tgg aaa cat tct aca gga att gac ata ggg gat agc	643
Ile Ile Arg Phe Trp Lys His Ser Thr Gly Ile Asp Ile Gly Asp Ser	
165 170 175	
tta act att cca gat gaa ttc acg gaa gac gaa aaa aaa tcc gga caa	691
Leu Thr Ile Pro Asp Glu Phe Thr Glu Asp Glu Lys Lys Ser Gly Gln	
180 185 190	
tgg tgg agg cag ctt ttg gca gga ggc att gct ggt gct gtc tct cga	739
Trp Trp Arg Gln Leu Leu Ala Gly Gly Ile Ala Gly Ala Val Ser Arg	
195 200 205	
aca agc act gcc cct ttg gac cgt ctg aaa atc atg atg cag gtt cac	787
Thr Ser Thr Ala Pro Leu Asp Arg Leu Lys Ile Met Met Gln Val His	
210 215 220 225	
ggt tca aaa tca gac aaa atg aac ata ttt ggt ggc ttt cga cag atg	835
Gly Ser Lys Ser Asp Lys Met Asn Ile Phe Gly Gly Phe Arg Gln Met	
230 235 240	
gta aaa gaa gga ggt atc cgc tcg ctt tgg agg gga aat ggt aca aac	883
Val Lys Glu Gly Gly Ile Arg Ser Leu Trp Arg Gly Asn Gly Thr Asn	
245 250 255	
gtc atc aaa att gct cct gag aca gct gtt aaa ttc tgg gca tat gaa	931
Val Ile Lys Ile Ala Pro Glu Thr Ala Val Lys Phe Trp Ala Tyr Glu	
260 265 270	
cag tac aag aag tta ctt act gaa gaa gga caa aaa ata gga aca ttt	979
Gln Tyr Lys Lys Leu Leu Thr Glu Glu Gly Gln Lys Ile Gly Thr Phe	
275 280 285	
gag aga ttt att tct ggt tcc atg gct gga gca act gca cag act ttt	1027
Glu Arg Phe Ile Ser Gly Ser Met Ala Gly Ala Thr Ala Gln Thr Phe	
290 295 300 305	
ata tat cca atg gag gtt atg aaa acc agg ctg gct gta ggc aaa act	1075
Ile Tyr Pro Met Glu Val Met Lys Thr Arg Leu Ala Val Gly Lys Thr	
310 315 320	
ggg cag tac tct gga ata tat gat tgt gcc aag aag att ttg aaa cat	1123
Gly Gln Tyr Ser Gly Ile Tyr Asp Cys Ala Lys Lys Ile Leu Lys His	
325 330 335	
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Glu Gly Leu Gly Ala Phe Tyr Lys Gly Tyr Val Pro Asn Leu Leu Gly	
340 345 350	

atc ata cct tat gca ggc ata gat ctt gct gtg tat gag ctc ttg aag	1219
Ile Ile Pro Tyr Ala Gly Ile Asp Leu Ala Val Tyr Glu Leu Leu Lys	
355 360 365	
tcc tat tgg ctg gat aat ttt gca aaa gat tct gta aac cct gga gtc	1267
Ser Tyr Trp Leu Asp Asn Phe Ala Lys Asp Ser Val Asn Pro Gly Val	
370 375 380 385	
atg gtg ttg ctg gga tgc ggt gcc tta tcc agc acc tgt ggt cag ctg	1315
Met Val Leu Leu Gly Cys Gly Ala Leu Ser Ser Thr Cys Gly Gln Leu	
390 395 400	
gcc agc tac cca ttg gct ttg gtg aga act cgc atg cag gct caa gcc	1363
Ala Ser Tyr Pro Leu Ala Leu Val Arg Thr Arg Met Gln Ala Gln Ala	
405 410 415	
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Ile Ile Ser Lys Glu Gly Ile Pro Gly Leu Tyr Arg Gly Ile Thr Pro	
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Asn Phe Met Lys Val Leu Pro Ala Val Gly Ile Ser Tyr Val Val Tyr	
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Gln Ala Thr Pro Gln Val Phe Asp Leu Leu Pro Ser Ser Ser Gln Arg
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Leu Asn Pro Gly Ala Leu Pro Val Leu Thr Asp Pro Ala Leu Asn
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Asp Leu Tyr Val Ile Ser Thr Phe Lys Leu Gln Thr Lys Ser Ser Ala
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Gly Ala Gly Ser Leu Glu Leu Tyr Leu Asp Cys Ile Gln Val Asp Ser	
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Ala Cys Asp Ser Cys Pro Asp Val Ser Asn Pro Asn Gln Ser Asp Val	
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 Ile Asn Pro Ala His Ala Ile Ser Leu Leu Ser Ala Leu Asn Glu Glu
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 Gln Leu Arg Asn Leu Ser Val Ala Asp His Ser Lys Thr Gln Val Gln
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 aag aaa gag aac aaa tct cta aaa aga gat aca aag gca ata ata gat 433
 Lys Lys Glu Asn Lys Ser Leu Lys Arg Asp Thr Lys Ala Ile Ile Asp
 50 55 60
 act gga ctt aaa aaa act aca cag tgc ccc aaa cta gaa gac tca gaa 481
 Thr Gly Leu Lys Lys Thr Thr Gln Cys Pro Lys Leu Glu Asp Ser Glu
 65 70 75
 aaa gaa tat gtt ctt gat ccc aaa ccg ccg ccg ttg act ttg gca cag 529
 Lys Glu Tyr Val Leu Asp Pro Lys Pro Pro Pro Leu Thr Leu Ala Gln
 80 85 90
 aag ttg ggc ctc att ggg cct cca cca cct cca ctg tca tca gat gaa 577
 Lys Leu Gly Leu Ile Gly Pro Pro Pro Pro Pro Leu Ser Ser Asp Glu
 95 100 105
 tgg gag aag gtg aaa cag cgc tct ctc ctg caa ggg gac tcc gtg caa 625
 Trp Glu Lys Val Lys Gln Arg Ser Leu Leu Gln Gly Asp Ser Val Gln
 110 115 120 125
 cca tgc ccc atc tgt aaa gaa gaa ttc gag ctt cgt cct cag gtg ttt 673
 Pro Cys Pro Ile Cys Lys Glu Glu Phe Glu Leu Arg Pro Gln Val Phe
 130 135 140
 agc ata cga ggg tgc tgc ttt cat gct ccc atg tgt tcc aca aag cat 721
 Ser Ile Arg Gly Cys Cys Phe His Ala Pro Met Cys Ser Thr Lys His
 145 150 155
 gtc ttc agg ctt ttg aaa agt tca caa ata aga aaa cct gtc ctc tct 769
 Val Phe Arg Leu Leu Lys Ser Ser Gln Ile Arg Lys Pro Val Leu Ser
 160 165 170

gta gaa aga acc agt atc aaa ccc gag tga t acacgatggg gccgcctgt 820
 Val Glu Arg Thr Ser Ile Lys Pro Glu *
 175 180

tcagaatcaa gtgtgtgacc agaatccaag cctactggag aggatgtgtt gttagaaagt 880
 ggtacagaaa cctgaggaaa acagtacctc ccacagatgc caagttaaga aaaaaattct 940
 ttgaaaaaaa gttcacagaa atcagccacc gcatcctgtg ctcatacaac accaacattg 1000
 aagagctctt tgcagaaatc gatcagtgtt tggccataaa tcgaagtgtt cttcagcagt 1060
 tggaagaaaa atgtggccat gagatcacag aagaggaatg ggagaaaatc caagtgcagg 1120
 ctctgcgccg ggagaccac gagtgcttca ttctgcctgg cccctctctc cgctgctggc 1180
 ggtcagcgcg tgggtgcagg caggcgttcc agagagatgg ccctcctgtc ctgctcacat 1240
 gtgttccacc atgcgtgtct gctggcacta gcaggagtcc tccgtgggag acaggcctcc 1300
 ttccatgcc tgtcctctct gccgatcctg gttccagaat agcattcacg agtgcgtaag 1360
 tcatagtcaa gtagagcgag gtcagtctga ggtataaagt tcgccaatcg ttcggtagtg 1420
 agcggccgtg tggtaggtgt aataagccgg gaatccgggc cggctactctc 1470

<210> 759
 <211> 914
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (12)..(899)

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 Met Ser Ser Asp Gly Glu Pro Leu Ser Arg Met Asp Ser
 1 5 10

gag gac agc ata agc agt act ata atg gat gta gac agc aca att tcc 98
 Glu Asp Ser Ile Ser Ser Thr Ile Met Asp Val Asp Ser Thr Ile Ser
 15 20 25

agt ggg cgt tca act cca gca atg atg aat gga caa gga agc act act 146
 Ser Gly Arg Ser Thr Pro Ala Met Met Asn Gly Gln Gly Ser Thr Thr
 30 35 40 45

tct tca agc aaa aat att gcc tat aat tgt tgt tgg gac cag tgc cag 194
 Ser Ser Ser Lys Asn Ile Ala Tyr Asn Cys Cys Trp Asp Gln Cys Gln
 50 55 60

gct tgc ttc aac tct agc cca gat ctg gca gat cac atc cgt tcc ata 242
 Ala Cys Phe Asn Ser Ser Pro Asp Leu Ala Asp His Ile Arg Ser Ile
 65 70 75

cat gta gat ggt cag cga gga ggg gta ttt gtt tgc tta tgg aaa ggt 290
 His Val Asp Gly Gln Arg Gly Gly Val Phe Val Cys Leu Trp Lys Gly
 80 85 90

tgt aaa gta tat aac act cca tct acc agt caa agt tgg tta caa agg 338

Cys	Lys	Val	Tyr	Asn	Thr	Pro	Ser	Thr	Ser	Gln	Ser	Trp	Leu	Gln	Arg	
95						100					105					
cat	atg	ctg	aca	cac	agt	gga	gac	aaa	cct	ttc	aag	tgt	gtt	gtt	ggt	386
His	Met	Leu	Thr	His	Ser	Gly	Asp	Lys	Pro	Phe	Lys	Cys	Val	Val	Gly	
110						115				120					125	
ggc	tgc	aat	gcc	agc	ttt	gct	tct	cag	gga	ggg	cta	gct	cgt	cat	gta	434
Gly	Cys	Asn	Ala	Ser	Phe	Ala	Ser	Gln	Gly	Gly	Leu	Ala	Arg	His	Val	
				130					135					140		
ccc	aca	cac	ttc	agt	cag	cag	aac	tcc	tca	aaa	gtt	tct	agc	cag	cca	482
Pro	Thr	His	Phe	Ser	Gln	Gln	Asn	Ser	Ser	Lys	Val	Ser	Ser	Gln	Pro	
			145					150					155			
aag	gcc	aaa	gaa	gaa	tct	cct	tct	aaa	gct	gga	atg	aac	aaa	agg	agg	530
Lys	Ala	Lys	Glu	Glu	Ser	Pro	Ser	Lys	Ala	Gly	Met	Asn	Lys	Arg	Arg	
		160					165					170				
aaa	tta	aag	aac	aaa	aga	cga	cgc	tca	tta	cca	cgg	cca	cat	gat	ttc	578
Lys	Leu	Lys	Asn	Lys	Arg	Arg	Arg	Ser	Leu	Pro	Arg	Pro	His	Asp	Phe	
	175					180					185					
ttc	gat	gca	caa	aca	ctg	gat	gcg	ata	aga	cat	cga	gcc	ata	tgc	ttt	626
Phe	Asp	Ala	Gln	Thr	Leu	Asp	Ala	Ile	Arg	His	Arg	Ala	Ile	Cys	Phe	
190					195					200					205	
aac	ctc	tca	gct	cat	ata	gaa	agt	tta	ggg	aag	gga	cac	agt	gtt	gtt	674
Asn	Leu	Ser	Ala	His	Ile	Glu	Ser	Leu	Gly	Lys	Gly	His	Ser	Val	Val	
				210					215					220		
ttt	cat	agt	cct	gta	ata	gct	aag	aga	aaa	gaa	gat	tct	ggg	aag	atc	722
Phe	His	Ser	Pro	Val	Ile	Ala	Lys	Arg	Lys	Glu	Asp	Ser	Gly	Lys	Ile	
			225					230					235			
aaa	ctt	ttg	ctt	cat	tgg	atg	cct	gaa	gac	att	ctg	cat	gat	gtg	tgg	770
Lys	Leu	Leu	Leu	His	Trp	Met	Pro	Glu	Asp	Ile	Leu	His	Asp	Val	Trp	
		240					245						250			
gtg	aat	gaa	agt	gaa	cga	cat	cag	tta	aaa	act	aaa	gta	gtt	cat	tta	818
Val	Asn	Glu	Ser	Glu	Arg	His	Gln	Leu	Lys	Thr	Lys	Val	Val	His	Leu	
		255				260					265					
tca	aag	cta	ccc	aaa	gat	act	gcc	ttg	ctt	ttg	gac	cca	aac	ata	tac	866
Ser	Lys	Leu	Pro	Lys	Asp	Thr	Ala	Leu	Leu	Leu	Asp	Pro	Asn	Ile	Tyr	
270					275					280					285	
aga	aca	atg	ccg	cag	aag	agg	ttg	aag	agg	taa	aaaaaaaaa	aaaaa				914
Arg	Thr	Met	Pro	Gln	Lys	Arg	Leu	Lys	Arg	*						
				290					295							

<210> 760
 <211> 913
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (18) .. (662)

<400> 760
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Met Asp Asn Ala Gly Lys Glu Arg Glu Ala Val
1 5 10

cag ctg atg gcg gag gcc gag aag cga gtc aag gcc tcc cac tcc ttc 98
Gln Leu Met Ala Glu Ala Glu Lys Arg Val Lys Ala Ser His Ser Phe
15 20 25

ctc cga ggg ctg ttt gga gga aac aca aga ata gaa gag gct tgt gaa 146
Leu Arg Gly Leu Phe Gly Gly Asn Thr Arg Ile Glu Glu Ala Cys Glu
30 35 40

atg tat acc aga gct gca aat atg ttc aag atg gct aaa aat tgg agt 194
Met Tyr Thr Arg Ala Ala Asn Met Phe Lys Met Ala Lys Asn Trp Ser
45 50 55

gct gca gga aac gca ttt tgt cag gca gcc aag ctc cac atg cag ctt 242
Ala Ala Gly Asn Ala Phe Cys Gln Ala Ala Lys Leu His Met Gln Leu
60 65 70 75

cag agc aaa cat gac tct gct acc agc ttt gtg gat gct gga aat gct 290
Gln Ser Lys His Asp Ser Ala Thr Ser Phe Val Asp Ala Gly Asn Ala
80 85 90

tac aaa aag gca gat ccc caa gag gct atc aac tgc tta aat gca gcc 338
Tyr Lys Lys Ala Asp Pro Gln Glu Ala Ile Asn Cys Leu Asn Ala Ala
95 100 105

atc gac att tac aca gac atg gga agg ttt aca att gca gcc aag cac 386
Ile Asp Ile Tyr Thr Asp Met Gly Arg Phe Thr Ile Ala Ala Lys His
110 115 120

cac att act att gca gag atc tat gag act gaa ctt gta gac att gag 434
His Ile Thr Ile Ala Glu Ile Tyr Glu Thr Glu Leu Val Asp Ile Glu
125 130 135

aag gct att gca cat tat gaa caa tct gct gat tat tac aaa gga gaa 482
Lys Ala Ile Ala His Tyr Glu Gln Ser Ala Asp Tyr Tyr Lys Gly Glu
140 145 150 155

gaa tcc aac agc tca gca aac aag tgt ctg ctg aag gtg gca gca tat 530
Glu Ser Asn Ser Ala Asn Lys Cys Leu Leu Lys Val Ala Ala Tyr
160 165 170

gct gcc cag ctt gag cag tac cag aaa gcc att gag atc tat gag cag 578
Ala Ala Gln Leu Glu Gln Tyr Gln Lys Ala Ile Glu Ile Tyr Glu Gln
175 180 185

gtt ggg gcc aac aca atg gaa tat ccc ttt gtg gaa tac agg cca aag 626
Val Gly Ala Asn Thr Met Glu Tyr Pro Phe Val Glu Tyr Arg Pro Lys
190 195 200

gat act tct tca aag ctg oct ttt gcc act cta tag agac gagttgaagg 676
Asp Thr Ser Ser Lys Leu Pro Phe Ala Thr Leu *
205 210 215

ccagcttgct cttgagaata tgaggaatgt tccagcatta ctgattcaga gatgtaaatt 736

attgaaaaac tctagagctc atgacgacag acagggaact tacctgagca gtgaggattg 796

gctcatatct gcttgacaga gttgacacat gtggctgatc aaagccttcc agggatgaga 856

cgaatgggac taatgaaggt ttgtttggca gcatacacct tatttgtag caaggac 913

<210> 761
 <211> 2047
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (369) .. (860)

<400> 761
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 ccgggggcccc ggcgacgtgg gccgcgcacg gccctggaaa agacgtcgcc tccccctcat 120
 ccgcctctct ctacaccgcgc cgctcccgcct tctctgctct gcgctgcggg ctccaggcgga 180
 acccggaacg gccgtctctt tccccgcgcc tccgcgcctt cctccttctc ctctctctcc 240
 tctctctctt ccttctcggc ttctctctca gcccggggcc ggagcggggg gtcggcggcg 300
 gccggttcgg gcggcgactc gcgtttcttt gggcggcggc gcttggccat gtcgtgtcgg 360
 ggaaggta atg agc cgc aga gcc ccg ggg tct cgg ctg agc agc ggc ggc 410
 Met Ser Arg Arg Ala Pro Gly Ser Arg Leu Ser Ser Gly Gly
 1 5 10
 ggc ggc ggc ggc acc aag tat ccg cgg agc tgg aat gac tgg caa ccc 458
 Gly Gly Gly Gly Thr Lys Tyr Pro Arg Ser Trp Asn Asp Trp Gln Pro
 15 20 25 30
 aga act gat agt gca tca gcc gac cca gat aat tta aaa tat tct tca 506
 Arg Thr Asp Ser Ala Ser Ala Asp Pro Asp Asn Leu Lys Tyr Ser Ser
 35 40 45
 tcc aga gat aga ggt ggt tct tcc tct tat gga ctg caa cct tca aat 554
 Ser Arg Asp Arg Gly Gly Ser Ser Ser Tyr Gly Leu Gln Pro Ser Asn
 50 55 60
 tca gct gtg gtg tct cgg caa agg cac gat gat acc aga gtc cac gct 602
 Ser Ala Val Val Ser Arg Gln Arg His Asp Asp Thr Arg Val His Ala
 65 70 75
 gac ata cag aat gac gaa aag ggt ggc tac agt gtc aat gga gga tct 650
 Asp Ile Gln Asn Asp Glu Lys Gly Gly Tyr Ser Val Asn Gly Gly Ser
 80 85 90
 ggg gaa aat act tat ggt cgg aag tcg ttg ggg caa gag ctg agg gtt 698
 Gly Glu Asn Thr Tyr Gly Arg Lys Ser Leu Gly Gln Glu Leu Arg Val
 95 100 105 110
 aac aat gtg acc agc cct gag ttc aca agt gtt cag cat ggc agt cgt 746
 Asn Asn Val Thr Ser Pro Glu Phe Thr Ser Val Gln His Gly Ser Arg
 115 120 125
 gct tta gcc acc aaa gac atg agg aaa tca cag gag aga tcg atg tct 794
 Ala Leu Ala Thr Lys Asp Met Arg Lys Ser Gln Glu Arg Ser Met Ser
 130 135 140
 tat tgt gat gag tct cga ctg tca aat ctt ctt cgg agg atc acc cgg 842
 Tyr Cys Asp Glu Ser Arg Leu Ser Asn Leu Leu Arg Arg Ile Thr Arg

145

150

155

gaa gac gac aga gac tga agattg gtcactgtaa agcagttgaa agaatttatt 896
 Glu Asp Asp Arg Asp *
 160

cagcaaccag aaaataagct ggtactagtt aaacaattgg ataatatctt ggctgctgta 956
 catgatgtgc ttaatgaaag tagcaaattg cttcaggagt tgagacagga gggagcttgc 1016
 tgtctcggcc ttctttgtgc ttctctgagc tatgaggctg agaagatctt caagtggatt 1076
 tttagcaaat ttagctcadc tgcaaaagat gaagttaaac tcctctactt atgtgccacc 1136
 taaaaagcac tagagactgt aggagaaaag aaagcctttt catctgtaat gcagcttgta 1196
 atgaccagcc tgcagtcaat tcttgaaaat gtggatacac cagaattgct ttgcaaatgt 1256
 gttaagtga tttcttttggg ggctcgatgt taccctcata ttttcagcac taattttagg 1316
 gatacagttg atatattagt tggatggcat agagatcata ctcagaaacc ttcgctcacg 1376
 cagcaggtat ctgggtgggt gcagagtttg gagccatttt gggtagctga tcttgcatth 1436
 cctacgactc ttcttggtca gtttctagaa gacatggaag catatgctga ggacctcagc 1496
 catgtggcct ctggggaatc agtggatgaa gacgtccctc ctccatcagt gtcacacca 1556
 aagctggctg cgcttctccg ggtatttagt actgtgctga ggagcattgg ggaacgcttc 1616
 agcccaattc gggtcctcca attactgagg catacgtaac agttgttctg tacagagtaa 1676
 tgagatgtgt gacggctgca aaccaggtgt tttttctgga ggctgtgttg acagctgcta 1736
 atgagtgtgt tgggtgtttg ctcggcagct tggatcctag catgactata cattgtgaca 1796
 tggtcattac atatggagta gaccaactgg agaattgcca gacttgtggt accaattata 1856
 tcactcagct cttgaattta ctcacgctga ttgttgacca gataaatacg aaactgccat 1916
 catcatttgt agaaaactgt ttataccatc atctaaacta ctattctggc gttatcataa 1976
 gacaaggggt tttgctgtag cccatctgtt tatcaagcaa tctcagcttg agatattcct 2036
 gtttgagac t 2047

<210> 762
 <211> 567
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (295) .. (465)

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 catctcctgc tggttaccac cttactcatt tctctccaac gatactggcc ttcttggtat 120
 tccttgaaca taccaagtat attctcttgc ctcagggact ttgcttctgc ccttctccat 180

tcttgggata	ctcttctccc	agttattctg	catgcctttc	tcccacacct	cttttaaata	240
tttgctttga	agtcaccttc	ttatcttttg	ccttgttgca	ctcctgaagg	caaa atg	297
					Met	
					1	
gat cac aag cag ctc tgc tgg agc cac cca caa aaa tct ggc cag agt	345					
Asp His Lys Gln Leu Cys Trp Ser His Pro Gln Lys Ser Gly Gln Ser						
5 10 15						
tct cgc tct tgt tgc atc tgc tca aac cag cat ggt ctg atc tgg aaa	393					
Ser Arg Ser Cys Cys Ile Cys Ser Asn Gln His Gly Leu Ile Trp Lys						
20 25 30						
tat agc ctc aat atg tgc ctc cag tgt tgc cat cag tac gtg aag gat	441					
Tyr Ser Leu Asn Met Cys Leu Gln Cys Cys His Gln Tyr Val Lys Asp						
35 40 45						
ata ggt ttc att aaa ttg gac taa gtgatcttcc ttgaatggat tatccaaggc	495					
Ile Gly Phe Ile Lys Leu Asp *						
50 55						
atccacacaa tgaaaaatca tattagctgt ttgtacataa aataaaaatg aagaaaatga	555					
agtcaaacga ca	567					

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<210> 763
<211> 888
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (589) .. (858)
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tatctagcac ttttgtgtct ctggccttg ccaagggttg ggattggccc ctcatgtccc	120
gcagagagaa gggactgaac caggagcccc aaggcagggg tctggccctc cagaagatgg	180
gtcaagagga agagagccct ccaagagagg agaggcccca gcagagtcca aaggtacagt	240
gttacctgtt taacaaaagg agaaggattt ggggaggctg agacctcaag acctgcttga	300
ctttgcacc tatcccgagg catctccgg actgctggca gctgccctac aacagagcca	360
ggaactgagt tgggtaccag ctttgtctcaa aatggtttct accatgaggc cgtggctctc	420
ttcaccagagg ccttgaagct caacccccag gaccaccgtt tatttgaaaa tcgttccttc	480
tgccatgagc gggtgggtca gccagcgtgg gccctggctg atgccagggt ggcccttacc	540
ctacggcctg gctggccccg gggcctcttc cgctgggcca aggcttg atg gga cta	597
	Met Gly Leu
	1
cag cgc ttc aga gag gca gct gct gtg ttt cag gaa act ctg aga ggt	645
Gln Arg Phe Arg Glu Ala Ala Val Phe Gln Glu Thr Leu Arg Gly	

5	10	15	
ggg tcc cag cct gac gca gcc cga gag ctc cgc tct tgc ctt ctc cac			693
Gly Ser Gln Pro Asp Ala Ala Arg Glu Leu Arg Ser Cys Leu Leu His			
20	25	30	35
ctc aca ctg cag ggt cag cga gga gga atc tgt gca cca cct ctg tca			741
Leu Thr Leu Gln Gly Gln Arg Gly Gly Ile Cys Ala Pro Pro Leu Ser			
	40	45	50
cct ggg gcc ctc cag cca ctt ccc cat gct gag ctg gca ccc tca ggc			789
Pro Gly Ala Leu Gln Pro Leu Pro His Ala Glu Leu Ala Pro Ser Gly			
	55	60	65
cta cct tcc ctc agg tgc cct cga agc act gct ttg agg tcc cct ggc			837
Leu Pro Ser Leu Arg Cys Pro Arg Ser Thr Ala Leu Arg Ser Pro Gly			
	70	75	80
ctg tct cca ctc ttg cat taa ccataatgtc accgaagcca cccctgtatt			888
Leu Ser Pro Leu Leu His *			
85	90		

<210> 764
 <211> 984
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (153)..(806)

<400> 764			
tatacagaggc actatagggga atttcgcccc gagcagtaat tcggcacgac ggggaaccgc			60
atcctcgcga tccacatccg catcgtcgtc cccccgacc gcgtcctgca gcagctgcca			120
gtggagccgc ctgacaagga ctgccatcca cc atg gtg aag ctg ggc tgc agc			173
	Met Val Lys Leu Gly Cys Ser		
	1	5	
ttc tct ggg aag cca ggt aaa gac cct ggg gac cag gat ggg gct gcc			221
Phe Ser Gly Lys Pro Gly Lys Asp Pro Gly Asp Gln Asp Gly Ala Ala			
	10	15	20
atg gac agt gtg cct ctg atc agc ccc ttg gac atc agc cag ctc cag			269
Met Asp Ser Val Pro Leu Ile Ser Pro Leu Asp Ile Ser Gln Leu Gln			
	25	30	35
ccg cca ctc cct gac cag gtg gtc atc aag aca cag aca gaa tac cag			317
Pro Pro Leu Pro Asp Gln Val Val Ile Lys Thr Gln Thr Glu Tyr Gln			
	40	45	50
ctg tcc tcc cca gac cag cag aat ttc cct gac ctg gag ggc cag agg			365
Leu Ser Ser Pro Asp Gln Gln Asn Phe Pro Asp Leu Glu Gly Gln Arg			
	60	65	70
ctg aac tgc agc cac cca gag gaa ggg cgc agg ctg ccc acc gca cgg			413
Leu Asn Cys Ser His Pro Glu Glu Gly Arg Arg Leu Pro Thr Ala Arg			
	75	80	85

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atg atc gcc ttc gcc atg gcg cta ctg ggc tgc gtg ctg atc atg tac      461
Met Ile Ala Phe Ala Met Ala Leu Leu Gly Cys Val Leu Ile Met Tyr
      90                      95                      100

aag gcc atc tgg tac gac cag ttc acc tgc ccc gac ggc ttc ctg ctg      509
Lys Ala Ile Trp Tyr Asp Gln Phe Thr Cys Pro Asp Gly Phe Leu Leu
      105                      110                      115

cgg cac aag atc tgc acg ccg ctg acc ctg gag atg tac tac acg gag      557
Arg His Lys Ile Cys Thr Pro Leu Thr Leu Glu Met Tyr Tyr Thr Glu
      120                      125                      130                      135

atg gac ccc gag cgc cac cgc agc atc ctg gcg gcc atc ggg gcc tac      605
Met Asp Pro Glu Arg His Arg Ser Ile Leu Ala Ala Ile Gly Ala Tyr
      140                      145                      150

ccg ctg agc cgc aag cac ggc acg gag acg ccg gcg gcc tgg ggg gac      653
Pro Leu Ser Arg Lys His Gly Thr Glu Thr Pro Ala Ala Trp Gly Asp
      155                      160                      165

ggc tac cgc gca gcc aag gag gag cgc aag ggg ccc acc cag gct ggg      701
Gly Tyr Arg Ala Ala Lys Glu Glu Arg Lys Gly Pro Thr Gln Ala Gly
      170                      175                      180

gcg gcg gcg gcg gcc acc gaa ccc ccc ggg aag ccg tcg gcc aag gcg      749
Ala Ala Ala Ala Ala Thr Glu Pro Pro Gly Lys Pro Ser Ala Lys Ala
      185                      190                      195

gag aag gag gcg gcg ccg aag gcg gcc ggg agc gcg gcg ccc ccg ccc      797
Glu Lys Glu Ala Ala Arg Lys Ala Ala Gly Ser Ala Ala Pro Pro Pro
      200                      205                      210                      215

gcg cag tga cgtctcc agccccgcag cccggccccg gcgtcctccg ccagctcctg      853
Ala Gln *

tgaccagcgc gtctcccgat gctctccgcc gtgttcgtgt cccagggcgc cctcgtctga      913

gccccgcccc cgtgggtctc tgactctgtc gcttttctct aagtaaagat ttcacgtcca      973

aaaaaaaaa a                                                                984

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<210> 765
 <211> 1538
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (237) .. (1451)

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<400> 765
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cgtccgggag acgtgtctgt ctgtgaggcg ctgggtgcac gtccccaggg ctctgggcta      120
ggaaggcagc ggcgaggtgc ctccccacgt acccctcgcg ggcccagccg agcaacgtgg      180

ggcgaaggcg gcggcgaagg cccgggctgg gacggttggc ggccggagtc ccagcc      236
atg gcg gag tct gtg gag cgc ctg cag cag ccg gtc cag gag ctg gag      284
Met Ala Glu Ser Val Glu Arg Leu Gln Gln Arg Val Gln Glu Leu Glu

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1	5	10	15	
cgg gaa ctt gcc cag gag agg agt ctg cag gtc ccg agg agc ggc gac				332
Arg Glu Leu Ala Gln Glu Arg Ser Leu Gln Val Pro Arg Ser Gly Asp	20	25	30	
gga ggg ggc ggc cgg gtc cgc atc gag aag atg agc tca gag gtg gtg				380
Gly Gly Gly Gly Arg Val Arg Ile Glu Lys Met Ser Ser Glu Val Val	35	40	45	
gat tcg aat ccc tac agc cgc ttg atg gca ttg aaa cga atg gga att				428
Asp Ser Asn Pro Tyr Ser Arg Leu Met Ala Leu Lys Arg Met Gly Ile	50	55	60	
gta agc gac tat gag aaa atc cgt acc ttt gcc gta gca ata gta ggt				476
Val Ser Asp Tyr Glu Lys Ile Arg Thr Phe Ala Val Ala Ile Val Gly	65	70	75	80
gtt ggt gga gta ggt agt gtg act gct gaa atg ctg aca aga tgt ggc				524
Val Gly Gly Val Gly Ser Val Thr Ala Glu Met Leu Thr Arg Cys Gly	85	90	95	
att ggt aag ttg cta ctc ttt gat tat gac aag gtg gaa cta gcc aat				572
Ile Gly Lys Leu Leu Leu Phe Asp Tyr Asp Lys Val Glu Leu Ala Asn	100	105	110	
atg aat aga ctt ttc ttc caa cct cat caa gca gga tta agt aaa gtt				620
Met Asn Arg Leu Phe Phe Gln Pro His Gln Ala Gly Leu Ser Lys Val	115	120	125	
caa gca gca gaa cat act ctg agg aac att aat cct gat gtt ctt ttt				668
Gln Ala Ala Glu His Thr Leu Arg Asn Ile Asn Pro Asp Val Leu Phe	130	135	140	
gaa gta cac aac tat aat ata acc aca gtg gaa aac ttt caa cat ttc				716
Glu Val His Asn Tyr Asn Ile Thr Thr Val Glu Asn Phe Gln His Phe	145	150	155	160
atg gat aga ata agt aat ggt ggg tta gaa gaa gga aaa cct gtt gat				764
Met Asp Arg Ile Ser Asn Gly Gly Leu Glu Glu Gly Lys Pro Val Asp	165	170	175	
cta gtt ctt agc tgt gtg gac aat ttt gaa gct cga atg aca ata aat				812
Leu Val Leu Ser Cys Val Asp Asn Phe Glu Ala Arg Met Thr Ile Asn	180	185	190	
aca gct tgt aat gaa ctt gga caa aca tgg atg gaa tct ggg gtc agt				860
Thr Ala Cys Asn Glu Leu Gly Gln Thr Trp Met Glu Ser Gly Val Ser	195	200	205	
gaa aat gca gtt tca ggg cat ata cag ctt ata att cct gga gaa tct				908
Glu Asn Ala Val Ser Gly His Ile Gln Leu Ile Ile Pro Gly Glu Ser	210	215	220	
gct tgt ttt gcg tgt gct cca cca ctt gta gtt gct gca aat att gat				956
Ala Cys Phe Ala Cys Ala Pro Pro Leu Val Val Ala Ala Asn Ile Asp	225	230	235	240
gaa aag act ctg aaa cga gaa ggt gtt tgt gca gcc agt ctt cct acc				1004
Glu Lys Thr Leu Lys Arg Glu Gly Val Cys Ala Ala Ser Leu Pro Thr	245	250	255	
act atg ggt gtg gtt gct ggg atc tta gta caa aac gtg tta aag ttt				1052
Thr Met Gly Val Val Ala Gly Ile Leu Val Gln Asn Val Leu Lys Phe				

260	265	270	
ctg tta aat ttt ggt act gtt agt ttt tac ctt gga tac aat gca atg			1100
Leu Leu Asn Phe Gly Thr Val Ser Phe Tyr Leu Gly Tyr Asn Ala Met			
275	280	285	
cag gat ttt ttt cct act atg tcc atg aag cca aat cct cag tgt gat			1148
Gln Asp Phe Phe Pro Thr Met Ser Met Lys Pro Asn Pro Gln Cys Asp			
290	295	300	
gac aga aat tgc agg aag cag cag gag gaa tat aag aaa aag gta gca			1196
Asp Arg Asn Cys Arg Lys Gln Gln Glu Glu Tyr Lys Lys Lys Val Ala			
305	310	315	320
gca ctg cct aaa caa gag gtt ata caa gaa gag gaa gag ata atc cat			1244
Ala Leu Pro Lys Gln Glu Val Ile Gln Glu Glu Glu Ile Ile His			
325	330	335	
gaa gat aat gaa tgg ggt att gag ctg gta tct gag gtt tca gaa gag			1292
Glu Asp Asn Glu Trp Gly Ile Glu Leu Val Ser Glu Val Ser Glu Glu			
340	345	350	
gaa ctg aaa aat ttt tca ggt cca gtt cca gac tta cct gaa gga att			1340
Glu Leu Lys Asn Phe Ser Gly Pro Val Pro Asp Leu Pro Glu Gly Ile			
355	360	365	
aca gtg gca tac aca att cca aaa aag caa gaa gat tct gtc act gag			1388
Thr Val Ala Tyr Thr Ile Pro Lys Lys Gln Glu Asp Ser Val Thr Glu			
370	375	380	
tta aca gtg gaa gat tct ggt gaa agc ttg gaa gac ctg atg gcc aaa			1436
Leu Thr Val Glu Asp Ser Gly Glu Ser Leu Glu Asp Leu Met Ala Lys			
385	390	395	400
atg aag aat atg tag ataatggact gggatatatt gtattttctca tgttaaagcc			1491
Met Lys Asn Met *			
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Asp Gln Arg Gln Arg Ser Leu Ser Thr Ser Gly Glu Ser Leu Tyr His		
5	10	15
gtc ctt ggg ttg gac aag aac gca acc tca gat gac att aaa aag tcc		152
Val Leu Gly Leu Asp Lys Asn Ala Thr Ser Asp Ile Lys Lys Ser		
20	25	30

tat cgg aag ctt gcc ttg aaa tat cac ccc gac aag aac ccc gac aac	200
Tyr Arg Lys Leu Ala Leu Lys Tyr His Pro Asp Lys Asn Pro Asp Asn	
35 40 45 50	
ccg gag gcc gcg gac aag ttt aag gag atc aac aac gcg cac gcc atc	248
Pro Glu Ala Ala Asp Lys Phe Lys Glu Ile Asn Asn Ala His Ala Ile	
55 60 65	
ctc acg gac gcc aca aaa agg aac atc tac gac aag tac ggc tcg ctg	296
Leu Thr Asp Ala Thr Lys Arg Asn Ile Tyr Asp Lys Tyr Gly Ser Leu	
70 75 80	
ggt ctc tac gtg gcc gag cag ttt ggg gaa gag aac gtg aac acc tac	344
Gly Leu Tyr Val Ala Glu Gln Phe Gly Glu Glu Asn Val Asn Thr Tyr	
85 90 95	
ttc gtg ctg tcc agc tgg tgg gcc aag gcc ctg ttt gtc ttc tgc ggc	392
Phe Val Leu Ser Ser Trp Trp Ala Lys Ala Leu Phe Val Phe Cys Gly	
100 105 110	
ctc ctc acg tgc tgc tac tgc tgc tgc tgt ctg tgc tgc tgc ttc aac	440
Leu Leu Thr Cys Cys Tyr Cys Cys Cys Cys Leu Cys Cys Cys Phe Asn	
115 120 125 130	
tgc tgc tgc ggg aag tgt aag ccc aag gcg cct gaa ggc gag gag acg	488
Cys Cys Cys Gly Lys Cys Lys Pro Lys Ala Pro Glu Gly Glu Glu Thr	
135 140 145	
gag ttc tac gtg tcc ccc gag gat ctg gag gca cag ctg cag tct gac	536
Glu Phe Tyr Val Ser Pro Glu Asp Leu Glu Ala Gln Leu Gln Ser Asp	
150 155 160	
gag agg gag gcc aca gac acg ccg atc gtc ata cag ccg gca tcc gcc	584
Glu Arg Glu Ala Thr Asp Thr Pro Ile Val Ile Gln Pro Ala Ser Ala	
165 170 175	
acc gag acc acc cag ctc aca gcc gac tcc cac ccc agc tac cac act	632
Thr Glu Thr Thr Gln Leu Thr Ala Asp Ser His Pro Ser Tyr His Thr	
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Asp Gly Phe Asn *	
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tgccctggcc ttgctggggc ccctcctgcc tccacgcca ccagcgctcg acccttgacc	807
cacgaagtgc gtagcatgca gtatttaaag cagtgtagct acggtcttct gtttttttcc	867
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gcttgagggg ccggaggcag gtgctgcctg gcagagctgt gttaccgtct tggcctcggg	1107
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 aggaaggact gactggacca gagggaccct ctggctcagg agggttgggt ccctgggagg 1827
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<213> Homo sapiens

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<400> 767

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 atg gga agc cga gca gac ggc ccc aga aca agc ggt cat gtg act ggg 168
 Met Gly Ser Arg Ala Asp Gly Pro Arg Thr Ser Gly His Val Thr Gly
 1 5 10 15
 aag atg gcc gtc ttt cct tgg cac tcc agg aat agg aac tac aaa gct 216
 Lys Met Ala Val Phe Pro Trp His Ser Arg Asn Arg Asn Tyr Lys Ala
 20 25 30
 gaa ttt gca tca tgc cga ctg gag gct gta cca ttg gag ttt ggg gac 264
 Glu Phe Ala Ser Cys Arg Leu Glu Ala Val Pro Leu Glu Phe Gly Asp
 35 40 45
 tat cac cct ctg aaa ccc ata act gtc aca gag tca aag aca aag aaa 312
 Tyr His Pro Leu Lys Pro Ile Thr Val Thr Glu Ser Lys Thr Lys Lys
 50 55 60
 gtg aac cgg aaa gga agc act tct tcc acg tcc tcc tcc tcc tcc agc 360
 Val Asn Arg Lys Gly Ser Thr Ser Ser Thr Ser Ser Ser Ser Ser
 65 70 75 80
 tcc gtg gtg gac ccg ctg agc agc gtc ctc gat ggg act gac ccc ctc 408
 Ser Val Val Asp Pro Leu Ser Ser Val Leu Asp Gly Thr Asp Pro Leu
 85 90 95
 tcc atg ttt gca gcc act gct gac ccc gca gcc ttg gca gct gcc atg 456
 Ser Met Phe Ala Ala Thr Ala Asp Pro Ala Ala Leu Ala Ala Met

100	105	110	
gac agc tcc aga agg aaa cgt gat aga gat gat aac tcc gtt gta gga			504
Asp Ser Ser Arg Arg Lys Arg Asp Arg Asp Asp Asn Ser Val Val Gly			
115	120	125	
tcg gat ttt gag cct tgg acc aac aaa cgg gga gaa atc ctt gcc cgg			552
Ser Asp Phe Glu Pro Trp Thr Asn Lys Arg Gly Glu Ile Leu Ala Arg			
130	135	140	
tac acc act acc gaa aag ctg tct att aat ctg ttt atg gga tct gaa			600
Tyr Thr Thr Thr Glu Lys Leu Ser Ile Asn Leu Phe Met Gly Ser Glu			
145	150	155	160
aaa ggc aaa gct ggg act gcc aca ttg gca atg tca gag aag gtg cgg			648
Lys Gly Lys Ala Gly Thr Ala Thr Leu Ala Met Ser Glu Lys Val Arg			
165	170	175	
acc cgg ctg gag gag ctg gat gac ttt gag gag ggt tcc caa aag gag			696
Thr Arg Leu Glu Glu Leu Asp Asp Phe Glu Glu Gly Ser Gln Lys Glu			
180	185	190	
ctg ttg aac ttg act cag cag gat tac gtg aac cgc ata gag gag ctc			744
Leu Leu Asn Leu Thr Gln Gln Asp Tyr Val Asn Arg Ile Glu Glu Leu			
195	200	205	
aac caa tcg ctg aag gat gcc tgg gcc tca gac cag aaa gtg aag gct			792
Asn Gln Ser Leu Lys Asp Ala Trp Ala Ser Asp Gln Lys Val Lys Ala			
210	215	220	
cta aaa ata gtt cat cca gga aag ctc gtg tac gag cgc atc ttt tcc			840
Leu Lys Ile Val His Pro Gly Lys Leu Val Tyr Glu Arg Ile Phe Ser			
225	230	235	240
atg tgt gtg gat agc cgc agc gtc tta cca gat cac ttt tct cca gag			888
Met Cys Val Asp Ser Arg Ser Val Leu Pro Asp His Phe Ser Pro Glu			
245	250	255	
aat gca aat gac acg gcc aag gaa aca tgc cta aat tgg ttt ttc aag			936
Asn Ala Asn Asp Thr Ala Lys Glu Thr Cys Leu Asn Trp Phe Phe Lys			
260	265	270	
att gcc tcc atc agg gaa ctc att cca aga ttt tac gtg gag gca tcc			984
Ile Ala Ser Ile Arg Glu Leu Ile Pro Arg Phe Tyr Val Glu Ala Ser			
275	280	285	
atc ctg aaa tgt aac aaa ttc ctc tcc aaa acg gga att tca gag tgc			1032
Ile Leu Lys Cys Asn Lys Phe Leu Ser Lys Thr Gly Ile Ser Glu Cys			
290	295	300	
ctg ccc cgg ttg aca tgc atg atc aga ggg atc gga gac cca cta gtg			1080
Leu Pro Arg Leu Thr Cys Met Ile Arg Gly Ile Gly Asp Pro Leu Val			
305	310	315	320
tcg gtg tat gcc cgt gcc tac ctg tgc cgg gtg gga atg gaa gtg gcc			1128
Ser Val Tyr Ala Arg Ala Tyr Leu Cys Arg Val Gly Met Glu Val Ala			
325	330	335	
cca cat ctc aaa gaa acc cta aat aag aac ttt ttt gac ttc ctc ctt			1176
Pro His Leu Lys Glu Thr Leu Asn Lys Asn Phe Phe Asp Phe Leu Leu			
340	345	350	
acg ttc aaa cag att cat ggg gat acg gtc cag aac cag ctg gtg gtc			1224
Thr Phe Lys Gln Ile His Gly Asp Thr Val Gln Asn Gln Leu Val Val			

355	360	365	
caa gga gtg gag ctc cca tct tac ctc ccc ttg tac ccg cct gcc atg Gln Gly Val Glu Leu Pro Ser Tyr Leu Pro Leu Tyr Pro Pro Ala Met 370 375 380			1272
gac tgg atc ttc cag tgc atc tcc tac cat gcc ccc gag gct ctg ctg Asp Trp Ile Phe Gln Cys Ile Ser Tyr His Ala Pro Glu Ala Leu Leu 385 390 395 400			1320
acc gag atg atg gaa agg tgt aag aaa cta gga aac aat gcc ttg ctg Thr Glu Met Met Glu Arg Cys Lys Lys Leu Gly Asn Asn Ala Leu Leu 405 410 415			1368
ttg aat tct gtg atg tct gcc ttc cgg gct gag ttc atc gcc aca agg Leu Asn Ser Val Met Ser Ala Phe Arg Ala Glu Phe Ile Ala Thr Arg 420 425 430			1416
tct atg gat ttc att ggc atg att aaa gag tgt gat gaa tct ggt ttc Ser Met Asp Phe Ile Gly Met Ile Lys Glu Cys Asp Glu Ser Gly Phe 435 440 445			1464
ccc aag cat ctt ctt ttt cga tca ctg gga tta aac ttg gcc ttg gct Pro Lys His Leu Leu Phe Arg Ser Leu Gly Leu Asn Leu Ala Leu Ala 450 455 460			1512
gat cct cct gag agt gac cga ctt cag att ctc aac gaa gct tgg aaa Asp Pro Pro Glu Ser Asp Arg Leu Gln Ile Leu Asn Glu Ala Trp Lys 465 470 475 480			1560
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gtg tgg gtg gaa tac acc tgc aag cat ttc acg aaa cga gag gtg aat Val Trp Val Glu Tyr Thr Cys Lys His Phe Thr Lys Arg Glu Val Asn 500 505 510			1656
acc gtt ttg gca gat gtc atc aag cac atg act cca gat cgt gca ttt Thr Val Leu Ala Asp Val Ile Lys His Met Thr Pro Asp Arg Ala Phe 515 520 525			1704
gaa gat tcc tac ccc cag ctt cag tta ata att aag aaa gtt att gcc Glu Asp Ser Tyr Pro Gln Leu Gln Leu Ile Ile Lys Lys Val Ile Ala 530 535 540			1752
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tgc atc atg gac gcc ttt atc aag cat caa caa gag ccc acc aag gac Cys Ile Met Asp Ala Phe Ile Lys His Gln Gln Glu Pro Thr Lys Asp 580 585 590			1896
ccg gtc atc ttg aat gcc ctt ttg cat gtt tgc aag acc atg cat gac Pro Val Ile Leu Asn Ala Leu Leu His Val Cys Lys Thr Met His Asp 595 600 605			1944
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gag aca aga aaa gta atg aaa gga aat cat tcc aga aag aca gct gca Glu Thr Arg Lys Val Met Lys Gly Asn His Ser Arg Lys Thr Ala Ala 675 680 685			2184
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gcg ggc atc ttc aca cgt ctc aat ctc tac ctg cat tct ggt cag gtg Ala Gly Ile Phe Thr Arg Leu Asn Leu Tyr Leu His Ser Gly Gln Val 705 710 715 720			2280
gcc ttg gcc aac cag tgc ctc tcc caa gct gat gct ttt ttc aaa gcc Ala Leu Ala Asn Gln Cys Leu Ser Gln Ala Asp Ala Phe Phe Lys Ala 725 730 735			2328
gct ata agc ctt gtt ccg gaa gtt cca aag atg att aat att gat ggg Ala Ile Ser Leu Val Pro Glu Val Pro Lys Met Ile Asn Ile Asp Gly 740 745 750			2376
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aaa acc ctg gcc aag gac gag gcc ctg aag cgc cag agc tcg ttg ggc Lys Thr Leu Ala Lys Asp Glu Ala Leu Lys Arg Gln Ser Ser Leu Gly			2760

865	870	875	880	
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Lys Leu Asn Gln Leu Ser Val Asn Leu Trp His Leu Ala Gln Arg His				
	900	905	910	
ggc tgt gca gac acc agg acc atg gtg aaa acg cta gaa tac atc aag				2904
Gly Cys Ala Asp Thr Arg Thr Met Val Lys Thr Leu Glu Tyr Ile Lys				
	915	920	925	
aag caa agc aaa caa cca gac atg act cat ctg acg gag ctg gcc ctc				2952
Lys Gln Ser Lys Gln Pro Asp Met Thr His Leu Thr Glu Leu Ala Leu				
	930	935	940	
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Arg Leu Pro Leu Gln Thr Arg Thr *				
	945	950		
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gcttcggcac	ttccgggagg	agccggaaat	aatttttgtg	ctcggcggag	gctctctagg		600
cgtagcagccc	agcgactcga	tagccggaag	tcatccttgc	tgaggctggg	gcaaccaccg		660
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				Met Ala Glu	Arg Ala		
				1	5		
gcg ctg gag	gag ctg gtg	aaa ctt	cag gga	gag cgc	gtg cga	ggc ctc	761
Ala Leu Glu	Glu Leu Val	Lys Leu	Gln Gly	Glu Arg	Val Arg	Gly Leu	
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Lys Gln Gln	Lys Ala Ser	Ala Glu	Leu Ile	Glu Glu	Glu Val	Ala Lys	
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Leu Leu Lys	Leu Lys Ala	Gln Leu	Gly Pro	Asp Glu	Ser Lys	Gln Lys	
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Phe Val Leu	Lys Thr Pro	Lys Gly	Thr Arg	Asp Tyr	Ser Pro	Arg Gln	
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Met Ala Val	Arg Glu Lys	Val Phe	Asp Val	Ile Ile	Arg Cys	Phe Lys	
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gcg cac ggt	gca gaa gtc	att gat	aca cct	gta ttt	gaa cta	aag gaa	1001
Arg His Gly	Ala Glu Val	Ile Asp	Thr Pro	Val Phe	Glu Leu	Lys Glu	
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aca ctg atg	gga aag tat	ggg gaa	gac tcc	aag ctt	atc tat	gac ctg	1049
Thr Leu Met	Gly Lys Tyr	Gly Glu	Asp Ser	Lys Leu	Ile Tyr	Asp Leu	
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Lys Asp Gln	Gly Gly Glu	Leu Leu	Ser Leu	Arg Tyr	Asp Leu	Thr Val	
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cct ttt gct	cgg tat ttg	gca atg	aat aaa	ctg acc	aac att	aaa cgc	1145
Pro Phe Ala	Arg Tyr Leu	Ala Met	Asn Lys	Leu Thr	Asn Ile	Lys Arg	
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Tyr His Ile	Ala Lys Val	Tyr Arg	Arg Asp	Asn Pro	Ala Met	Thr Arg	
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Gly Arg Tyr	Arg Glu Phe	Tyr Gln	Cys Asp	Phe Asp	Ile Ala	Gly Asn	
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Phe Asp Pro Met Ile Pro Asp Ala Glu Cys Leu Lys Ile Met Cys Glu	
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Ile Leu Ser Ser Leu Gln Ile Gly Asp Phe Leu Val Lys Val Asn Asp	
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Lys Phe Arg Thr Ile Cys Ser Ser Val Asp Lys Leu Asp Lys Val Ser	
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Trp Glu Glu Val Lys Asn Glu Met Val Gly Glu Lys Gly Leu Ala Pro	
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Ser Leu Val Glu Gln Leu Leu Gln Asp Pro Lys Leu Ser Gln Asn Lys	
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Glu Glu Arg Leu Lys Leu Val Ser Glu Leu Trp Asp Ala Gly Ile Lys	
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Ala Glu Leu Leu Tyr Lys Lys Asn Pro Lys Leu Leu Asn Gln Leu Gln	
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Tyr Cys Glu Glu Ala Gly Ile Pro Leu Val Ala Ile Ile Gly Glu Gln	
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Thr Gly Gln Pro Leu Cys Ile Cys *	
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 Met Leu Thr
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 ccg ccg ttg ctc ctg ctg ctg ccc ctg ctc tca gct ctg gtc gcg gcg 523
 Pro Pro Leu Leu Leu Leu Leu Pro Leu Leu Ser Ala Leu Val Ala Ala
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 Ala Ile Asp Ala Pro Lys Thr Cys Ser Pro Lys Gln Phe Ala Cys Arg
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 Asp Gln Ile Thr Cys Ile Ser Lys Gly Trp Arg Cys Asp Gly Glu Arg
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 Asp Cys Pro Asp Gly Ser Asp Glu Ala Pro Glu Ile Cys Pro Gln Ser
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 Lys Ala Gln Arg Cys Gln Pro Asn Glu His Asn Cys Leu Gly Thr Glu
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 Leu Cys Val Pro Met Ser Arg Leu Cys Asn Gly Val Gln Asp Cys Met
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 Thr Cys Tyr Cys Asn Ser Ser Phe Gln Leu Gln Ala Asp Gly Lys Thr
 135 140 145
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 Cys Lys Asp Phe Asp Glu Cys Ser Val Tyr Gly Thr Cys Ser Gln Leu
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 Cys Thr Asn Thr Asp Gly Ser Phe Ile Cys Gly Cys Val Glu Gly Tyr
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 Thr Tyr Leu Ser Gly Ala Gln Val Ser Thr Ile Thr Pro Thr Ser Thr
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Trp Val His Val Gly Asp Ser Ala Ala Gln Thr Gln Leu Lys Cys Ala			
245	250	255	
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Arg Met Pro Gly Leu Lys Gly Phe Val Asp Glu His Thr Ile Asn Ile			
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Ser Leu Ser Leu His His Val Glu Gln Met Ala Ile Asp Trp Leu Thr			
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Gly Asn Phe Tyr Phe Val Asp Asp Ile Asp Asp Arg Ile Phe Val Cys			
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Asn Arg Asn Gly Asp Thr Cys Val Thr Leu Leu Asp Leu Glu Leu Tyr			
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Asn Pro Lys Gly Ile Ala Leu Asp Pro Ala Met Gly Lys Val Phe Phe			
325	330	335	
act gac tat ggg cag atc cca aag gtg gaa cgc tgt gac atg gat ggg			1531
Thr Asp Tyr Gly Gln Ile Pro Lys Val Glu Arg Cys Asp Met Asp Gly			
340	345	350	355
cag aac cgc acc aag ctc gtc gac agc aag att gtg ttt cct cat ggc			1579
Gln Asn Arg Thr Lys Leu Val Asp Ser Lys Ile Val Phe Pro His Gly			
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Ile Thr Leu Asp Leu Val Ser Arg Leu Val Tyr Trp Ala Asp Ala Tyr			
375	380	385	
ctg gac tat att gaa gtg gtg gac tat gag ggc aag ggc cgc cag acc			1675
Leu Asp Tyr Ile Glu Val Val Asp Tyr Glu Gly Lys Gly Arg Gln Thr			
390	395	400	
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Ile Ile Gln Gly Ile Leu Ile Glu His Leu Tyr Gly Leu Thr Val Phe			
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Glu Asn Tyr Leu Tyr Ala Thr Asn Ser Asp Asn Ala Asn Ala Gln Gln			
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aag acg agt gtg atc cgt gtg aac cgc ttt aac agc acc gag tac cag			1819
Lys Thr Ser Val Ile Arg Val Asn Arg Phe Asn Ser Thr Glu Tyr Gln			
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Val Val Thr Arg Val Asp Lys Gly Gly Ala Leu His Ile Tyr His Gln			
455	460	465	
agg cgt cag ccc cga gtg agg agc cat gcc tgt gaa aac gac cag tat			1915
Arg Arg Gln Pro Arg Val Arg Ser His Ala Cys Glu Asn Asp Gln Tyr			
470	475	480	
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Gly Lys Pro Gly Gly Cys Ser Asp Ile Cys Leu Leu Ala Asn Ser His			

485	490	495	
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cct gag ctg aac cac gcc ttt ggc ctg tgt cac cat ggc aac tac ctc Pro Glu Leu Asn His Ala Phe Gly Leu Cys His His Gly Asn Tyr Leu			2731

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Phe Trp Thr Glu Tyr Arg Ser Gly Ser Val Tyr Arg Leu Glu Arg Gly				
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Val Gly Gly Ala Pro Pro Thr Val Thr Leu Leu Arg Ser Glu Arg Pro				
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Thr Asn Lys Cys Arg Val Asn Asn Gly Gly Cys Ser Ser Leu Cys Leu				
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gcc acc cct ggg agc cgc cag tgc gcc tgt gct gag gac cag gtg ttg				2971
Ala Thr Pro Gly Ser Arg Gln Cys Ala Cys Ala Glu Asp Gln Val Leu				
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Asp Ala Asp Gly Val Thr Cys Leu Ala Asn Pro Ser Tyr Val Pro Pro				
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Pro Gln Cys Gln Pro Gly Glu Phe Ala Cys Ala Asn Ser Arg Cys Ile				
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Gln Glu Arg Trp Lys Cys Asp Gly Asp Asn Asp Cys Leu Asp Asn Ser				
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gat gag gcc cca gcc ctc tgc cat cag cac acc tgc ccc tcg gac cga				3163
Asp Glu Ala Pro Ala Leu Cys His Gln His Thr Cys Pro Ser Asp Arg				
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Phe Lys Cys Glu Asn Asn Arg Cys Ile Pro Asn Arg Trp Leu Cys Asp				
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Gly Asp Asn Asp Cys Gly Asn Ser Glu Asp Glu Ser Asn Ala Thr Cys				
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Ser Ala Arg Thr Cys Pro Pro Asn Gln Phe Ser Cys Ala Ser Gly Arg				
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Cys Ile Pro Ile Ser Trp Thr Cys Asp Leu Asp Asp Asp Cys Gly Asp				
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Thr Gln Phe Thr Cys Asn Asn Gly Arg Cys Ile Asn Ile Asn Trp Arg				
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Cys Asp Asn Asp Asn Asp Cys Gly Asp Asn Ser Asp Glu Ala Gly Cys				

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atc gcc ctg gac ttc cac ctc agc cag agc gcc ctc tac tgg acc gac Ile Ala Leu Asp Phe His Leu Ser Gln Ser Ala Leu Tyr Trp Thr Asp 1300 1305 1310 1315			4411
gtg gtg gag gac aag atc tac cgc ggg aag ctg ctg gac aac gga gcc Val Val Glu Asp Lys Ile Tyr Arg Gly Lys Leu Leu Asp Asn Gly Ala 1320 1325 1330			4459
ctg act agt ttc gag gtg gtg att cag tat ggc ctg gcc aca ccc gag Leu Thr Ser Phe Glu Val Val Ile Gln Tyr Gly Leu Ala Thr Pro Glu 1335 1340 1345			4507
ggc ctg gct gta gac tgg att gca ggc aac atc tac tgg gtg gag agt Gly Leu Ala Val Asp Trp Ile Ala Gly Asn Ile Tyr Trp Val Glu Ser 1350 1355 1360			4555
aac ctg gat cag atc gag gtg gcc aag ctg gat ggg acc ctc cgg acc Asn Leu Asp Gln Ile Glu Val Ala Lys Leu Asp Gly Thr Leu Arg Thr 1365 1370 1375			4603
acc ctg ctg gcc ggt gac att gag cac cca agg gca atc gca ctg gat Thr Leu Leu Ala Gly Asp Ile Glu His Pro Arg Ala Ile Ala Leu Asp 1380 1385 1390 1395			4651
ccc cgg gat ggg atc ctg ttt tgg aca gac tgg gat gcc agc ctg ccc Pro Arg Asp Gly Ile Leu Phe Trp Thr Asp Trp Asp Ala Ser Leu Pro 1400 1405 1410			4699
cgc att gag gca gcc tcc atg agt ggg gct ggg cgc cgc acc gtg cac Arg Ile Glu Ala Ala Ser Met Ser Gly Ala Gly Arg Arg Thr Val His 1415 1420 1425			4747
cgg gag acc ggc tct ggg ggc tgg ccc aac ggg ctc acc gtg gac tac Arg Glu Thr Gly Ser Gly Gly Trp Pro Asn Gly Leu Thr Val Asp Tyr 1430 1435 1440			4795
ctg gag aag cgc atc ctt tgg att gac gcc agg tca gat gcc att tac Leu Glu Lys Arg Ile Leu Trp Ile Asp Ala Arg Ser Asp Ala Ile Tyr 1445 1450 1455			4843
tca gcc cgt tac gac ggc tct ggc cac atg gag gtg ctt cgg gga cac Ser Ala Arg Tyr Asp Gly Ser Gly His Met Glu Val Leu Arg Gly His 1460 1465 1470 1475			4891
gag ttc ctg tcg cac ccg ttt gca gtg acg ctg tac ggg ggg gag gtc Glu Phe Leu Ser His Pro Phe Ala Val Thr Leu Tyr Gly Gly Glu Val 1480 1485 1490			4939
tac tgg act gac tgg cga aca aac aca ctg gct aag gcc aac aag tgg Tyr Trp Thr Asp Trp Arg Thr Asn Thr Leu Ala Lys Ala Asn Lys Trp 1495 1500 1505			4987
acc ggc cac aat gtc acc gtg gta cag agg acc aac acc cag ccc ttt Thr Gly His Asn Val Thr Val Val Gln Arg Thr Asn Thr Gln Pro Phe			5035

1510	1515	1520	
gac ctg cag gtg tac cac ccc tcc cgc cag ccc atg gct ccc aat ccc Asp Leu Gln Val Tyr His Pro Ser Arg Gln Pro Met Ala Pro Asn Pro 1525 1530 1535			5083
tgt gag gcc aat ggg ggc cag ggc ccc tgc tcc cac ctg tgt ctc atc Cys Glu Ala Asn Gly Gly Gln Gly Pro Cys Ser His Leu Cys Leu Ile 1540 1545 1550 1555			5131
aac tac aac cgg acc gtg tcc tgc gcc tgc ccc cac ctc atg aag ctc Asn Tyr Asn Arg Thr Val Ser Cys Ala Cys Pro His Leu Met Lys Leu 1560 1565 1570			5179
cac aag gac aac acc acc tgc tat gag ttt aag aag ttc ctg ctg tac His Lys Asp Asn Thr Thr Cys Tyr Glu Phe Lys Lys Phe Leu Leu Tyr 1575 1580 1585			5227
gca cgt cag atg gag atc cga ggt gtg gac ctg gat gct ccc tac tac Ala Arg Gln Met Glu Ile Arg Gly Val Asp Leu Asp Ala Pro Tyr Tyr 1590 1595 1600			5275
aac tac atc atc tcc ttc acg gtg ccc gac atc gac aac gtc aca gtg Asn Tyr Ile Ile Ser Phe Thr Val Pro Asp Ile Asp Asn Val Thr Val 1605 1610 1615			5323
cta gac tac gat gcc cgc gag cag cgt gtg tac tgg tct gac gtg cgg Leu Asp Tyr Asp Ala Arg Glu Gln Arg Val Tyr Trp Ser Asp Val Arg 1620 1625 1630 1635			5371
aca cag gcc atc aag cgg gcc ttc atc aac ggc aca ggc gtg gag aca Thr Gln Ala Ile Lys Arg Ala Phe Ile Asn Gly Thr Gly Val Glu Thr 1640 1645 1650			5419
gtc gtc tct gca gac ttg cca aat gcc cac ggg ctg gct gtg gac tgg Val Val Ser Ala Asp Leu Pro Asn Ala His Gly Leu Ala Val Asp Trp 1655 1660 1665			5467
gtc tcc cga aac ctg ttc tgg aca agc tat gac acc aat aag aag cag Val Ser Arg Asn Leu Phe Trp Thr Ser Tyr Asp Thr Asn Lys Lys Gln 1670 1675 1680			5515
atc aat gtg gcc cgg ctg gat ggc tcc ttc aag aac gca gtg gtg cag Ile Asn Val Ala Arg Leu Asp Gly Ser Phe Lys Asn Ala Val Val Gln 1685 1690 1695			5563
ggc ctg gag cag ccc cat ggc ctt gtc gtc cac cct ctg cgt ggg aag Gly Leu Glu Gln Pro His Gly Leu Val Val His Pro Leu Arg Gly Lys 1700 1705 1710 1715			5611
ctc tac tgg acc gat ggt gac aac atc agc atg gcc aac atg gat ggc Leu Tyr Trp Thr Asp Gly Asp Asn Ile Ser Met Ala Asn Met Asp Gly 1720 1725 1730			5659
agc aat cgc acc ctg ctc ttc agt ggc cag aag ggc ccc gtg ggc ctg Ser Asn Arg Thr Leu Leu Phe Ser Gly Gln Lys Gly Pro Val Gly Leu 1735 1740 1745			5707
gct att gac ttc cct gaa agc aaa ctc tac tgg atc agc tcc ggg aac Ala Ile Asp Phe Pro Glu Ser Lys Leu Tyr Trp Ile Ser Ser Gly Asn 1750 1755 1760			5755
cat acc atc aac cgc tgc aac ctg gat ggg agt ggg ctg gag gtc atc His Thr Ile Asn Arg Cys Asn Leu Asp Gly Ser Gly Leu Glu Val Ile			5803

1765	1770	1775	
gat gcc atg cgg agc cag ctg ggc aag gcc acc gcc ctg gcc atc atg Asp Ala Met Arg Ser Gln Leu Gly Lys Ala Thr Ala Leu Ala Ile Met 1780	1785	1790	1795 5851
ggg gac aag ctg tgg tgg gct gat cag gtg tgc gaa aag atg ggc aca Gly Asp Lys Leu Trp Trp Ala Asp Gln Val Ser Glu Lys Met Gly Thr 1800	1805	1810	5899
tgc agc aag gct gac ggc tgc ggc tcc gtg gtc ctt cgg aac agc acc Cys Ser Lys Ala Asp Gly Ser Gly Ser Val Val Leu Arg Asn Ser Thr 1815	1820	1825	5947
acc ctg gtg atg cac atg aag gtc tat gac gag agc atc cag ctg gac Thr Leu Val Met His Met Lys Val Tyr Asp Glu Ser Ile Gln Leu Asp 1830	1835	1840	5995
cat aag ggc acc aac ccc tgc agt gtc aac aac ggt gac tgc tcc cag His Lys Gly Thr Asn Pro Cys Ser Val Asn Asn Gly Asp Cys Ser Gln 1845	1850	1855	6043
ctc tgc ctg ccc acg tca gag acg acc cgc tcc tgc atg tgc aca gcc Leu Cys Leu Pro Thr Ser Glu Thr Thr Arg Ser Cys Met Cys Thr Ala 1860	1865	1870	1875 6091
ggc tat agc ctc cgg agt ggc cag cag gcc tgc gag ggc gta ggt tcc Gly Tyr Ser Leu Arg Ser Gly Gln Gln Ala Cys Glu Gly Val Gly Ser 1880	1885	1890	6139
ttt ctc ctg tac tct gtg cat gag gga atc agg gga att ccc ctg gat Phe Leu Leu Tyr Ser Val His Glu Gly Ile Arg Gly Ile Pro Leu Asp 1895	1900	1905	6187
ccc aat gac aag tca gat gcc ctg gtc cca gtg tcc ggg acc tgc ctg Pro Asn Asp Lys Ser Asp Ala Leu Val Pro Val Ser Gly Thr Ser Leu 1910	1915	1920	6235
gct gtc ggc atc gac ttc cac gct gaa aat gac acc atc tac tgg gtg Ala Val Gly Ile Asp Phe His Ala Glu Asn Asp Thr Ile Tyr Trp Val 1925	1930	1935	6283
gac atg ggc ctg agc acg atc agc cgg gcc aag cgg gac cag acg tgg Asp Met Gly Leu Ser Thr Ile Ser Arg Ala Lys Arg Asp Gln Thr Trp 1940	1945	1950	1955 6331
cgt gaa gac gtg gtg acc aat ggc att ggc cgt gtg gag ggc att gca Arg Glu Asp Val Val Thr Asn Gly Ile Gly Arg Val Glu Gly Ile Ala 1960	1965	1970	6379
gtg gac tgg atc gca ggc aac atc tac tgg aca gac cag ggc ttt gat Val Asp Trp Ile Ala Gly Asn Ile Tyr Trp Thr Asp Gln Gly Phe Asp 1975	1980	1985	6427
gtc atc gag gtc gcc cgg ctc aat ggc tcc ttc cgc tac gtg gtg atc Val Ile Glu Val Ala Arg Leu Asn Gly Ser Phe Arg Tyr Val Val Ile 1990	1995	2000	6475
tcc cag ggt cta gac aag ccc cgg gcc atc acc gtc cac ccg gag aaa Ser Gln Gly Leu Asp Lys Pro Arg Ala Ile Thr Val His Pro Glu Lys 2005	2010	2015	6523
ggg tac ttg ttc tgg act gag tgg ggt cag tat ccg cgt att gag cgg Gly Tyr Leu Phe Trp Thr Glu Trp Gly Gln Tyr Pro Arg Ile Glu Arg			6571

2020	2025	2030	2035	
tct cgg cta gat ggc acg gag cgt gtg gtg ctg gtc aac gtc agc atc Ser Arg Leu Asp Gly Thr Glu Arg Val Val Leu Val Asn Val Ser Ile	2040	2045	2050	6619
agc tgg ccc aac ggc atc tca gtg gac tac cag gat ggg aag ctg tac Ser Trp Pro Asn Gly Ile Ser Val Asp Tyr Gln Asp Gly Lys Leu Tyr	2055	2060	2065	6667
tgg tgc gat gca cgg aca gac aag att gaa cgg atc gac ctg gag aca Trp Cys Asp Ala Arg Thr Asp Lys Ile Glu Arg Ile Asp Leu Glu Thr	2070	2075	2080	6715
ggg gag aac cgc gag gtg gtt ctg tcc agc aac aac atg gac atg ttt Gly Glu Asn Arg Glu Val Val Leu Ser Ser Asn Asn Met Asp Met Phe	2085	2090	2095	6763
tca gtg tct gtg ttt gag gat ttc atc tac tgg agt gac agg act cat Ser Val Ser Val Phe Glu Asp Phe Ile Tyr Trp Ser Asp Arg Thr His	2100	2105	2110	6811
gcc aac ggc tct atc aag cgc ggg agc aaa gac aat gcc aca gac tcc Ala Asn Gly Ser Ile Lys Arg Gly Ser Lys Asp Asn Ala Thr Asp Ser	2120	2125	2130	6859
gtg ccc ctg cga acc ggc atc ggc gtc cag ctt aaa gac atc aaa gtc Val Pro Leu Arg Thr Gly Ile Gly Val Gln Leu Lys Asp Ile Lys Val	2135	2140	2145	6907
ttc aac cgg gac cgg cag aaa ggc acc aac gtg tgc gcg gtg gcc aat Phe Asn Arg Asp Arg Gln Lys Gly Thr Asn Val Cys Ala Val Ala Asn	2150	2155	2160	6955
ggc ggg tgc cag cag ctg tgc ctg tac cgg ggc cgt ggg cag cgg gcc Gly Gly Cys Gln Gln Leu Cys Leu Tyr Arg Gly Arg Gly Gln Arg Ala	2165	2170	2175	7003
tgc gcc tgt gcc cac ggg atg ctg gct gaa gac gga gca tcg tgc cgc Cys Ala Cys Ala His Gly Met Leu Ala Glu Asp Gly Ala Ser Cys Arg	2180	2185	2190	7051
gag tat gcc ggc tac ctg ctc tac tca gag cgc acc att ctc aag agt Glu Tyr Ala Gly Tyr Leu Leu Tyr Ser Glu Arg Thr Ile Leu Lys Ser	2200	2205	2210	7099
atc cac ctg tcg gat gag cgc aac ctc aat gcg ccc gtg cag ccc ttc Ile His Leu Ser Asp Glu Arg Asn Leu Asn Ala Pro Val Gln Pro Phe	2215	2220	2225	7147
gag gac cct gag cac atg aag aac gtc atc gcc ctg gcc ttt gac tac Glu Asp Pro Glu His Met Lys Asn Val Ile Ala Leu Ala Phe Asp Tyr	2230	2235	2240	7195
cgg gca ggc acc tct cgg ggc acc ccc aat cgc atc ttc ttc agc gac Arg Ala Gly Thr Ser Pro Gly Thr Pro Asn Arg Ile Phe Phe Ser Asp	2245	2250	2255	7243
atc cac ttt ggg aac atc caa cag atc aac gac gat ggc tcc agg agg Ile His Phe Gly Asn Ile Gln Gln Ile Asn Asp Asp Gly Ser Arg Arg	2260	2265	2270	7291
atc acc att gtg gaa aac gtg ggc tcc gtg gaa ggc ctg gcc tat cac Ile Thr Ile Val Glu Asn Val Gly Ser Val Glu Gly Leu Ala Tyr His				7339

2280	2285	2290	
cgt ggc tgg gac act ctc tat tgg aca agc tac acg aca tcc acc atc			7387
Arg Gly Trp Asp Thr Leu Tyr Trp Thr Ser Tyr Thr Thr Ser Thr Ile			
2295	2300	2305	
acg cgc cac aca gtg gac cag acc cgc cca ggg gcc ttc gag cgt gag			7435
Thr Arg His Thr Val Asp Gln Thr Arg Pro Gly Ala Phe Glu Arg Glu			
2310	2315	2320	
acc gtc atc act atg tct gga gat gac cac cca cgg gcc ttc gtt ttg			7483
Thr Val Ile Thr Met Ser Gly Asp Asp His Pro Arg Ala Phe Val Leu			
2325	2330	2335	
gac gag tgc cag aac ctc atg ttc tgg acc aac tgg aat gag cag cat			7531
Asp Glu Cys Gln Asn Leu Met Phe Trp Thr Asn Trp Asn Glu Gln His			
2340	2345	2350	2355
ccc agc atc atg cgg gcg gcg ctc tcg gga gcc aat gtc ctg acc ctt			7579
Pro Ser Ile Met Arg Ala Ala Leu Ser Gly Ala Asn Val Leu Thr Leu			
2360	2365	2370	
atc gag aag gac atc cgt acc ccc aat ggc ctg gcc atc gac cac cgt			7627
Ile Glu Lys Asp Ile Arg Thr Pro Asn Gly Leu Ala Ile Asp His Arg			
2375	2380	2385	
gcc gag aag ctc tac ttc tct gac gcc acc ctg gac aag atc gag cgg			7675
Ala Glu Lys Leu Tyr Phe Ser Asp Ala Thr Leu Asp Lys Ile Glu Arg			
2390	2395	2400	
tgc gag tat gac ggc tcc cac cgc tat gtg atc cta aag tca gag cct			7723
Cys Glu Tyr Asp Gly Ser His Arg Tyr Val Ile Leu Lys Ser Glu Pro			
2405	2410	2415	
gtc cac ccc ttc ggg ctg gcc gtg tat ggg gag cac att ttc tgg act			7771
Val His Pro Phe Gly Leu Ala Val Tyr Gly Glu His Ile Phe Trp Thr			
2420	2425	2430	2435
gac tgg gtg cgg cgg gca gtg cag cgg gcc aac aag cac gtg ggc agc			7819
Asp Trp Val Arg Arg Ala Val Gln Arg Ala Asn Lys His Val Gly Ser			
2440	2445	2450	
aac atg aag ctg ctg cgc gtg gac atc ccc cag cag ccc atg ggc atc			7867
Asn Met Lys Leu Leu Arg Val Asp Ile Pro Gln Gln Pro Met Gly Ile			
2455	2460	2465	
atc gcc gtg gcc aac gac acc aac agc tgt gaa ctc tct cca tgc cga			7915
Ile Ala Val Ala Asn Asp Thr Asn Ser Cys Glu Leu Ser Pro Cys Arg			
2470	2475	2480	
atc aac aac ggt ggc tgc cag gac ctg tgt ctg ctc act cac cag ggc			7963
Ile Asn Asn Gly Gly Cys Gln Asp Leu Cys Leu Leu Thr His Gln Gly			
2485	2490	2495	
cat gtc aac tgc tca tgc cga ggg ggc cga atc ctc cag gat gac ctc			8011
His Val Asn Cys Ser Cys Arg Gly Gly Arg Ile Leu Gln Asp Asp Leu			
2500	2505	2510	2515
acc tgc cga gcg gtg aat tcc tct tgc cga gca caa gat gag ttt gag			8059
Thr Cys Arg Ala Val Asn Ser Ser Cys Arg Ala Gln Asp Glu Phe Glu			
2520	2525	2530	
tgt gcc aat ggc gag tgc atc aac ttc agc ctg acc tgc gac ggc gtc			8107
Cys Ala Asn Gly Glu Cys Ile Asn Phe Ser Leu Thr Cys Asp Gly Val			

2535	2540	2545	
ccc cac tgc aag gac aag tcc gat gag aag cca tcc tac tgc aac tcc Pro His Cys Lys Asp Lys Ser Asp Glu Lys Pro Ser Tyr Cys Asn Ser 2550 2555 2560			8155
cgc cgc tgc aag aag act ttc cgg cag tgc agc aat ggg cgc tgt gtg Arg Arg Cys Lys Lys Thr Phe Arg Gln Cys Ser Asn Gly Arg Cys Val 2565 2570 2575			8203
tcc aac atg ctg tgg tgc aac ggg gcc gac gac tgt ggg gat ggc tct Ser Asn Met Leu Trp Cys Asn Gly Ala Asp Asp Cys Gly Asp Gly Ser 2580 2585 2590 2595			8251
gac gag atc cct tgc aac aag aca gcc tgt ggt gtg ggc gag ttc cgc Asp Glu Ile Pro Cys Asn Lys Thr Ala Cys Gly Val Gly Glu Phe Arg 2600 2605 2610			8299
tgc cgg gac ggg acc tgc atc ggg aac tcc agc cgc tgc aac cag ttt Cys Arg Asp Gly Thr Cys Ile Gly Asn Ser Ser Arg Cys Asn Gln Phe 2615 2620 2625			8347
gtg gat tgt gag gac gcc tca gat gag atg aac tgc agt gcc acc gac Val Asp Cys Glu Asp Ala Ser Asp Glu Met Asn Cys Ser Ala Thr Asp 2630 2635 2640			8395
tgc agc agc tac ttc cgc ctg ggc gtg aag ggc gtg ctc ttc cag ccc Cys Ser Ser Tyr Phe Arg Leu Gly Val Lys Gly Val Leu Phe Gln Pro 2645 2650 2655			8443
tgc gag cgg acc tca ctc tgc tac gca ccc agc tgg gtg tgt gat ggc Cys Glu Arg Thr Ser Leu Cys Tyr Ala Pro Ser Trp Val Cys Asp Gly 2660 2665 2670 2675			8491
gcc aat gac tgt ggg gac tac agt gat gag cgc gac tgc cca ggt gtg Ala Asn Asp Cys Gly Asp Tyr Ser Asp Glu Arg Asp Cys Pro Gly Val 2680 2685 2690			8539
aaa cgc ccc aga tgc cct ctg aat tac ttc gcc tgc cct agt ggg cgc Lys Arg Pro Arg Cys Pro Leu Asn Tyr Phe Ala Cys Pro Ser Gly Arg 2695 2700 2705			8587
tgc atc ccc atg agc tgg acg tgt gac aaa gag gat gac tgt gaa cat Cys Ile Pro Met Ser Trp Thr Cys Asp Lys Glu Asp Asp Cys Glu His 2710 2715 2720			8635
ggc gag gac gag acc cac tgc aac aag ttc tgc tca gag gcc cag ttt Gly Glu Asp Glu Thr His Cys Asn Lys Phe Cys Ser Glu Ala Gln Phe 2725 2730 2735			8683
gag tgc cag aac cat cgc tgc atc tcc aag cag tgg ctg tgt gac ggc Glu Cys Gln Asn His Arg Cys Ile Ser Lys Gln Trp Leu Cys Asp Gly 2740 2745 2750 2755			8731
agc gat gac tgt ggg gat ggc tca gac gag gct gct cac tgt gaa ggc Ser Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ala His Cys Glu Gly 2760 2765 2770			8779
aag acg tgc ggc ccc tcc tcc ttc tcc tgc cct ggc acc cac gtg tgc Lys Thr Cys Gly Pro Ser Ser Phe Ser Cys Pro Gly Thr His Val Cys 2775 2780 2785			8827
gtc ccc gag cgc tgg ctc tgt gac ggt gac aaa gac tgt gct gat ggt Val Pro Glu Arg Trp Leu Cys Asp Gly Asp Lys Asp Cys Ala Asp Gly 2790 2795 2800			8875

2790	2795	2800	
gca gac gag agc atc gca gct ggt tgc ttg tac aac agc act tgt gac Ala Asp Glu Ser Ile Ala Ala Gly Cys Leu Tyr Asn Ser Thr Cys Asp 2805	2810	2815	8923
gac cgt gag ttc atg tgc cag aac cgc cag tgc atc ccc aag cac ttc Asp Arg Glu Phe Met Cys Gln Asn Arg Gln Cys Ile Pro Lys His Phe 2820	2825	2830 2835	8971
gtg tgt gac cac gac cgt gac tgt gca gat ggc tct gat gag tcc ccc Val Cys Asp His Asp Arg Asp Cys Ala Asp Gly Ser Asp Glu Ser Pro 2840	2845	2850	9019
gag tgt gag tac ccg acc tgc ggc ccc agt gag ttc cgc tgt gcc aat Glu Cys Glu Tyr Pro Thr Cys Gly Pro Ser Glu Phe Arg Cys Ala Asn 2855	2860	2865	9067
ggg cgc tgt ctg agc tcc cgc cag tgg gag tgt gat ggc gag aat gac Gly Arg Cys Leu Ser Ser Arg Gln Trp Glu Cys Asp Gly Glu Asn Asp 2870	2875	2880	9115
tgc cac gac cag agt gac gag gct ccc aag aac cca cac tgc acc agc Cys His Asp Gln Ser Asp Glu Ala Pro Lys Asn Pro His Cys Thr Ser 2885	2890	2895	9163
cca gag cac aag tgc aat gcc tcg tca cag ttc ctg tgc agc agt ggg Pro Glu His Lys Cys Asn Ala Ser Ser Gln Phe Leu Cys Ser Ser Gly 2900	2905	2910 2915	9211
cgc tgt gtg gct gag gca ctg ctc tgc aac ggc cag gat gac tgt ggc Arg Cys Val Ala Glu Ala Leu Leu Cys Asn Gly Gln Asp Asp Cys Gly 2920	2925	2930	9259
gac agc tcg gac gag cgt ggc tgc cac atc aat gag tgt ctc agc cgc Asp Ser Ser Asp Glu Arg Gly Cys His Ile Asn Glu Cys Leu Ser Arg 2935	2940	2945	9307
aag ctc agt ggc tgc agc cag gac tgt gag gac ctc aag atc ggc ttc Lys Leu Ser Gly Cys Ser Gln Asp Cys Glu Asp Leu Lys Ile Gly Phe 2950	2955	2960	9355
aag tgc cgc tgt cgc cct ggc ttc cgg ctg aag gac gac ggc cgg acg Lys Cys Arg Cys Arg Pro Gly Phe Arg Leu Lys Asp Asp Gly Arg Thr 2965	2970	2975	9403
tgt gct gat gtg gac gag tgc agc acc acc ttc ccc tgc agc cag cgc Cys Ala Asp Val Asp Glu Cys Ser Thr Thr Phe Pro Cys Ser Gln Arg 2980	2985	2990 2995	9451
tgc atc aac acc cat ggc agc tat aag tgt ctg tgt gtg gag ggc tat Cys Ile Asn Thr His Gly Ser Tyr Lys Cys Leu Cys Val Glu Gly Tyr 3000	3005	3010	9499
gca ccc cgc ggc ggc gac ccc cac agc tgc aag gct gtg act gac gag Ala Pro Arg Gly Gly Asp Pro His Ser Cys Lys Ala Val Thr Asp Glu 3015	3020	3025	9547
gaa ccg ttt ctg atc ttc gcc aac cgg tac tac ctg cgc aag ctc aac Glu Pro Phe Leu Ile Phe Ala Asn Arg Tyr Tyr Leu Arg Lys Leu Asn 3030	3035	3040	9595
ctg gac ggg tcc aac tac acg tta ctt aag cag ggc ctg aac aac gcc Leu Asp Gly Ser Asn Tyr Thr Leu Leu Lys Gln Gly Leu Asn Asn Ala			9643

3045	3050	3055	
gtt gcc ttg gat ttt gac tac cga gag cag atg atc tac tgg aca gat Val Ala Leu Asp Phe Asp Tyr Arg Glu Gln Met Ile Tyr Trp Thr Asp 3060 3065 3070 3075			9691
gtg acc acc cag ggc agc atg atc cga agg atg cac ctt aac ggg agc Val Thr Thr Gln Gly Ser Met Ile Arg Arg Met His Leu Asn Gly Ser 3080 3085 3090			9739
aat gtg cag gtc cta cac cgt aca ggc ctc agc aac ccc gat ggg ctg Asn Val Gln Val Leu His Arg Thr Gly Leu Ser Asn Pro Asp Gly Leu 3095 3100 3105			9787
gct gtg gac tgg gtg ggt ggc aac ctg tac tgg tgc gac aaa ggc cgg Ala Val Asp Trp Val Gly Gly Asn Leu Tyr Trp Cys Asp Lys Gly Arg 3110 3115 3120			9835
gac acc atc gag gtg tcc aag ctc aat ggg gcc tat cgg acg gtg ctg Asp Thr Ile Glu Val Ser Lys Leu Asn Gly Ala Tyr Arg Thr Val Leu 3125 3130 3135			9883
gtc agc tct ggc ctc cgt gag ccc agg gct ctg gtg gtg gat gtg cag Val Ser Ser Gly Leu Arg Glu Pro Arg Ala Leu Val Val Asp Val Gln 3140 3145 3150 3155			9931
aat ggg tac ctg tac tgg aca gac tgg ggt gac cat tca ctg atc ggc Asn Gly Tyr Leu Tyr Trp Thr Asp Trp Gly Asp His Ser Leu Ile Gly 3160 3165 3170			9979
cgc atc ggc atg gat ggg tcc agc cgc agc gtc atc gtg gac acc aag Arg Ile Gly Met Asp Gly Ser Ser Arg Ser Val Ile Val Asp Thr Lys 3175 3180 3185			10027
atc aca tgg ccc aat ggc ctg acg ctg gac tat gtc act gag cgc atc Ile Thr Trp Pro Asn Gly Leu Thr Leu Asp Tyr Val Thr Glu Arg Ile 3190 3195 3200			10075
tac tgg gcc gac gcc cgc gag gac tac att gaa ttt gcc agc ctg gat Tyr Trp Ala Asp Ala Arg Glu Asp Tyr Ile Glu Phe Ala Ser Leu Asp 3205 3210 3215			10123
ggc tcc aat cgc cac gtt gtg ctg agc cag gac atc ccg cac atc ttt Gly Ser Asn Arg His Val Val Leu Ser Gln Asp Ile Pro His Ile Phe 3220 3225 3230 3235			10171
gca ctg acc ctg ttt gag gac tac gtc tac tgg acc gac tgg gaa aca Ala Leu Thr Leu Phe Glu Asp Tyr Val Tyr Trp Thr Asp Trp Glu Thr 3240 3245 3250			10219
aag tcc att aac cga gcc cac aag acc aca ggc acc aac aaa acg ctc Lys Ser Ile Asn Arg Ala His Lys Thr Thr Gly Thr Asn Lys Thr Leu 3255 3260 3265			10267
ctc atc agc acg ctg cac cgg ccc atg gac ctg cat gtc ttc cat gcc Leu Ile Ser Thr Leu His Arg Pro Met Asp Leu His Val Phe His Ala 3270 3275 3280			10315
ctg cgc cag cca gac gtg ccc aat cac ccc tgc aag gtc aac aat ggt Leu Arg Gln Pro Asp Val Pro Asn His Pro Cys Lys Val Asn Asn Gly 3285 3290 3295			10363
ggc tgc agc aac ctg tgc ctg ctg tcc ccc ggg gga ggg cac aaa tgt Gly Cys Ser Asn Leu Cys Leu Leu Ser Pro Gly Gly Gly His Lys Cys			10411

3300	3305	3310	3315	
gcc tgc ccc acc aac ttc tac ctg ggc agc gat ggg cgc acc tgt gtg Ala Cys Pro Thr Asn Phe Tyr Leu Gly Ser Asp Gly Arg Thr Cys Val 3320 3325 3330				10459
tcc aac tgc acg gct agc cag ttt gta tgc aag aac gac aag tgc atc Ser Asn Cys Thr Ala Ser Gln Phe Val Cys Lys Asn Asp Lys Cys Ile 3335 3340 3345				10507
ccc ttc tgg tgg aag tgt gac acc gag gac gac tgc ggg gac cac tca Pro Phe Trp Trp Lys Cys Asp Thr Glu Asp Asp Cys Gly Asp His Ser 3350 3355 3360				10555
gac gag ccc ccg gac tgc cct gag ttc aag tgc cgg ccc gga cag ttc Asp Glu Pro Pro Asp Cys Pro Glu Phe Lys Cys Arg Pro Gly Gln Phe 3365 3370 3375				10603
cag tgc tcc aca ggt atc tgc aca aac cct gcc ttc atc tgc gat ggc Gln Cys Ser Thr Gly Ile Cys Thr Asn Pro Ala Phe Ile Cys Asp Gly 3380 3385 3390 3395				10651
gac aat gac tgc cag gac aac agt gac gag gcc aac tgt gac atc cac Asp Asn Asp Cys Gln Asp Asn Ser Asp Glu Ala Asn Cys Asp Ile His 3400 3405 3410				10699
gtc tgc ttg ccc agt cag ttc aaa tgc acc aac acc aac cgc tgt att Val Cys Leu Pro Ser Gln Phe Lys Cys Thr Asn Thr Asn Arg Cys Ile 3415 3420 3425				10747
ccc ggc atc ttc cgc tgc aat ggg cag gac aac tgc gga gat ggg gag Pro Gly Ile Phe Arg Cys Asn Gly Gln Asp Asn Cys Gly Asp Gly Glu 3430 3435 3440				10795
gat gag agg gac tgc ccc gag gtg acc tgc gcc ccc aac cag ttc cag Asp Glu Arg Asp Cys Pro Glu Val Thr Cys Ala Pro Asn Gln Phe Gln 3445 3450 3455				10843
tgc tcc att acc aaa cgg tgc atc ccc cgg gtc tgg gtc tgc gac cgg Cys Ser Ile Thr Lys Arg Cys Ile Pro Arg Val Trp Val Cys Asp Arg 3460 3465 3470 3475				10891
gac aat gac tgt gtg gat ggc agt gat gag gcc gcc aac tgc acc cag Asp Asn Asp Cys Val Asp Gly Ser Asp Glu Pro Ala Asn Cys Thr Gln 3480 3485 3490				10939
atg acc tgt ggt gtg gac gag ttc cgc tgc aag gat tcg ggc cgc tgc Met Thr Cys Gly Val Asp Glu Phe Arg Cys Lys Asp Ser Gly Arg Cys 3495 3500 3505				10987
atc cca gcg cgt tgg aag tgt gac gga gag gat gac tgt ggg gat ggc Ile Pro Ala Arg Trp Lys Cys Asp Gly Glu Asp Asp Cys Gly Asp Gly 3510 3515 3520				11035
tcg gat gag ccc aag gaa gag tgt gat gaa cgc acc tgt gag cca tac Ser Asp Glu Pro Lys Glu Glu Cys Asp Glu Arg Thr Cys Glu Pro Tyr 3525 3530 3535				11083
cag ttc cgc tgc aag aac aac cgc tgc gtg ccc ggc cgc tgg cag tgc Gln Phe Arg Cys Lys Asn Asn Arg Cys Val Pro Gly Arg Trp Gln Cys 3540 3545 3550 3555				11131
gac tac gac aac gat tgc ggt gac aac tcc gat gaa gag agc tgc acc Asp Tyr Asp Asn Asp Cys Gly Asp Asn Ser Asp Glu Glu Ser Cys Thr 3560 3565 3570 3575				11179

3560	3565	3570	
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Pro Arg Pro Cys Ser Glu Ser Glu Phe Ser Cys Ala Asn Gly Arg Cys			
3575	3580	3585	
atc gcg ggg cgc tgg aaa tgc gat gga gac cac gac tgc gcg gac ggc			11275
Ile Ala Gly Arg Trp Lys Cys Asp Gly Asp His Asp Cys Ala Asp Gly			
3590	3595	3600	
tcg gac gag aaa gac tgc acc ccc cgc tgt gac atg gac cag ttc cag			11323
Ser Asp Glu Lys Asp Cys Thr Pro Arg Cys Asp Met Asp Gln Phe Gln			
3605	3610	3615	
tgc aag agc ggc cac tgc atc ccc ctg cgc tgg cgc tgt gac gca gac			11371
Cys Lys Ser Gly His Cys Ile Pro Leu Arg Trp Arg Cys Asp Ala Asp			
3620	3625	3630	3635
gcc gac tgc atg gac ggc agc gac gag gag gcc tgc ggc act ggc gtg			11419
Ala Asp Cys Met Asp Gly Ser Asp Glu Glu Ala Cys Gly Thr Gly Val			
3640	3645	3650	
cgg acc tgc ccc ctg gac gag ttc cag tgc aac aac acc ttg tgc aag			11467
Arg Thr Cys Pro Leu Asp Glu Phe Gln Cys Asn Asn Thr Leu Cys Lys			
3655	3660	3665	
cgg ctg gcc tgg aag tgc gat ggc gag gat gac tgt ggg gac aac tca			11515
Pro Leu Ala Trp Lys Cys Asp Gly Glu Asp Asp Cys Gly Asp Asn Ser			
3670	3675	3680	
gat gag aac ccc gag gag tgt gcc cgg ttc gtg tgc cct ccc aac cgg			11563
Asp Glu Asn Pro Glu Glu Cys Ala Arg Phe Val Cys Pro Pro Asn Arg			
3685	3690	3695	
ccc ttc cgt tgc aag aat gac cgc gtc tgt ctg tgg atc ggg cgc caa			11611
Pro Phe Arg Cys Lys Asn Asp Arg Val Cys Leu Trp Ile Gly Arg Gln			
3700	3705	3710	3715
tgc gat ggc acg gac aac tgt ggg gat ggg act gat gaa gag gac tgt			11659
Cys Asp Gly Thr Asp Asn Cys Gly Asp Gly Thr Asp Glu Glu Asp Cys			
3720	3725	3730	
gag ccc ccc aca gcc cac acc acc cac tgc aaa gac aag aag gag ttt			11707
Glu Pro Pro Thr Ala His Thr Thr His Cys Lys Asp Lys Lys Glu Phe			
3735	3740	3745	
ctg tgc cgg aac cag cgc tgc ctc tcc tcc tcc ctg cgc tgc aac atg			11755
Leu Cys Arg Asn Gln Arg Cys Leu Ser Ser Ser Leu Arg Cys Asn Met			
3750	3755	3760	
ttc gat gac tgc ggg gac ggc tct gac gag gag gac tgc agc atc gac			11803
Phe Asp Asp Cys Gly Asp Gly Ser Asp Glu Glu Asp Cys Ser Ile Asp			
3765	3770	3775	
ccc aag ctg acc agc tgc gcc acc aat gcc agc atc tgt ggg gac gag			11851
Pro Lys Leu Thr Ser Cys Ala Thr Asn Ala Ser Ile Cys Gly Asp Glu			
3780	3785	3790	3795
gca cgc tgc gtg cgc acc gag aaa gcg gcc tac tgt gcc tgc cgc tgc			11899
Ala Arg Cys Val Arg Thr Glu Lys Ala Ala Tyr Cys Ala Cys Arg Ser			
3800	3805	3810	
ggc ttc cac acc gtg ccc ggc cag ccc gga tgc caa gac atc aac gag			11947
Gly Phe His Thr Val Pro Gly Gln Pro Gly Cys Gln Asp Ile Asn Glu			

3815	3820	3825	
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ggc cac ctc tgc agc tgc gct cgg aac ttc atg aag acg cac aac acc Gly His Leu Cys Ser Cys Ala Arg Asn Phe Met Lys Thr His Asn Thr 3845 3850 3855			12043
tgc aag gcc gaa ggc tct gag tac cag gtc ctg tac atc gct gat gac Cys Lys Ala Glu Gly Ser Glu Tyr Gln Val Leu Tyr Ile Ala Asp Asp 3860 3865 3870 3875			12091
aat gag atc cgc agc ctg ttc ccc ggc cac ccc cat tcg gct tac gag Asn Glu Ile Arg Ser Leu Phe Pro Gly His Pro His Ser Ala Tyr Glu 3880 3885 3890			12139
cag gca ttc cag ggt gac gag agt gtc cgc att gat gct atg gat gtc Gln Ala Phe Gln Gly Asp Glu Ser Val Arg Ile Asp Ala Met Asp Val 3895 3900 3905			12187
cat gtc aag gct ggc cgt gtc tat tgg acc aac tgg cac acg ggc acc His Val Lys Ala Gly Arg Val Tyr Trp Thr Asn Trp His Thr Gly Thr 3910 3915 3920			12235
atc tcc tac cgc agc ctg cca cct gct gcg cct cct acc act tcc aac Ile Ser Tyr Arg Ser Leu Pro Pro Ala Ala Pro Pro Thr Thr Ser Asn 3925 3930 3935			12283
cgc cac cgg cga cag att gac cgg ggt gtc acc cac ctc aac att tca Arg His Arg Arg Gln Ile Asp Arg Gly Val Thr His Leu Asn Ile Ser 3940 3945 3950 3955			12331
ggg ctg aag atg ccc aga ggc atc gcc atc gac tgg gtg gcc gga aac Gly Leu Lys Met Pro Arg Gly Ile Ala Ile Asp Trp Val Ala Gly Asn 3960 3965 3970			12379
gtg tac tgg acc gac tcg ggc cga gat gtg att gag gtg gcg cag atg Val Tyr Trp Thr Asp Ser Gly Arg Asp Val Ile Glu Val Ala Gln Met 3975 3980 3985			12427
aag ggc gag aac cgc aag acg ctc atc tcg ggc atg att gac gag ccc Lys Gly Glu Asn Arg Lys Thr Leu Ile Ser Gly Met Ile Asp Glu Pro 3990 3995 4000			12475
cac gcc att gtg gtg gac cca ctg agg ggg acc atg tac tgg tca gac His Ala Ile Val Val Asp Pro Leu Arg Gly Thr Met Tyr Trp Ser Asp 4005 4010 4015			12523
tgg ggc aac cac ccc aag att gag acg gca gcg atg gat ggg acg ctt Trp Gly Asn His Pro Lys Ile Glu Thr Ala Ala Met Asp Gly Thr Leu 4020 4025 4030 4035			12571
cgg gag aca ctg gtg cag gac aac att cag tgg ccc aca ggc ctg gcc Arg Glu Thr Leu Val Gln Asp Asn Ile Gln Trp Pro Thr Gly Leu Ala 4040 4045 4050			12619
gtg gat tat cac aat gag cgg ctg tac tgg gca gac gcc aag ctt tca Val Asp Tyr His Asn Glu Arg Leu Tyr Trp Ala Asp Ala Lys Leu Ser 4055 4060 4065			12667
gtc atc ggc agc atc cgg ctc aat ggc acg gac ccc att gtg gct gct Val Ile Gly Ser Ile Arg Leu Asn Gly Thr Asp Pro Ile Val Ala Ala			12715

4070	4075	4080	
gac agc aaa cga ggc cta agt cac ccc ttc agc atc gac gtc ttt gag			12763
Asp Ser Lys Arg Gly Leu Ser His Pro Phe Ser Ile Asp Val Phe Glu			
4085	4090	4095	
gat tac atc tat ggt gtc acc tac atc aat aat cgt gtc ttc aag atc			12811
Asp Tyr Ile Tyr Gly Val Thr Tyr Ile Asn Asn Arg Val Phe Lys Ile			
4100	4105	4110	4115
cat aag ttt ggc cac agc ccc ttg gtc aac ctg aca ggg ggc ctg agc			12859
His Lys Phe Gly His Ser Pro Leu Val Asn Leu Thr Gly Gly Leu Ser			
4120	4125	4130	
cac gcc tct gac gtg gtc ctt tac cat cag cac aag cag ccc gaa gtg			12907
His Ala Ser Asp Val Val Leu Tyr His Gln His Lys Gln Pro Glu Val			
4135	4140	4145	
acc aac cca tgt gac cgc aag aaa tgc gag tgg ctc tgc ctg ctg agc			12955
Thr Asn Pro Cys Asp Arg Lys Lys Cys Glu Trp Leu Cys Leu Leu Ser			
4150	4155	4160	
ccc agt ggg cct gtc tgc acc tgt ccc aat ggg aag cgg ctg gac aac			13003
Pro Ser Gly Pro Val Cys Thr Cys Pro Asn Gly Lys Arg Leu Asp Asn			
4165	4170	4175	
ggc aca tgc gtg cct gtg ccc tct cca acg ccc ccc cca gat gct ccc			13051
Gly Thr Cys Val Pro Val Pro Ser Pro Thr Pro Pro Pro Asp Ala Pro			
4180	4185	4190	4195
cgg cct gga acc tgt aac ctg cag tgc ttc aac ggt ggc agc tgt ttc			13099
Arg Pro Gly Thr Cys Asn Leu Gln Cys Phe Asn Gly Gly Ser Cys Phe			
4200	4205	4210	
ctc aat gca cgg agg cag ccc aag tgc cgc tgc caa ccc cgc tac acg			13147
Leu Asn Ala Arg Arg Gln Pro Lys Cys Arg Cys Gln Pro Arg Tyr Thr			
4215	4220	4225	
ggt gac aag tgt gaa ctg gac cag tgc tgg gag cac tgt cgc aat ggg			13195
Gly Asp Lys Cys Glu Leu Asp Gln Cys Trp Glu His Cys Arg Asn Gly			
4230	4235	4240	
ggc acc tgt gct gcc tcc ccc tct ggc atg ccc acg tgc cgg tgc ccc			13243
Gly Thr Cys Ala Ala Ser Pro Ser Gly Met Pro Thr Cys Arg Cys Pro			
4245	4250	4255	
acg ggc ttc acg ggc ccc aaa tgc acc cag cag gtg tgt gcg ggc tac			13291
Thr Gly Phe Thr Gly Pro Lys Cys Thr Gln Gln Val Cys Ala Gly Tyr			
4260	4265	4270	4275
tgt gcc aac aac agc acc tgc act gtc aac cag ggc aac cag ccc cag			13339
Cys Ala Asn Asn Ser Thr Cys Thr Val Asn Gln Gly Asn Gln Pro Gln			
4280	4285	4290	
tgc cga tgc cta ccc ggc ttc ctg ggc gac cgc tgc cag tac cgg cag			13387
Cys Arg Cys Leu Pro Gly Phe Leu Gly Asp Arg Cys Gln Tyr Arg Gln			
4295	4300	4305	
tgc tct ggc tac tgt gag aac ttt ggc aca tgc cag atg gct gct gat			13435
Cys Ser Gly Tyr Cys Glu Asn Phe Gly Thr Cys Gln Met Ala Ala Asp			
4310	4315	4320	
ggc tcc cga caa tgc cgc tgc act gcc tac ttt gag gga tcg agg tgt			13483
Gly Ser Arg Gln Cys Arg Cys Thr Ala Tyr Phe Glu Gly Ser Arg Cys			

4325	4330	4335	
gag gtg aac aag tgc agc cgc tgt ctc gaa ggg gcc tgt gtg gtc aac Glu Val Asn Lys Cys Ser Arg Cys Leu Glu Gly Ala Cys Val Val Asn 4340 4345 4350 4355			13531
aag cag agt ggg gat gtc acc tgc aac tgc acg gat ggc cgg gtg gcc Lys Gln Ser Gly Asp Val Thr Cys Asn Cys Thr Asp Gly Arg Val Ala 4360 4365 4370			13579
ccc agc tgt ctg acc tgc gtc ggc cac tgc agc aat ggc ggc tcc tgt Pro Ser Cys Leu Thr Cys Val Gly His Cys Ser Asn Gly Gly Ser Cys 4375 4380 4385			13627
acc atg aac agc aaa atg atg cct gag tgc cag tgc cca ccc cac atg Thr Met Asn Ser Lys Met Met Pro Glu Cys Gln Cys Pro Pro His Met 4390 4395 4400			13675
aca ggg ccc cgg tgt gag gag cac gtc ttc agc cag cag cag cca gga Thr Gly Pro Arg Cys Glu Glu His Val Phe Ser Gln Gln Gln Pro Gly 4405 4410 4415			13723
cat ata gcc tcc atc cta atc cct ctg ctg ttg ctg ctg ctg ctg gtt His Ile Ala Ser Ile Leu Ile Pro Leu Leu Leu Leu Leu Leu Val 4420 4425 4430 4435			13771
ctg gtg gcc gga gtg gta ttc tgg tat aag cgg cga gtc caa ggg gct Leu Val Ala Gly Val Val Phe Trp Tyr Lys Arg Arg Val Gln Gly Ala 4440 4445 4450			13819
aag ggc ttc cag cac caa cgg atg acc aac ggg gcc atg aac gtg gag Lys Gly Phe Gln His Gln Arg Met Thr Asn Gly Ala Met Asn Val Glu 4455 4460 4465			13867
att gga aac ccc acc tac aag atg tac gaa ggc gga gag cct gat gat Ile Gly Asn Pro Thr Tyr Lys Met Tyr Glu Gly Gly Glu Pro Asp Asp 4470 4475 4480			13915
gtg gga ggc cta ctg gac gct gac ttt gcc ctg gac cct gac aag ccc Val Gly Gly Leu Leu Asp Ala Asp Phe Ala Leu Asp Pro Asp Lys Pro 4485 4490 4495			13963
acc aac ttc acc aac ccc gtg tat gcc aca ctc tac atg ggg ggc cat Thr Asn Phe Thr Asn Pro Val Tyr Ala Thr Leu Tyr Met Gly Gly His 4500 4505 4510 4515			14011
ggc agt cgc cac tcc ctg gcc agc acg gac gag aag cga gaa ctc ctg Gly Ser Arg His Ser Leu Ala Ser Thr Asp Glu Lys Arg Glu Leu Leu 4520 4525 4530			14059
ggc cgg ggc cct gag gac gag ata ggg gac ccc ttg gca tag ggcctg Gly Arg Gly Pro Glu Asp Glu Ile Gly Asp Pro Leu Ala *			14108
4535 4540 4545			
ccccgtcgga ctgccccag aaagcctcct gccccctgcc ggtgaagtcc ttcagtgage			14168
ccctccccag ccagcccttc cctggccccg ccggaatgat aaatgtaaaa atgaaggaat			14228
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tccctgcctg ctccctggca ccccatgct gccttcaggg agacaggcag ggagggcttg			14348
gggctgcacc tcctaccctc ccaccagaac gcacccact gggagagctg gtggtgcagc			14408

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cttccccctcc ctgtataaga cacttttgcca aggcctctccc ctctcgcccc atccctgctt 14468
gcccgcctccc acagcttcct gagggetaat tctgggaagg gagagttctt tgctgcccc 14528
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gggccacacc caggaaggga aagcgggcag ccccgttttg gggacgtgaa cgttttaata 14828
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aaaaaaaaa a 14899

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<212> DNA
<213> Homo sapiens

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<222> (195) .. (1373)

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tttttttttt tggtttcggg ttctgtcacc tccaggetga gccgggctgg cggaagagggc 180
acgtgcgctg ctga atg gag ctg gtc gct ggt tgc tac gag cag gtc ctc 230
Met Glu Leu Val Ala Gly Cys Tyr Glu Gln Val Leu
1 5 10
ttt ggg ttc gct gta cac ccg gag ccc gag gct tgc ggc gac cac gag 278
Phe Gly Phe Ala Val His Pro Glu Pro Glu Ala Cys Gly Asp His Glu
15 20 25
caa tgg act ctt gtg gct gac ttc act cac cat gct cac act gcc tcc 326
Gln Trp Thr Leu Val Ala Asp Phe Thr His His Ala His Thr Ala Ser
30 35 40
ttg tca gca gta gct gta aat agt cgt ttt gtg gtc act ggg agc aaa 374
Leu Ser Ala Val Ala Val Asn Ser Arg Phe Val Val Thr Gly Ser Lys
45 50 55 60
gat gaa aca att cac att tat gac atg aaa aag aag att gag cat ggg 422
Asp Glu Thr Ile His Ile Tyr Asp Met Lys Lys Lys Ile Glu His Gly
65 70 75
gct cta gtg cat cac agt ggt aca ata act tgc ctg aaa ttc tat ggc 470
Ala Leu Val His His Ser Gly Thr Ile Thr Cys Leu Lys Phe Tyr Gly
80 85 90
aac agg cat tta atc agt gga gcg gaa gat gga ctc atc tgt atc tgg 518
Asn Arg His Leu Ile Ser Gly Ala Glu Asp Gly Leu Ile Cys Ile Trp
95 100 105

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gat gca aag aaa tgg gaa tgc ctg aag tca att aaa gct cac aaa gga Asp Ala Lys Lys Trp Glu Cys Leu Lys Ser Ile Lys Ala His Lys Gly 110 115 120	566
cag gtg acc ttc ctt tct att cac cca tct ggc aag ttg gcc ctg tcg Gln Val Thr Phe Leu Ser Ile His Pro Ser Gly Lys Leu Ala Leu Ser 125 130 135 140	614
gtt ggt aca gat aaa act tta aga acg tgg aat ctt gta gaa gga aga Val Gly Thr Asp Lys Thr Leu Arg Thr Trp Asn Leu Val Glu Gly Arg 145 150 155	662
tca gca ttc ata aaa aat ata aaa caa aat gct cac ata gta gaa tgg Ser Ala Phe Ile Lys Asn Ile Lys Gln Asn Ala His Ile Val Glu Trp 160 165 170	710
tcc cca aga gga gag cag tat gta gtt atc ata cag aat aaa ata gac Ser Pro Arg Gly Glu Gln Tyr Val Val Ile Ile Gln Asn Lys Ile Asp 175 180 185	758
atc tat cag ctt gac act gca tcc att agt ggc acc atc aca aat gaa Ile Tyr Gln Leu Asp Thr Ala Ser Ile Ser Gly Thr Ile Thr Asn Glu 190 195 200	806
aag aga att tcc tct gtt aaa ttt ctt tca gag tct gtc ctt gca gtg Lys Arg Ile Ser Ser Val Lys Phe Leu Ser Glu Ser Val Leu Ala Val 205 210 215 220	854
gct gga gat gaa gaa gtt ata agg ttt ttt gac tgt gat tca cta gtg Ala Gly Asp Glu Glu Val Ile Arg Phe Phe Asp Cys Asp Ser Leu Val 225 230 235	902
tgc ctc tgc gaa ttt aaa gct cat gaa aac agg gta aag gac atg ttc Cys Leu Cys Glu Phe Lys Ala His Glu Asn Arg Val Lys Asp Met Phe 240 245 250	950
agt ttt gaa att cca gag cat cat gtt att gtt tca gca tcg agt gat Ser Phe Glu Ile Pro Glu His His Val Ile Val Ser Ala Ser Ser Asp 255 260 265	998
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tct tta ctc tgt gaa ata aac act aat gcc agg ctg acg tgt ctt gga Ser Leu Leu Cys Glu Ile Asn Thr Asn Ala Arg Leu Thr Cys Leu Gly 285 290 295 300	1094
gtg tgg cta gac aaa gtg gca gac atg aaa gaa agc ctt cct cca gct Val Trp Leu Asp Lys Val Ala Asp Met Lys Glu Ser Leu Pro Pro Ala 305 310 315	1142
gca gag cct tct cct gta agt aaa gaa cag tcc aaa att ggc aaa aag Ala Glu Pro Ser Pro Val Ser Lys Glu Gln Ser Lys Ile Gly Lys Lys 320 325 330	1190
gag cct ggt gac aca gtg cac aaa gaa gaa aag cgg tca aaa cct aac Glu Pro Gly Asp Thr Val His Lys Glu Glu Lys Arg Ser Lys Pro Asn 335 340 345	1238
aca aag aaa cgc ggt tta aca ggt gac agt aag aaa gca aca aaa gaa Thr Lys Lys Arg Gly Leu Thr Gly Asp Ser Lys Lys Ala Thr Lys Glu 350 355 360	1286

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agt ggc ctg ata tca acc aag aag agg aaa atg gta gaa atg ttg gaa      1334
Ser Gly Leu Ile Ser Thr Lys Lys Arg Lys Met Val Glu Met Leu Glu
365                      370                      375                      380

aag aag agg aaa aag aag aaa ata aaa cca atg cag tga atcacagatg      1383
Lys Lys Arg Lys Lys Lys Lys Ile Lys Pro Met Gln *
                      385                      390

tctcctgaaa gaactctttt agatgaaatc attctactca aatgtacctt aatttttttt      1443

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cactttttaga tggttttttt taaaaaaaaa aaaaaa                        1538

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 <213> Homo sapiens

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tgccgtgtca tggaggctca gtctctgagc agccattgaa ggggaaggaa ctgcgggtgt      180

gtgtgtgtat gtgtgtgtgt atgtgtgtgc gcgcgtgcgt gcgtgtgtgt gcgcgcgcta      240

gtgtgtggac aaggagggtgg gggcagctga gttagagtcc caactcttgg actccatttg      300

ctattctctt ctttctcccc cacacctatc tggtggtggt agtgggcgtt tatatttgcg      360

tctcttttca ttcatttcta aatctcttaa aaattttggg ttgggggtat tggggaaggc      420

aggaaagggg aaaggagagt agtagctgaa gagcaagagg aggac      atg gag atg      474
                      Met Glu Met
                      1

aag aag aag att aac ctg gag tta agg aac aga tcc ccg gag gag gtg      522
Lys Lys Lys Ile Asn Leu Glu Leu Arg Asn Arg Ser Pro Glu Glu Val
      5                      10                      15

aca gag tta gtc ctt gat aat tgc ctg tgt gtc aat ggg gaa att gaa      570
Thr Glu Leu Val Leu Asp Asn Cys Leu Cys Val Asn Gly Glu Ile Glu
      20                      25                      30                      35

ggc ctg aat gat act ttc aaa gaa cta gaa ttt ctg agt atg gct aat      618
Gly Leu Asn Asp Thr Phe Lys Glu Leu Glu Phe Leu Ser Met Ala Asn
                      40                      45                      50

gtg gaa cta agt tgc ctg gcc cgg ctt ccc agc tta aat aaa ctt cga      666
Val Glu Leu Ser Ser Leu Ala Arg Leu Pro Ser Leu Asn Lys Leu Arg
                      55                      60                      65

aaa ttg gag ctt agt gat aat ata att tct gga ggc ttg gaa gtc ctg      714
Lys Leu Glu Leu Ser Asp Asn Ile Ile Ser Gly Gly Leu Glu Val Leu

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70	75	80	
gca gag aaa tgt cca aat ctt acc tac ctc aat ctg agt gga aac aaa			762
Ala Glu Lys Cys Pro Asn Leu Thr Tyr Leu Asn Leu Ser Gly Asn Lys			
85	90	95	
ata aaa gat ctc agt aca gta gaa gct ctg caa aat ctt aaa aat ttg			810
Ile Lys Asp Leu Ser Thr Val Glu Ala Leu Gln Asn Leu Lys Asn Leu			
100	105	110	115
aaa agt ctt gac ctg ttt aac tgt gag atc aca aac ctg gaa gat tat			858
Lys Ser Leu Asp Leu Phe Asn Cys Glu Ile Thr Asn Leu Glu Asp Tyr			
120	125	130	
aga gaa agt att ttt gaa cta ctg cag caa atc aca tac tta gat gga			906
Arg Glu Ser Ile Phe Glu Leu Leu Gln Gln Ile Thr Tyr Leu Asp Gly			
135	140	145	
ttt gat cag gag gat aat gaa gcg ccg gac tct gaa gag gag gat gat			954
Phe Asp Gln Glu Asp Asn Glu Ala Pro Asp Ser Glu Glu Glu Asp Asp			
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gag gat gga gat gaa gat gat gaa gag gaa gag gaa aat gaa gct ggt			1002
Glu Asp Gly Asp Glu Asp Asp Glu Glu Glu Glu Glu Asn Glu Ala Gly			
165	170	175	
cca ccg gaa gga tat gag gaa gag gag gag gaa gag gag gat gag gat			1050
Pro Pro Glu Gly Tyr Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp			
180	185	190	195
gag gat gaa gat gaa gat gaa gca ggt tca gag ttg gga gag gga gaa			1098
Glu Asp Glu Asp Glu Asp Glu Ala Gly Ser Glu Leu Gly Glu Gly Glu			
200	205	210	
gag gaa gtg ggc ctc tca tac tta atg aaa gaa gaa att cag gat gaa			1146
Glu Glu Val Gly Leu Ser Tyr Leu Met Lys Glu Glu Ile Gln Asp Glu			
215	220	225	
gaa gat gat gat gac tat gtt gaa gaa ggg gaa gaa gag gaa gaa gag			1194
Glu Asp Asp Asp Asp Tyr Val Glu Glu Gly Glu Glu Glu Glu Glu			
230	235	240	
gaa gaa gga ggt ctt cga ggg gag aag agg aaa cga gat gct gaa gac			1242
Glu Glu Gly Gly Leu Arg Gly Glu Lys Arg Lys Arg Asp Ala Glu Asp			
245	250	255	
gat gga gag gaa gaa gat gac tag atcattctaa gaccagattc tctaattgttt			1296
Asp Gly Glu Glu Glu Asp Asp *			
260	265		
ctgggtgtgc aatagagtga tcacatcttt gttcttctcat gtacgatagc tatecctaca			1356
gaagataatg tgtaactttt tataggaaaa gtgtgggtttt actatttttg ccttatcatt			1416
ccaaataaga actagtctgt taatgatcat attgtatgta gagaaaaatt ttcattgact			1476
cccattgtgg aattocctag caatttattt agacttaatt ttttaaattc aagcttactg			1536
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 Gly Pro Pro Thr Pro Arg Ser Pro Lys Ala Gln Arg Pro Val Ala Cys
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ccc aaa gga gac tcc gga gag tcc tca gca ctt tgt tga acgtggtggt 776
 Pro Lys Gly Asp Ser Gly Glu Ser Ser Ala Leu Cys *
 230 235

gagagcacac gtcctcgtct cattcctgat cgaacgcggg ggtgagagca cacgtcctcg 836

tctcgttcgt gacagaacgc ggtggtgaga gcacacgtcg tcgtttcgat cctgatcgaa 896

cgcggtggtg agagcgcacg tcctcgtctc gttcctgaac gaacgcgggtg gtgagagccc 956

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 Ala Leu Glu Ala Ala Gly Gly Pro Pro Glu Glu Thr Leu Ser Leu Trp
 5 10 15

aaa cgg gag caa gct cgg ctg aag gcc cac gtc gta gac cgg gac acc 151
 Lys Arg Glu Gln Ala Arg Leu Lys Ala His Val Val Asp Arg Asp Thr
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gag gcg tgg cag cga gac ccc gcc ttc tcg ggt ctg cag agg gtc ggg 199
 Glu Ala Trp Gln Arg Asp Pro Ala Phe Ser Gly Leu Gln Arg Val Gly
 35 40 45

ggc gtt gac gtg tcc ttc gtg aaa ggg gac agt gtc cgc gct tgt gct 247
 Gly Val Asp Val Ser Phe Val Lys Gly Asp Ser Val Arg Ala Cys Ala
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tcc ctg gtg gtg ctc agc ttc cct gag ctc gag gtg gtg tat gag gag 295
 Ser Leu Val Val Leu Ser Phe Pro Glu Leu Glu Val Val Tyr Glu Glu
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agc cgc atg gtc agc ctc aca gcc ccc tac gtg tcg ggc ttc ctg gcc 343
 Ser Arg Met Val Ser Leu Thr Ala Pro Tyr Val Ser Gly Phe Leu Ala
 85 90 95

ttc cga gag gtg ccc ttc ttg ctg gag ctg gtg caa cag ctg cgg gag 391
 Phe Arg Glu Val Pro Phe Leu Leu Glu Leu Val Gln Gln Leu Arg Glu
 100 105 110

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aag gag ccg ggc ctc atg ccc cag gtc ctt ctt gtg gat gga aac ggg      439
Lys Glu Pro Gly Leu Met Pro Gln Val Leu Leu Val Asp Gly Asn Gly
      115                      120                      125

gta ctc cac cac cga ggc ttt ggg gtg gcc tgc cac ctt ggc gtc ctt      487
Val Leu His His Arg Gly Phe Gly Val Ala Cys His Leu Gly Val Leu
      130                      135                      140                      145

aca gac ctg ccg tgt gtt ggg gtg gcc aag aaa ctt ctg cag gtg gat      535
Thr Asp Leu Pro Cys Val Gly Val Ala Lys Lys Leu Leu Gln Val Asp
                        150                      155                      160

ggg ctg gag aac aac gcc ctg cac aag gag aag atc cga ctc ctg cag      583
Gly Leu Glu Asn Asn Ala Leu His Lys Glu Lys Ile Arg Leu Leu Gln
                        165                      170                      175

act cga gga gac tca ttc cct ctg ctg gga gac tct ggg act gtc ctg      631
Thr Arg Gly Asp Ser Phe Pro Leu Leu Gly Asp Ser Gly Thr Val Leu
      180                      185                      190

gga atg gcc ctg agg agc cac gac cgc agc acc agg ccc ctc tac atc      679
Gly Met Ala Leu Arg Ser His Asp Arg Ser Thr Arg Pro Leu Tyr Ile
      195                      200                      205

tcc gtg ggc cac agg atg agc ctg gag gcc gct gtg cgc ctg act tgc      727
Ser Val Gly His Arg Met Ser Leu Glu Ala Ala Val Arg Leu Thr Cys
      210                      215                      220                      225

tgc tgc tgc agg ttc cgg atc cca gag ccc gtg cgc cag gct gac atc      775
Cys Cys Cys Arg Phe Arg Ile Pro Glu Pro Val Arg Gln Ala Asp Ile
                        230                      235                      240

tgc tcc cga gag cac atc cgc aag tcg ctg gga ctc ccc ggg cca ccc      823
Cys Ser Arg Glu His Ile Arg Lys Ser Leu Gly Leu Pro Gly Pro Pro
                        245                      250                      255

aca ccg agg agc ccg aag gcg cag agg cca gtg gca tgc ccc aaa gga      871
Thr Pro Arg Ser Pro Lys Ala Gln Arg Pro Val Ala Cys Pro Lys Gly
                        260                      265                      270

gac tcc gga gag tcc tca gca ctt tgt tga a cgtggtggtg agagcacacg      922
Asp Ser Gly Glu Ser Ser Ala Leu Cys *
      275                      280

tcctcgtctc attcctgac gaacgcggtg gtgagagcac acgtcctcgt ctcgttcgtg      982

acagaacgcg gtggtgagag cacacgtcgt cgtttcgac ctgatcgaac gcggtggtga      1042

gagcgcacgt cctcgtctcg ttcctgaacg aacgcggtgg tgagagccca cgtcgtggtc      1102

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ggagctttctc tttgtgggcg ggcgcgaggg cgcctagggg gttatactgg ggaacgtgcc      180
tgcgcgtgct tggatagttc atttaaagcc cccatccctg caaggtggtg ctttctacca      240
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    Met Asn Leu Phe Asn Leu Asp Arg Phe Gly Phe Glu Lys Arg Asn
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Lys Ile Glu Glu Ala Pro Glu Ala Thr Pro Gln Pro Ser Gln Pro Gly
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cct tct tca cca att tct ctt agt gct gaa gag gag aat gct gaa ggg      383
Pro Ser Ser Pro Ile Ser Leu Ser Ala Glu Glu Glu Asn Ala Glu Gly
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gaa gtt agc agg gca aac act cct gat tca gat ata act gaa aaa aca      431
Glu Val Ser Arg Ala Asn Thr Pro Asp Ser Asp Ile Thr Glu Lys Thr
           50           55           60

gaa gat tct agt gtt cca gaa act cca gat aat gaa aga aaa gca agt      479
Glu Asp Ser Ser Val Pro Glu Thr Pro Asp Asn Glu Arg Lys Ala Ser
           65           70           75

ata tca tat ttc aaa aat caa aga gga ata cag tat att gat ttg tct      527
Ile Ser Tyr Phe Lys Asn Gln Arg Gly Ile Gln Tyr Ile Asp Leu Ser
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tct gat agt gaa gat gtc gtt tcc cca aat tgc tcc aat aca gtt caa      575
Ser Asp Ser Glu Asp Val Val Ser Pro Asn Cys Ser Asn Thr Val Gln
           100           105           110

gag aaa aca ttc aac aaa gat aca gtg att ata gtt tct gag cca tct      623
Glu Lys Thr Phe Asn Lys Asp Thr Val Ile Ile Val Ser Glu Pro Ser
           115           120           125

gaa gat gaa gag tcc caa ggc ctt cct acc atg gca cgt aga aat gat      671
Glu Asp Glu Glu Ser Gln Gly Leu Pro Thr Met Ala Arg Arg Asn Asp
           130           135           140

gat att tca gaa ctg gaa gac ctt tcg gaa ttg gaa gac ctt aaa gat      719
Asp Ile Ser Glu Leu Glu Asp Leu Ser Glu Leu Glu Asp Leu Lys Asp
           145           150           155

gct aaa ctt cag act ttg aag gaa ctt ttt cca caa aga agt gac aat      767
Ala Lys Leu Gln Thr Leu Lys Glu Leu Phe Pro Gln Arg Ser Asp Asn
           160           165           170           175

gat tta ctt aag ttg att gaa tca aca agc act atg gat gga gca att      815
Asp Leu Leu Lys Leu Ile Glu Ser Thr Ser Thr Met Asp Gly Ala Ile
           180           185           190

gct gct gcc ttg ctg atg ttt ggt gat gca ggt ggt ggg ccc agg aaa      863
Ala Ala Ala Leu Leu Met Phe Gly Asp Ala Gly Gly Gly Pro Arg Lys
           195           200           205

aga aaa tta tct tct tct tca gag cca tat gag gaa gat gaa ttt aat      911

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Arg	Lys	Leu	Ser	Ser	Ser	Ser	Glu	Pro	Tyr	Glu	Glu	Asp	Glu	Phe	Asn	
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gat	gat	caa	tct	ata	aaa	aag	aca	aga	ctg	gat	cat	gga	gag	gaa	tca	959
Asp	Asp	Gln	Ser	Ile	Lys	Lys	Thr	Arg	Leu	Asp	His	Gly	Glu	Glu	Ser	
		225				230					235					
aat	gag	tct	gca	gaa	tct	agc	agt	aat	tgg	gaa	aag	cag	gaa	agt	att	1007
Asn	Glu	Ser	Ala	Glu	Ser	Ser	Asn	Trp	Glu	Lys	Gln	Glu	Ser	Ile		
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Val	Leu	Lys	Leu	Gln	Lys	Glu	Phe	Pro	Asn	Phe	Asp	Lys	Gln	Glu	Leu	
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Arg	Glu	Val	Leu	Lys	Glu	His	Glu	Trp	Met	Tyr	Thr	Glu	Ala	Leu	Glu	
			275					280					285			
tct	cta	aaa	gtg	ttt	gca	gaa	gac	caa	gat	atg	caa	tat	gca	tca	caa	1151
Ser	Leu	Lys	Val	Phe	Ala	Glu	Asp	Gln	Asp	Met	Gln	Tyr	Ala	Ser	Gln	
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Ser	Glu	Val	Pro	Asn	Gly	Lys	Glu	Val	Ser	Ser	Arg	Ser	Gln	Asn	Tyr	
		305				310					315					
cct	aaa	aat	gca	act	aaa	aca	aaa	cta	aaa	cag	aaa	ttt	tca	atg	aaa	1247
Pro	Lys	Asn	Ala	Thr	Lys	Thr	Lys	Leu	Lys	Gln	Lys	Phe	Ser	Met	Lys	
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Ala	Gln	Asn	Gly	Phe	Asn	Lys	Lys	Lys	Lys	Lys	Asn	Val	Phe	Asn	Pro	
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Lys	Arg	Val	Val	Glu	Asp	Ser	Glu	Tyr	Asp	Ser	Gly	Ser	Asp	Val	Gly	
			355					360					365			
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Ser	Ser	Leu	Asp	Glu	Asp	Tyr	Ser	Ser	Gly	Glu	Glu	Val	Met	Glu	Asp	
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Gly	Tyr	Lys	Gly	Lys	Ile	Leu	His	Phe	Leu	Gln	Asp	Ala	Ser	Ile	Gly	
		385				390					395					
gaa	ctt	act	ttg	att	cct	cag	tgt	tct	cag	aaa	aag	gct	cag	aag	ata	1487
Glu	Leu	Thr	Leu	Ile	Pro	Gln	Cys	Ser	Gln	Lys	Lys	Ala	Gln	Lys	Ile	
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Thr	Glu	Leu	Arg	Pro	Phe	Asn	Ser	Trp	Glu	Ala	Leu	Phe	Thr	Lys	Met	
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Ser	Lys	Thr	Asn	Gly	Leu	Ser	Glu	Asp	Leu	Ile	Trp	His	Cys	Lys	Thr	
			435					440					445			
ctg	atc	caa	gaa	aga	gat	gta	gtt	ata	agg	ctt	atg	aac	aaa	tgt	gaa	1631
Leu	Ile	Gln	Glu	Arg	Asp	Val	Val	Ile	Arg	Leu	Met	Asn	Lys	Cys	Glu	
		450				455						460				
gac	att	tca	aat	aaa	ttg	acc	aaa	caa	gtt	acc	atg	ctt	act	gga	aat	1679

Asp	Ile	Ser	Asn	Lys	Leu	Thr	Lys	Gln	Val	Thr	Met	Leu	Thr	Gly	Asn		
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480					485					490					495		
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Ser	Leu	Lys	Pro	Tyr	Gln	Lys	Val	Gly	Leu	Asn	Trp	Leu	Ala	Leu	Val		
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cat	aaa	cat	gga	ctt	aat	ggc	att	ttg	gca	gat	gaa	atg	ggc	cta	gga	1823	
His	Lys	His	Gly	Leu	Asn	Gly	Ile	Leu	Ala	Asp	Glu	Met	Gly	Leu	Gly		
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Lys	Thr	Ile	Gln	Ala	Ile	Ala	Phe	Leu	Ala	Tyr	Leu	Tyr	Gln	Glu	Gly		
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Asn	Asn	Gly	Pro	His	Leu	Ile	Val	Val	Pro	Ala	Ser	Thr	Ile	Asp	Asn		
			545				550					555					
tgg	tta	agg	gaa	gtt	aat	tta	tgg	tgc	cct	act	ttg	aag	gtc	ctc	tgt	1967	
Trp	Leu	Arg	Glu	Val	Asn	Leu	Trp	Cys	Pro	Thr	Leu	Lys	Val	Leu	Cys		
560					565					570					575		
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Tyr	Tyr	Gly	Ser		Gln	Glu	Glu	Arg	Lys	Gln	Ile	Arg	Phe	Asn	Ile	His	
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Ser	Arg	Tyr	Glu	Asp	Tyr	Asn	Val	Ile	Val	Thr	Thr	Tyr	Asn	Cys	Ala		
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Ile	Ser	Ser	Ser	Asp	Asp	Arg	Ser	Leu	Phe	Arg	Arg	Leu	Lys	Leu	Asn		
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tac	gca	att	ttt	gat	gag	ggc	cat	atg	ctg	aag	aat	atg	ggc	tcc	att	2159	
Tyr	Ala	Ile	Phe	Asp	Glu	Gly	His	Met	Leu	Lys	Asn	Met	Gly	Ser	Ile		
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cgc	tac	cag	cac	ctt	atg	aca	att	aat	gca	aat	aac	cgt	ttg	ctg	ctc	2207	
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Thr	Gly	Thr	Pro	Val	Gln	Asn	Asn	Leu	Leu	Glu	Leu	Met	Ser	Leu	Leu		
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Asn	Phe	Val	Met	Pro	His	Met	Phe	Ser	Ser	Ser	Thr	Ser	Glu	Ile	Arg		
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aga	atg	ttt	tcc	tct	aag	aca	aaa	tca	gca	gat	gag	caa	agc	ata	tat	2351	
Arg	Met	Phe	Ser	Ser	Lys	Thr	Lys	Ser	Ala	Asp	Glu	Gln	Ser	Ile	Tyr		
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gaa	aag	gag	aga	ata	gca	cat	gca	aaa	caa	att	ata	aag	cca	ttt	att	2399	
Glu	Lys	Glu	Arg	Ile	Ala	His	Ala	Lys	Gln	Ile	Ile	Lys	Pro	Phe	Ile		
				705			710				715						
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Asp Arg Ile Glu Leu Cys Ala Met Ser Glu Lys Gln Glu Gln Leu Tyr	
740 745 750	
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Leu Gly Leu Phe Asn Arg Leu Lys Lys Ser Ile Asn Asn Leu Val Thr	
755 760 765	
gaa aaa aac aca gaa atg tgc aat gtc atg atg cag ttg agg aaa atg	2591
Glu Lys Asn Thr Glu Met Cys Asn Val Met Met Gln Leu Arg Lys Met	
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785 790 795	
aag gaa atg tct cag ctt atg cta aag gaa cct aca cat tgt gag gct	2687
Lys Glu Met Ser Gln Leu Met Leu Lys Glu Pro Thr His Cys Glu Ala	
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Asn Pro Asp Leu Ile Phe Glu Asp Met Glu Val Met Thr Asp Phe Glu	
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850 855 860	
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Ile Leu Ser Glu Leu Lys Gln Lys Gly Asp Arg Val Val Leu Phe Ser	
865 870 875	
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Gln Phe Thr Met Met Leu Asp Ile Leu Glu Val Leu Leu Lys His His	
880 885 890 895	
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930 935 940	
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Asn Val Val Ile Leu His Asp Ile Asp Cys Asn Pro Tyr Asn Asp Lys	
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Val Ile Lys Leu Ile Ser Gln Gly Thr Ile Glu Glu Ser Met Leu Lys
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att aac caa cag aaa ttg aaa cta gaa cag gat atg act aca gta gat 3263
 Ile Asn Gln Gln Lys Leu Lys Leu Glu Gln Asp Met Thr Thr Val Asp
 995 1000 1005

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 1010 1015 1020

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 Thr Ser Met Gly Leu *
 1025

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tttgtaacaa atatgctaata gcttttagaaa tgtcagtatt tttgtaatta tttctacctc 3665

caaatatata tatattgtct ttcactggat aatgtgtgta gatttttaca tgtgccttat 3725

ttgacaatgc ttatgtcttg tttttgcttg tctcatttga agttcttttt tattatgtta 3785

aagaatgcag ctgtatagat tatatagctt tcattttatt gctatttgaa gcagatgttc 3845

accaatgtca gcaagaactc aacctgaatt taaagggtggc attccatata ctaacatccc 3905

ccaggctctc tcaagtactt ctgctgaaac aaatttattt ggctaggcac taagttgttt 3965

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 Ser Asn Leu Val Gly Ala Arg Ile Pro Arg Gly Lys Val Ile Thr Thr
 15 20 25 30

gca cga ggg agt tcg act ggc gaa ctg gaa ggc cac gcc tcc tcc cgc 146
 Ala Arg Gly Ser Ser Thr Gly Glu Leu Glu Gly His Ala Ser Ser Arg
 35 40 45

ctg ccc cct cag ccc tgt ggc tgg ggg cag agc tca gac tta tta tct	194
Leu Pro Pro Gln Pro Cys Gly Trp Gly Gln Ser Ser Asp Leu Leu Ser	
50 55 60	
agg ata gat ttg gat gaa cta atg aaa aaa gat gaa ccg cct ctt gat	242
Arg Ile Asp Leu Asp Glu Leu Met Lys Lys Asp Glu Pro Pro Leu Asp	
65 70 75	
ttt cct gat acc ctg gaa gga ttt gaa tat gct ttt aat gaa aag gga	290
Phe Pro Asp Thr Leu Glu Gly Phe Glu Tyr Ala Phe Asn Glu Lys Gly	
80 85 90	
cag tta aga cac ata aaa act ggg gaa cca ttt gtt ttt aac tac cgg	338
Gln Leu Arg His Ile Lys Thr Gly Glu Pro Phe Val Phe Asn Tyr Arg	
95 100 105 110	
gaa gat tta cac aga tgg aac cag aaa aga tac gag gct cta gga gag	386
Glu Asp Leu His Arg Trp Asn Gln Lys Arg Tyr Glu Ala Leu Gly Glu	
115 120 125	
atc atc acg aag tat gta tat gag ctc ctg gaa aag gat tgt aat ttg	434
Ile Ile Thr Lys Tyr Val Tyr Glu Leu Leu Glu Lys Asp Cys Asn Leu	
130 135 140	
aaa aaa gta tct att cca gta gat gcc act gag agt gaa cca aag agt	482
Lys Lys Val Ser Ile Pro Val Asp Ala Thr Glu Ser Glu Pro Lys Ser	
145 150 155	
ttt atc ttt atg agt gag gat gct ttg aca aat cca cag aaa ctg atg	530
Phe Ile Phe Met Ser Glu Asp Ala Leu Thr Asn Pro Gln Lys Leu Met	
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gtt tta att cat ggt agt ggt gtt gtc agg gca ggg cag tgg gct aga	578
Val Leu Ile His Gly Ser Gly Val Val Arg Ala Gly Gln Trp Ala Arg	
175 180 185 190	
aga ctt att ata aat gaa gat ctg gac agt ggc aca cag ata ccg ttt	626
Arg Leu Ile Ile Asn Glu Asp Leu Asp Ser Gly Thr Gln Ile Pro Phe	
195 200 205	
att aaa aga gct gtg gct gaa gga tat gga gta ata gta cta aat ccc	674
Ile Lys Arg Ala Val Ala Glu Gly Tyr Gly Val Ile Val Leu Asn Pro	
210 215 220	
aat gaa aac tat att gaa gta gaa aag ccg aag ata cac gta cag tca	722
Asn Glu Asn Tyr Ile Glu Val Glu Lys Pro Lys Ile His Val Gln Ser	
225 230 235	
tca tct gat agt tca gat gaa cca gca gaa aaa ccg gaa aga aaa gat	770
Ser Ser Asp Ser Ser Asp Glu Pro Ala Glu Lys Arg Glu Arg Lys Asp	
240 245 250	
aaa gtt tct aaa gaa aca aag aag cga cgt gat ttc tat gag aag tat	818
Lys Val Ser Lys Glu Thr Lys Lys Arg Arg Asp Phe Tyr Glu Lys Tyr	
255 260 265 270	
cgt aac aac aaa aaa aaa aaa aaa aaa aca cag aag ggg ggc cag gta	866
Arg Asn Asn Lys Lys Lys Lys Lys Lys Thr Gln Lys Gly Gly Gln Val	
275 280 285	
caa caa tac aac ctg ata atg agt cat aat aca att cac tag acca	912
Gln Gln Tyr Asn Leu Ile Met Ser His Asn Thr Ile His *	
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 Ala Lys Pro Gly Lys Ser Ser Ser Leu Glu Met Thr Pro Tyr Asn Thr
 15 20 25

cct cag cta tct cca gca acc act cca gca aat aaa aag aat cga tta 145
 Pro Gln Leu Ser Pro Ala Thr Thr Pro Ala Asn Lys Lys Asn Arg Leu
 30 35 40

cct ata gca act cgg agc aga agc cgc acc aat atg cta atg gac cta 193
 Pro Ile Ala Thr Arg Ser Arg Ser Arg Thr Asn Met Leu Met Asp Leu
 45 50 55 60

cat atg gac cat gaa gga tca tct caa gaa acc atc cag gag gtg caa 241
 His Met Asp His Glu Gly Ser Ser Gln Glu Thr Ile Gln Glu Val Gln
 65 70 75

cca gaa gag gtg ttg gtc att tcc tta ggt aca ggt ccc cag ctt act 289
 Pro Glu Glu Val Leu Val Ile Ser Leu Gly Thr Gly Pro Gln Leu Thr
 80 85 90

cca ggg atg atg tca gaa aat gag gtc cta aac atg cag ctt tgc gat 337
 Pro Gly Met Met Ser Glu Asn Glu Val Leu Asn Met Gln Leu Ser Asp
 95 100 105

gga gga caa gga gat gtc cct gtt gat gaa aac aaa ctc cat ggt aaa 385
 Gly Gly Gln Gly Asp Val Pro Val Asp Glu Asn Lys Leu His Gly Lys
 110 115 120

cct gat aaa acc ttg cgc ttt tcc ctc tgc agt gat aat ctg gaa gga 433
 Pro Asp Lys Thr Leu Arg Phe Ser Leu Cys Ser Asp Asn Leu Glu Gly
 125 130 135 140

ata tct gaa ggt cct tca aat cgc tcc aat tca gtg tcc tcc cta gac 481
 Ile Ser Glu Gly Pro Ser Asn Arg Ser Asn Ser Val Ser Ser Leu Asp
 145 150 155

cta gaa gga gag tct gtg tca gaa ctt gga gca gga cct tct ggc agt 529
 Leu Glu Gly Glu Ser Val Ser Glu Leu Gly Ala Gly Pro Ser Gly Ser
 160 165 170

aat gga gtt gaa gct cta cag ctg tta gaa cat gag caa gct aca aca 577
 Asn Gly Val Glu Ala Leu Gln Leu Leu Glu His Glu Gln Ala Thr Thr
 175 180 185

cag gat aac ctt gat gat aag cta agg aag ttt gaa att cgt gac atg 625
 Gln Asp Asn Leu Asp Asp Lys Leu Arg Lys Phe Glu Ile Arg Asp Met

190	195	200	
atg gga tta aca gat gat agg gac ata tca gaa aca gtg agt gag acc Met Gly Leu Thr Asp Asp Arg Asp Ile Ser Glu Thr Val Ser Glu Thr 205 210 215 220			673
tgg agt aca gac gtc ttg gga agt gac ttt gac cct aat att gat gaa Trp Ser Thr Asp Val Leu Gly Ser Asp Phe Asp Pro Asn Ile Asp Glu 225 230 235			721
gat cgc ttg caa gaa att gca ggt gct gca gca gag aac atg tta ggc Asp Arg Leu Gln Glu Ile Ala Gly Ala Ala Ala Glu Asn Met Leu Gly 240 245 250			769
agt ttg ctg tgc ctc cca ggt tca ggg tca gtg ctt ctt gac ccc tgc Ser Leu Leu Cys Leu Pro Gly Ser Gly Ser Val Leu Leu Asp Pro Cys 255 260 265			817
act ggt tct acc ata tca gag aca aca agt gaa gct tgg agt gta gag Thr Gly Ser Thr Ile Ser Glu Thr Thr Ser Glu Ala Trp Ser Val Glu 270 275 280			865
gta ttg cca agt gac tca gag gcc cca gac cta aag cag gag gag cgt Val Leu Pro Ser Asp Ser Glu Ala Pro Asp Leu Lys Gln Glu Glu Arg 285 290 295 300			913
ctg caa gaa ctg gag agc tgt tct gga ctg ggt agc aca tct gat gat Leu Gln Glu Leu Glu Ser Cys Ser Gly Leu Gly Ser Thr Ser Asp Asp 305 310 315			961
acg gat gtc agg gag gtc agt tcc cgc ccc agc aca cca ggc ctc agt Thr Asp Val Arg Glu Val Ser Ser Arg Pro Ser Thr Pro Gly Leu Ser 320 325 330			1009
gtt gtg tcc ggc ata agt gca acc tct gag gat att ccc aat aag att Val Val Ser Gly Ile Ser Ala Thr Ser Glu Asp Ile Pro Asn Lys Ile 335 340 345			1057
gaa gac ctg aga tct gag tgc agc tct gat ttt ggg ggt aaa gat tct Glu Asp Leu Arg Ser Glu Cys Ser Ser Asp Phe Gly Gly Lys Asp Ser 350 355 360			1105
gtc act agt cca gac atg gat gaa ata act cac gat ttt ctt tat ata Val Thr Ser Pro Asp Met Asp Glu Ile Thr His Asp Phe Leu Tyr Ile 365 370 375 380			1153
ctt cag cca aaa caa cat ttt caa cac att gaa gca gaa gca gac atg Leu Gln Pro Lys Gln His Phe Gln His Ile Glu Ala Glu Ala Asp Met 385 390 395			1201
aga atc cag ctg tct tct agt gcc cac cag ctg acc tct cct cct tct Arg Ile Gln Leu Ser Ser Ser Ala His Gln Leu Thr Ser Pro Pro Ser 400 405 410			1249
cag tca gag tct ctg ctg gcc atg ttt gat cca ctg tct tca cat gaa Gln Ser Glu Ser Leu Leu Ala Met Phe Asp Pro Leu Ser Ser His Glu 415 420 425			1297
ggg gct tct gct gtg gta agg cca aag gtt cac tat gct agg cca tcg Gly Ala Ser Ala Val Val Arg Pro Lys Val His Tyr Ala Arg Pro Ser 430 435 440			1345
cat cca cca cca gat ccc cca atc ctg gaa gga gct gtg gga gga aat His Pro Pro Pro Asp Pro Pro Ile Leu Glu Gly Ala Val Gly Gly Asn 445 450 455 460 465 470			1393

445	450	455	460	
gag gcc agg ttg cca aac ttt ggt tcc cat gtt tta act cca gct gaa				1441
Glu Ala Arg Leu Pro Asn Phe Gly Ser His Val Leu Thr Pro Ala Glu				
	465	470	475	
atg gag gca ttc aag caa agg cat tct tac cct gag aga cta gtt cga				1489
Met Glu Ala Phe Lys Gln Arg His Ser Tyr Pro Glu Arg Leu Val Arg				
	480	485	490	
agc agg agc tct gat ata gta tct tct gtc cgg aga ccc atg agt gac				1537
Ser Arg Ser Ser Asp Ile Val Ser Ser Val Arg Arg Pro Met Ser Asp				
	495	500	505	
ccc agc tgg aac cgg cgt cca gga aat gaa gag cga gaa ctc cct cca				1585
Pro Ser Trp Asn Arg Arg Pro Gly Asn Glu Glu Arg Glu Leu Pro Pro				
	510	515	520	
gct gca gcc att ggt gct act tct ttg gtg gct gca cct cat tca tca				1633
Ala Ala Ala Ile Gly Ala Thr Ser Leu Val Ala Ala Pro His Ser Ser				
	525	530	535	540
tct tca tcc ccg agt aag gac tcc tca aga gga gag act gaa gaa cgc				1681
Ser Ser Ser Pro Ser Lys Asp Ser Ser Arg Gly Glu Thr Glu Glu Arg				
	545	550	555	
aaa gat agc gat gat gag aaa tca gac agg aac aga cct tgg tgg aga				1729
Lys Asp Ser Asp Asp Glu Lys Ser Asp Arg Asn Arg Pro Trp Trp Arg				
	560	565	570	
aaa cgt ttt gtt tca gcc atg cct aaa gct cct ata cca ttt aga aag				1777
Lys Arg Phe Val Ser Ala Met Pro Lys Ala Pro Ile Pro Phe Arg Lys				
	575	580	585	
aaa gaa aaa caa gaa aaa gac aaa gat gat ctg ggg cct gac aga ttc				1825
Lys Glu Lys Gln Glu Lys Asp Lys Asp Asp Leu Gly Pro Asp Arg Phe				
	590	595	600	
tca aca ctc aca gat gat ccc agc cct aga ctc agt gca caa gct cag				1873
Ser Thr Leu Thr Asp Asp Pro Ser Pro Arg Leu Ser Ala Gln Ala Gln				
	605	610	615	620
gtg gct gag gat att ctg gac aaa tac agg aat gcc att aaa cgg acc				1921
Val Ala Glu Asp Ile Leu Asp Lys Tyr Arg Asn Ala Ile Lys Arg Thr				
	625	630	635	
agc ccc agt gat gga gca atg gca aac tat gaa agt aca gag gtt atg				1969
Ser Pro Ser Asp Gly Ala Met Ala Asn Tyr Glu Ser Thr Glu Val Met				
	640	645	650	
ggt gat ggt gaa agt gca cat gat tct ccc cgt gac gaa gca ctg cag				2017
Gly Asp Gly Glu Ser Ala His Asp Ser Pro Arg Asp Glu Ala Leu Gln				
	655	660	665	
aac atc tcg gct gat gat ctc cca gac tct gca agc caa gca gcc cac				2065
Asn Ile Ser Ala Asp Asp Leu Pro Asp Ser Ala Ser Gln Ala Ala His				
	670	675	680	
ccg cag gat tca gct ttc tct tac aga gat gca aaa aag aaa ctg agg				2113
Pro Gln Asp Ser Ala Phe Ser Tyr Arg Asp Ala Lys Lys Lys Leu Arg				
	685	690	695	700
ctt gct ctt tgc tct gcg gac tct gtt gcc ttc cca gtg ctg acc cat				2161
Leu Ala Leu Cys Ser Ala Asp Ser Val Ala Phe Pro Val Leu Thr His				

2106

960	965	970	
ctg aga atg tgc tct acg att atg aac ctc ctg agc ctg gcc aat gag			2977
Leu Arg Met Cys Ser Thr Ile Met Asn Leu Leu Ser Leu Ala Asn Glu			
975	980	985	
gac tct gtc cct gga gcg gat gac ttt gtt cct gtg ttg gtg ttt gtg			3025
Asp Ser Val Pro Gly Ala Asp Asp Phe Val Pro Val Leu Val Phe Val			
990	995	1000	
ttg ata aag gca aat cca ccc tgt ttg ctg tct act gtg cag tat atc			3073
Leu Ile Lys Ala Asn Pro Pro Cys Leu Leu Ser Thr Val Gln Tyr Ile			
1005	1010	1015	1020
agt agc ttt tat gct agc tgt ctg tct gga gag gag tcc tat tgg tgg			3121
Ser Ser Phe Tyr Ala Ser Cys Leu Ser Gly Glu Glu Ser Tyr Trp Trp			
1025	1030	1035	
atg cag ttc aca gca gca gta gaa ttc att aaa acc atc gat gac cga			3169
Met Gln Phe Thr Ala Ala Val Glu Phe Ile Lys Thr Ile Asp Asp Arg			
1040	1045	1050	
aag tga ccaagaccaa ggcccaccaa ggcagcagac tgттаатсag асааасаgаt			3225
Lys *			
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	1 5 10		

gcc aag cca gga aaa agt agc agt tta gaa atg act ccc tac aat aca	97
Ala Lys Pro Gly Lys Ser Ser Ser Leu Glu Met Thr Pro Tyr Asn Thr	
15 20 25	
cct cag cta tct cca gca acc act cca gca aat aaa aag aat cga tta	145
Pro Gln Leu Ser Pro Ala Thr Thr Pro Ala Asn Lys Lys Asn Arg Leu	
30 35 40	
cct ata gca act cgg agc aga agc cgc acc aat atg cta atg gac cta	193
Pro Ile Ala Thr Arg Ser Arg Ser Arg Thr Asn Met Leu Met Asp Leu	
45 50 55 60	
cat atg gac cat gaa gga tca tct caa gaa acc atc cag gag gtg caa	241
His Met Asp His Glu Gly Ser Ser Gln Glu Thr Ile Gln Glu Val Gln	
65 70 75	
cca gaa gag gtg ttg gtc att tcc tta ggt aca ggt ccc cag ctt act	289
Pro Glu Glu Val Leu Val Ile Ser Leu Gly Thr Gly Pro Gln Leu Thr	
80 85 90	
cca ggg atg atg tca gaa aat gag gtc cta aac atg cag ctt tcg gat	337
Pro Gly Met Met Ser Glu Asn Glu Val Leu Asn Met Gln Leu Ser Asp	
95 100 105	
gga gga caa gga gat gtc cct gtt gat gaa aac aaa ctc cat ggt aaa	385
Gly Gly Gln Gly Asp Val Pro Val Asp Glu Asn Lys Leu His Gly Lys	
110 115 120	
cct gat aaa acc ttg cgc ttt tcc ctc tgc agt gat aat ctg gaa gga	433
Pro Asp Lys Thr Leu Arg Phe Ser Leu Cys Ser Asp Asn Leu Glu Gly	
125 130 135 140	
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Ile Ser Glu Gly Pro Ser Asn Arg Ser Asn Ser Val Ser Ser Leu Asp	
145 150 155	
cta gaa gga gag tct gtg tca gaa ctt gga gca gga cct tct ggc agt	529
Leu Glu Gly Glu Ser Val Ser Glu Leu Gly Ala Gly Pro Ser Gly Ser	
160 165 170	
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Asn Gly Val Glu Ala Leu Gln Leu Glu His Glu Gln Ala Thr Thr	
175 180 185	
cag gat aac ctt gat gat aag cta agg aag ttt gaa att cgt gac atg	625
Gln Asp Asn Leu Asp Asp Lys Leu Arg Lys Phe Glu Ile Arg Asp Met	
190 195 200	
atg gga tta aca gat gat agg gac ata tca gaa aca gtg agt gag acc	673
Met Gly Leu Thr Asp Asp Arg Asp Ile Ser Glu Thr Val Ser Glu Thr	
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Trp Ser Thr Asp Val Leu Gly Ser Asp Phe Asp Pro Asn Ile Asp Glu	
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gat cgc ttg caa gaa att gca ggt gct gca gca gag aac atg tta ggc	769
Asp Arg Leu Gln Glu Ile Ala Gly Ala Ala Ala Glu Asn Met Leu Gly	
240 245 250	
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Ser Leu Leu Cys Leu Pro Gly Ser Gly Ser Val Leu Leu Asp Pro Cys	
255 260 265	

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ctg caa gaa ctg gag agc tgt tct gga ctg ggt agc aca tct gat gat Leu Gln Glu Leu Glu Ser Cys Ser Gly Leu Gly Ser Thr Ser Asp Asp 305 310 315	961
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gaa gac ctg aga tct gag tgc agc tct gat ttt ggg ggt aaa gat tct Glu Asp Leu Arg Ser Glu Cys Ser Ser Asp Phe Gly Gly Lys Asp Ser 350 355 360	1105
gtc act agt cca gac atg gat gaa ata act cac ggt gcc cac cag ctg Val Thr Ser Pro Asp Met Asp Glu Ile Thr His Gly Ala His Gln Leu 365 370 375 380	1153
acc tct cct cct tct cag tca gag tct ctg ctg gcc atg ttt gat cca Thr Ser Pro Pro Ser Gln Ser Glu Ser Leu Leu Ala Met Phe Asp Pro 385 390 395	1201
ctg tct tca cat gaa ggg gct tct gct gtg gta agg cca aag gtt cac Leu Ser Ser His Glu Gly Ala Ser Ala Val Val Arg Pro Lys Val His 400 405 410	1249
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gct gtg gga gga aat gag gcc agg ttg cca aac ttt ggt tcc cat gtt Ala Val Gly Gly Asn Glu Ala Arg Leu Pro Asn Phe Gly Ser His Val 430 435 440	1345
tta act cca gct gaa atg gag gca ttc aag caa agg cat tct tac cct Leu Thr Pro Ala Glu Met Glu Ala Phe Lys Gln Arg His Ser Tyr Pro 445 450 455 460	1393
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aga ccc atg agt gac ccc agc tgg aac cgg cgt cca gga aat gaa gag Arg Pro Met Ser Asp Pro Ser Trp Asn Arg Arg Pro Gly Asn Glu Glu 480 485 490	1489
cga gaa ctc cct cca gct gca gcc att ggt gct act tct ttg gtg gct Arg Glu Leu Pro Pro Ala Ala Ala Ile Gly Ala Thr Ser Leu Val Ala 495 500 505	1537
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Glu Thr Glu Glu Arg Lys Asp Ser Asp Asp Glu Lys Ser Asp Arg Asn	
525 530 535 540	
aga cct tgg tgg aga aaa cgt ttt gtt tca gcc atg cct aaa gct cct	1681
Arg Pro Trp Trp Arg Lys Arg Phe Val Ser Ala Met Pro Lys Ala Pro	
545 550 555	
ata cca ttt aga aag aaa gaa aaa caa gaa aaa gac aaa gat gat ctg	1729
Ile Pro Phe Arg Lys Lys Glu Lys Gln Glu Lys Asp Lys Asp Asp Leu	
560 565 570	
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Gly Pro Asp Arg Phe Ser Thr Leu Thr Asp Asp Pro Ser Pro Arg Leu	
575 580 585	
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Ser Ala Gln Ala Gln Val Ala Glu Asp Ile Leu Asp Lys Tyr Arg Asn	
590 595 600	
gcc att aaa cgg acc agc ccc agt gat gga gca atg gca aac tat gaa	1873
Ala Ile Lys Arg Thr Ser Pro Ser Asp Gly Ala Met Ala Asn Tyr Glu	
605 610 615 620	
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Ser Thr Glu Val Met Gly Asp Gly Glu Ser Ala His Asp Ser Pro Arg	
625 630 635	
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Asp Glu Ala Leu Gln Asn Ile Ser Ala Asp Asp Leu Pro Asp Ser Ala	
640 645 650	
agc caa gca gcc cac ccg cag gat tca gct ttc tct tac aga gat gca	2017
Ser Gln Ala Ala His Pro Gln Asp Ser Ala Phe Ser Tyr Arg Asp Ala	
655 660 665	
aaa aag aaa ctg agg ctt gct ctt tgc tct gcg gac tct gtt gcc ttc	2065
Lys Lys Lys Leu Arg Leu Ala Leu Cys Ser Ala Asp Ser Val Ala Phe	
670 675 680	
cca gtg ctg acc cat tca aca agg aat ggt tta cca gac cac aca gac	2113
Pro Val Leu Thr His Ser Thr Arg Asn Gly Leu Pro Asp His Thr Asp	
685 690 695 700	
cca gaa gac aat gaa att gta tgc ttc tta aaa gtt caa ata gct gaa	2161
Pro Glu Asp Asn Glu Ile Val Cys Phe Leu Lys Val Gln Ile Ala Glu	
705 710 715	
gca att aat tta caa gat aag aat cta atg gct caa ctt caa gaa aca	2209
Ala Ile Asn Leu Gln Asp Lys Asn Leu Met Ala Gln Leu Gln Glu Thr	
720 725 730	
atg cgc tgt gtg tgc cgt ttt gat aat agg act tgt agg aaa ctg ctg	2257
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cct cag cta tct cca gca acc act cca gca aat aaa aag aat cga tta 145
Pro Gln Leu Ser Pro Ala Thr Thr Pro Ala Asn Lys Lys Asn Arg Leu
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Pro Ile Ala Thr Arg Ser Arg Ser Arg Thr Asn Met Leu Met Asp Leu
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Pro Gly Met Met Ser Glu Asn Glu Val Leu Asn Met Gln Leu Ser Asp
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Gln Ser Glu Ser Leu Leu Ala Met Phe Asp Pro Leu Ser Ser His Glu	
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Ile Val Asn Leu Phe Val Asn Glu Ser Val Thr Asn Ala Thr Leu Ile	
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Asn Glu Leu Val Arg Lys Ser Thr Glu Ala Pro Val Thr Pro Asn Thr	
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Met Asp Phe Val Phe Ser Leu Val Asn Ser Phe Leu Gly Glu Phe Leu
1 5 10 15
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Phe Asp Ile Ala Arg Asn Val Leu Glu Leu Ile Tyr Ala Gln Thr Leu
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Phe Phe Ile Phe Leu Leu Phe Phe Pro Ser Phe Thr Gly Val Leu Cys
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Val Leu Ile Ile Thr Tyr Leu Tyr Trp Gln Ile Thr Glu Gly Arg Lys	
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Ile Met Ile Arg Leu Leu His Glu Gln Ile Ile Asn Glu Gly Lys Asp	
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Gly Lys Ala Ala Ala Thr Gln Pro Ala Lys Ser Pro Gly Ala Gln Leu	20 25 30	
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Lys Ile His Ser Val Asp Gln Gly Ala Glu His Met Leu Ile Leu Ser	100 105 110	
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Ser Asp Gly Lys Pro Phe Glu Tyr Asp Asn Tyr Ser Met Lys His Leu	115 120 125	
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Trp Gly Gln Asn Leu His Gly Gln Leu Gly Val Gly Arg Lys Phe Pro	165 170 175	
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Gly His Thr Glu Ser Lys Asp Asp Pro Ser Leu Ile Glu Gly Leu Asp		

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Ile	Phe	Ser	Ser	Pro	Ala	Cys	Leu	Thr	Gly	Ser	Phe	Leu	Arg	Lys	Arg														
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Arg	Thr	Thr	Glu	Met	Met	Pro	Val	Tyr	Leu	Asp	Leu	Asn	Lys	Ala	Arg														
			435				440				445																		
aac	atc	ttc	agg	gag	tta	acc	caa	aag	gac	tgg	att	act	aac	atg	ata	1508													
Asn	Ile	Phe	Arg	Glu	Leu	Thr	Gln	Lys	Asp	Trp	Ile	Thr	Asn	Met	Ile														
			450			455				460				465															
acc	acc	tgc	ctc	aaa	gat	aat	ctg	ctc	aaa	aga	ctt	cca	ttt	cat	tct	1556													
Thr	Thr	Cys	Leu	Lys	Asp	Asn	Leu	Leu	Lys	Arg	Leu	Pro	Phe	His	Ser														
			470					475					480																
cca	ccc	caa	gaa	gct	tta	gaa	att	ttc	ttc	ctt	ctc	cca	gaa	tgt	cct	1604													
Pro	Pro	Gln	Glu	Ala	Leu	Glu	Ile	Phe	Phe	Leu	Leu	Pro	Glu	Cys	Pro														

485	490	495	
gtg atg cat att tcc aac aac tgg gag agc ctt gtg gtt cca ttt gca Val Met His Ile Ser Asn Asn Trp Glu Ser Leu Val Val Pro Phe Ala 500 505 510			1652
aag gtt gtt tgt aaa atg agt gac cag tct tca ctg gtt ctg gaa gag Lys Val Val Cys Lys Met Ser Asp Gln Ser Ser Leu Val Leu Glu Glu 515 520 525			1700
tat tgg gca act ctg caa gaa tcc act ttc agc aaa ctg gtc cag atg Tyr Trp Ala Thr Leu Gln Glu Ser Thr Phe Ser Lys Leu Val Gln Met 530 535 540 545			1748
ttt aaa aca gcc gtc ata tgc cag ttg gat tac tgg gat gaa agt gct Phe Lys Thr Ala Val Ile Cys Gln Leu Asp Tyr Trp Asp Glu Ser Ala 550 555 560			1796
gag gag aat ggt aat gtt caa gct ctc cta gaa atg ttg aag aag ctg Glu Glu Asn Gly Asn Val Gln Ala Leu Leu Glu Met Leu Lys Lys Leu 565 570 575			1844
cac agg gta aac cag gtg aaa tgt caa cta cct gaa agt att ttc caa His Arg Val Asn Gln Val Lys Cys Gln Leu Pro Glu Ser Ile Phe Gln 580 585 590			1892
gta gac gaa ctc ttg cac cgt ctc aat ttt ttt gta gaa gta tgc aga Val Asp Glu Leu Leu His Arg Leu Asn Phe Phe Val Glu Val Cys Arg 595 600 605			1940
agg tac ttg tgg aaa atg act gtg gac gct tca gaa aat gta caa tgc Arg Tyr Leu Trp Lys Met Thr Val Asp Ala Ser Glu Asn Val Gln Cys 610 615 620 625			1988
tgc gtc ata ttc agt cac ttt cca ttt atc ttt aat aat ctg tcg aaa Cys Val Ile Phe Ser His Phe Pro Phe Ile Phe Asn Asn Leu Ser Lys 630 635 640			2036
att aaa cta cta cat aca gac aca ctt tta aaa ata gag agt aaa aaa Ile Lys Leu Leu His Thr Asp Thr Leu Leu Lys Ile Glu Ser Lys Lys 645 650 655			2084
cat aaa gct tat ctt agg tcg gca gca att gag gaa gaa aga gag tct His Lys Ala Tyr Leu Arg Ser Ala Ala Ile Glu Glu Glu Arg Glu Ser 660 665 670			2132
gaa ttc gct ttg agg ccc acg ttt gat cta aca gtc aga agg aat cac Glu Phe Ala Leu Arg Pro Thr Phe Asp Leu Thr Val Arg Arg Asn His 675 680 685			2180
ttg att gag gat gtt ttg aat cag cta agt caa ttt gag aat gaa gac Leu Ile Glu Asp Val Leu Asn Gln Leu Ser Gln Phe Glu Asn Glu Asp 690 695 700 705			2228
ctg agg aaa gag tta tgg gtt tca ttt agt gga gaa att ggg tat gac Leu Arg Lys Glu Leu Trp Val Ser Phe Ser Gly Glu Ile Gly Tyr Asp 710 715 720			2276
ctc gga gga gtc aag aaa gag ttc ttc tac tgt ctg ttt gca gag atg Leu Gly Gly Val Lys Lys Glu Phe Phe Tyr Cys Leu Phe Ala Glu Met 725 730 735			2324
atc cag ccg gaa tat ggg atg ttc atg tat cct gaa ggg gct tcc tgc Ile Gln Pro Glu Tyr Gly Met Phe Met Tyr Pro Glu Gly Ala Ser Cys			2372

740	745	750	
atg tgg ttt cct gtc aag cct aaa ttt gag aag aaa aga tac ttc ttt Met Trp Phe Pro Val Lys Pro Lys Phe Glu Lys Lys Arg Tyr Phe Phe 755 760 765			2420
ttt ggg gtt cta tgt gga ctt tcc ctg ttc aat tgc aat gtt gcc aac Phe Gly Val Leu Cys Gly Leu Ser Leu Phe Asn Cys Asn Val Ala Asn 770 775 780 785			2468
ctc cct ttc cca ctg gca ctg ttt aag aaa ctt ttg gac caa atg cca Leu Pro Phe Pro Leu Ala Leu Phe Lys Lys Leu Leu Asp Gln Met Pro 790 795 800			2516
tca ttg gaa gac ttg aaa gaa ctc agt cct gat ttg gga aag aat ttg Ser Leu Glu Asp Leu Lys Glu Leu Ser Pro Asp Leu Gly Lys Asn Leu 805 810 815			2564
caa aca ctt ctg gat gat gaa ggt gat aac ttt gag gaa gta ttt tac Gln Thr Leu Leu Asp Asp Glu Gly Asp Asn Phe Glu Glu Val Phe Tyr 820 825 830			2612
atc cat ttt aat gtg cac tgg gac aga aac gac aca aac tta att cct Ile His Phe Asn Val His Trp Asp Arg Asn Asp Thr Asn Leu Ile Pro 835 840 845			2660
aat gga agt agc ata act gtc aac cag act aac aag aga gac tat gtt Asn Gly Ser Ser Ile Thr Val Asn Gln Thr Asn Lys Arg Asp Tyr Val 850 855 860 865			2708
tct aag tat atc aat tac att ttc aac gac tct gta aag gcg gtt tat Ser Lys Tyr Ile Asn Tyr Ile Phe Asn Asp Ser Val Lys Ala Val Tyr 870 875 880			2756
gaa gaa ttt cgg aga gga ttt tat aaa atg tgc gac gaa gac att atc Glu Glu Phe Arg Arg Gly Phe Tyr Lys Met Cys Asp Glu Asp Ile Ile 885 890 895			2804
aaa tta ttc cac ccc gaa gaa ctg aag gat gtg att gtt gga aat aca Lys Leu Phe His Pro Glu Glu Leu Lys Asp Val Ile Val Gly Asn Thr 900 905 910			2852
gat tat gat tgg aaa aca ttt gaa aag aat gca cgt tat gaa cca gga Asp Tyr Asp Trp Lys Thr Phe Glu Lys Asn Ala Arg Tyr Glu Pro Gly 915 920 925			2900
tat aac agt tca cat ccc acc ata gtg atg ttt tgg aag gct ttc cac Tyr Asn Ser Ser His Pro Thr Ile Val Met Phe Trp Lys Ala Phe His 930 935 940 945			2948
aaa ttg act ctg gaa gaa aag aaa aaa ttc ctt gta ttt ctt aca gga Lys Leu Thr Leu Glu Glu Lys Lys Lys Phe Leu Val Phe Leu Thr Gly 950 955 960			2996
act gac aga cta caa atg aaa gat tta aat aat atg aaa ata aca ttt Thr Asp Arg Leu Gln Met Lys Asp Leu Asn Asn Met Lys Ile Thr Phe 965 970 975			3044
tgc tgt cct gaa agt tgg aat gaa aga gac cct ata aga gca ctg aca Cys Cys Pro Glu Ser Trp Asn Glu Arg Asp Pro Ile Arg Ala Leu Thr 980 985 990			3092
tgt ttc agt gtc ctc ttc ctc cct aaa tat tct aca atg gaa aca gtt Cys Phe Ser Val Leu Phe Leu Pro Lys Tyr Ser Thr Met Glu Thr Val			3140

995	1000	1005	
gaa gaa gcg ctt caa gaa gcc atc aac aac aac aga gga ttt ggc tga			3188
Glu Glu Ala Leu Gln Glu Ala Ile Asn Asn Asn Arg Gly Phe Gly *			
1010	1015	1020	1025
ccagcttgct tgtccaacag ccttattttg ttgttggtat cgttggtggt gttgttggtg			3248
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atttctgtct ctagtataa gcaggaaaga gggatgaaga agagggttta ctggccggtt			3368
agaaccctgt actgtattct ctcccttgga taccctatg cctacatcat attccttacc			3428
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Pro Leu Leu Thr Val Arg Gly Ser Glu Gly Leu Tyr Met Val Asn Gly			
10 15 20			
cca cca cat ttt aca gaa agc aca gtg ttt cca agg gaa tct ggg aag		149	
Pro Pro His Phe Thr Glu Ser Thr Val Phe Pro Arg Glu Ser Gly Lys			
25 30 35			
aat tgc aaa gtc tgt atc ttt agt aag gat ggg acc ttg ttt gcc tgg		197	
Asn Cys Lys Val Cys Ile Phe Ser Lys Asp Gly Thr Leu Phe Ala Trp			
40 45 50			
ggc aat gga gaa aaa gta aat att atc agt gtc act aac aag gga cta		245	
Gly Asn Gly Glu Lys Val Asn Ile Ile Ser Val Thr Asn Lys Gly Leu			
55 60 65			
ctg cac tcc ttc gac ctc ctg aag gca gtt tgc ctt gaa ttc tca ccc		293	
Leu His Ser Phe Asp Leu Leu Lys Ala Val Cys Leu Glu Phe Ser Pro			
70 75 80 85			
aaa aat act gtc ctg gca acg tgg cag cct tac agt act tct aaa gat		341	
Lys Asn Thr Val Leu Ala Thr Trp Gln Pro Tyr Ser Thr Ser Lys Asp			
90 95 100			
ggc aca gct ggg ata ccc aac cta caa ctt tat gat gtg aaa act ggg		389	
Gly Thr Ala Gly Ile Pro Asn Leu Gln Leu Tyr Asp Val Lys Thr Gly			
105 110 115			
aca tgt ttg aaa tct ttc atc cag aaa aaa atg caa aat tgg tgt cca		437	
Thr Cys Leu Lys Ser Phe Ile Gln Lys Lys Met Gln Asn Trp Cys Pro			
120 125 130			

tcc tgg tca gaa gat gaa act ctt tgt gcc cgc aat gtt aac aat gaa Ser Trp Ser Glu Asp Glu Thr Leu Cys Ala Arg Asn Val Asn Asn Glu 135 140 145	485
gtt cac ttc ttt gaa aac aac aat ttt aac aca att gca aat aaa ttg Val His Phe Phe Glu Asn Asn Asn Phe Asn Thr Ile Ala Asn Lys Leu 150 155 160 165	533
cat ttg caa aaa att aat gat ttt gta tta tca cct gga ccc caa cca His Leu Gln Lys Ile Asn Asp Phe Val Leu Ser Pro Gly Pro Gln Pro 170 175 180	581
tac aag gtg gct gtc tat gtt cca gga agt aaa ggt gca cct tca ttt Tyr Lys Val Ala Val Tyr Val Pro Gly Ser Lys Gly Ala Pro Ser Phe 185 190 195	629
gtt aga tta tat cag tac ccc aac ttt gct gga cct cat gca gct tta Val Arg Leu Tyr Gln Tyr Pro Asn Phe Ala Gly Pro His Ala Ala Leu 200 205 210	677
gct aat aaa agt ttc ttt aag gca gat aaa gtt aca atg ctg tgg aat Ala Asn Lys Ser Phe Phe Lys Ala Asp Lys Val Thr Met Leu Trp Asn 215 220 225	725
aaa aaa gct act gct gtg ttg gta ata gct agc aca gat gtt gac aag Lys Lys Ala Thr Ala Val Leu Val Ile Ala Ser Thr Asp Val Asp Lys 230 235 240 245	773
aca gga gct tcc tac tat gga gaa caa act cta cac tac att gca aca Thr Gly Ala Ser Tyr Tyr Gly Glu Gln Thr Leu His Tyr Ile Ala Thr 250 255 260	821
aat gga gaa agt gct gta gtg caa tta cca aaa aat ggc ccc att tat Asn Gly Glu Ser Ala Val Val Gln Leu Pro Lys Asn Gly Pro Ile Tyr 265 270 275	869
gat gta gtt tgg aat tct agt tct act gag ttt tgt gct gta tat ggt Asp Val Val Trp Asn Ser Ser Ser Thr Glu Phe Cys Ala Val Tyr Gly 280 285 290	917
ttt atg cct gcc aaa gcg aca att ttc aac ttg aaa tgt gat cct gta Phe Met Pro Ala Lys Ala Thr Ile Phe Asn Leu Lys Cys Asp Pro Val 295 300 305	965
ttt gac ttt gga act ggt cct cgt aat gca gcc tac tat agc cct cat Phe Asp Phe Gly Thr Gly Pro Arg Asn Ala Ala Tyr Tyr Ser Pro His 310 315 320 325	1013
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gaa gtg tgg gat gtg aaa aac tac aaa ctt att tct aaa ccg gtg gct Glu Val Trp Asp Val Lys Asn Tyr Lys Leu Ile Ser Lys Pro Val Ala 345 350 355	1109
tct gat tct aca tat ttt gct tgg tgc ccg gat ggt gag cat att tta Ser Asp Ser Thr Tyr Phe Ala Trp Cys Pro Asp Gly Glu His Ile Leu 360 365 370	1157
aca gct aca tgt gct ccc agg tta cgg gtt aat aat gga tac aaa att Thr Ala Thr Cys Ala Pro Arg Leu Arg Val Asn Asn Gly Tyr Lys Ile 375 380 385	1205

tgg cat tat act ggc tct atc ttg cac aag tat gat gtg cca tca aat	1253
Trp His Tyr Thr Gly Ser Ile Leu His Lys Tyr Asp Val Pro Ser Asn	
390 395 400 405	
gca gaa tta tgg cag gtt tct tgg cag cca ttt ttg gat gga ata ttt	1301
Ala Glu Leu Trp Gln Val Ser Trp Gln Pro Phe Leu Asp Gly Ile Phe	
410 415 420	
cca gca aaa aca ata act tac caa gca gtt cca agt gaa gta ccc aat	1349
Pro Ala Lys Thr Ile Thr Tyr Gln Ala Val Pro Ser Glu Val Pro Asn	
425 430 435	
gag gaa cct aaa gtt gca aca gct tat aga ccc cca gct tta aga aat	1397
Glu Glu Pro Lys Val Ala Thr Tyr Arg Pro Pro Ala Leu Arg Asn	
440 445 450	
aaa cca atc acc aat tcc aaa ttg cat gaa gag gaa cca cct cag aat	1445
Lys Pro Ile Thr Asn Ser Lys Leu His Glu Glu Glu Pro Pro Gln Asn	
455 460 465	
atg aaa cca caa tca gga aac gat aag cca tta tca aaa aca gct ctt	1493
Met Lys Pro Gln Ser Gly Asn Asp Lys Pro Leu Ser Lys Thr Ala Leu	
470 475 480 485	
aaa aat caa agg aag cat gaa gct aag aaa gct gca aag cag gaa gca	1541
Lys Asn Gln Arg Lys His Glu Ala Lys Lys Ala Ala Lys Gln Glu Ala	
490 495 500	
aga agt gac aag agt cca gat ttg gca cct act cct gcc cca cag agc	1589
Arg Ser Asp Lys Ser Pro Asp Leu Ala Pro Thr Pro Ala Pro Gln Ser	
505 510 515	
aca cca cga aac act gtc tct cag tca att tct ggg gac cct gag ata	1637
Thr Pro Arg Asn Thr Val Ser Gln Ser Ile Ser Gly Asp Pro Glu Ile	
520 525 530	
gac aaa aaa atc aag aac cta aag aag aaa ctg aaa gca atc gaa caa	1685
Asp Lys Lys Ile Lys Asn Leu Lys Lys Lys Leu Lys Ala Ile Glu Gln	
535 540 545	
ctg aaa gaa caa gca gca act gga aaa cag cta gaa aaa aat cag ttg	1733
Leu Lys Glu Gln Ala Ala Thr Gly Lys Gln Leu Glu Lys Asn Gln Leu	
550 555 560 565	
gag aaa att cag aaa gaa aca gcc ctt ctc cag gag ctg gaa gat ttg	1781
Glu Lys Ile Gln Lys Glu Thr Ala Leu Leu Gln Glu Leu Glu Asp Leu	
570 575 580	
gaa ttg ggt att taa agattcacgg aaagcaagtt gatgaccaga aatcagtgca	1836
Glu Leu Gly Ile *	
585	
aacacatctt ctgttaaacc cattggtata cacagaatat tcctgtgccc acacttaatg	1896
tcaatctata attttaacca tttatccaag attctactaa gtgtaaaatt atttaataat	1956
gtctattaaa ttgatattta tatcttgcat cctatatcat gtcaatatgt gatatagaaa	2016
agagatacgt gaatttttta gctaagcttg acagattgaa agacaagtgt catttttttt	2076
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 Met Gly Thr Pro Arg Ala Gln His Pro
 1 5
 ccg cct ccc cag ctg ctg ttc cta att ctg ctg agc tgt ccc tgg atc 159
 Pro Pro Pro Gln Leu Leu Phe Leu Ile Leu Leu Ser Cys Pro Trp Ile
 10 15 20 25
 cag ggt ctg ccc ctg aag gag gag gag ata ttg cca gag cct gga agt 207
 Gln Gly Leu Pro Leu Lys Glu Glu Glu Ile Leu Pro Glu Pro Gly Ser
 30 35 40
 gag acc ccc acg gtg gcc tct gag gcc ctg gct gaa ctg ctt cat ggg 255
 Glu Thr Pro Thr Val Ala Ser Glu Ala Leu Ala Glu Leu His Gly
 45 50 55
 gcc ctg ctg agg agg ggc cca gag atg ggc tac ctg cca ggg cct ccc 303
 Ala Leu Leu Arg Arg Gly Pro Glu Met Gly Tyr Leu Pro Gly Pro Pro
 60 65 70
 ctt ggg cct gag gga gga gag gag gag acg acg acc acc atc atc acc 351
 Leu Gly Pro Glu Gly Gly Glu Glu Glu Thr Thr Thr Thr Ile Ile Thr
 75 80 85
 acg aca act gtt acc act acg gtg acc agc cca gtt ctg tgt aat aac 399
 Thr Thr Thr Val Thr Thr Val Thr Ser Pro Val Leu Cys Asn Asn
 90 95 100 105
 aac atc tcc gag ggc gaa ggg tat gtg gag tct cca gat ctg ggg agc 447
 Asn Ile Ser Glu Gly Glu Gly Tyr Val Glu Ser Pro Asp Leu Gly Ser
 110 115 120
 ccc gtc agc cgc acc ctg ggg ctc ctg gac tgc act tac agc atc cat 495
 Pro Val Ser Thr Leu Gly Leu Leu Asp Cys Thr Tyr Ser Ile His
 125 130 135
 gtc tac cct ggc tac ggc att gag atc cag gtg cag acg ctg aac ctg 543
 Val Tyr Pro Gly Tyr Gly Ile Glu Ile Gln Val Gln Thr Leu Asn Leu
 140 145 150
 tca cag gaa gag gag ctc ctg gtg ctg gct ggt ggg gga tcc cca ggc 591
 Ser Gln Glu Glu Glu Leu Leu Val Leu Ala Gly Gly Gly Ser Pro Gly
 155 160 165
 ctg gcc ccc cga ctc ctg gcc aac tca tcc atg ctt gga gaa gga caa 639
 Leu Ala Pro Arg Leu Leu Ala Asn Ser Ser Met Leu Gly Glu Gly Gln
 170 175 180 185

gtc ctt cgg agc cca acc aac cgg ctg ctt ctg cac ttc cag agc cca	687
Val Leu Arg Ser Pro Thr Asn Arg Leu Leu Leu His Phe Gln Ser Pro	
190 195 200	
cgg gtc cca agg ggc ggt ggc ttc agg atc cac tat cag gcc tac ctc	735
Arg Val Pro Arg Gly Gly Gly Phe Arg Ile His Tyr Gln Ala Tyr Leu	
205 210 215	
ctg agc tgt ggc ttc cct ccc cgg ccg gcc cat ggg gac gtg agt gtg	783
Leu Ser Cys Gly Phe Pro Pro Arg Pro Ala His Gly Asp Val Ser Val	
220 225 230	
acg gac ctg cac cct ggg ggc act gcc acc ttt cac tgt gat tcg ggc	831
Thr Asp Leu His Pro Gly Gly Thr Ala Thr Phe His Cys Asp Ser Gly	
235 240 245	
tac cag ctg cag gga gag gag acc ctc atc tgc ctc aat ggc acc cgg	879
Tyr Gln Leu Gln Gly Glu Glu Thr Leu Ile Cys Leu Asn Gly Thr Arg	
250 255 260 265	
cca tcc tgg aac ggt gaa acc ccc agc tgc atg gca tcc tgt ggt ggc	927
Pro Ser Trp Asn Gly Glu Thr Pro Ser Cys Met Ala Ser Cys Gly Gly	
270 275 280	
acc atc cac aat gcc acc ctg ggc cgc atc gtg tcc cca gag cct ggg	975
Thr Ile His Asn Ala Thr Leu Gly Arg Ile Val Ser Pro Glu Pro Gly	
285 290 295	
gga gcc gta ggg ccc aac ctc acc tgc cgt tgg gtc att gaa gca gct	1023
Gly Ala Val Gly Pro Asn Leu Thr Cys Arg Trp Val Ile Glu Ala Ala	
300 305 310	
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Glu Gly Arg Arg Leu His Leu His Phe Glu Arg Val Ser Leu Asp Glu	
315 320 325	
gac aat gac cgg ctg atg gtg cgc tca ggg ggc agc ccc cta tcc ccc	1119
Asp Asn Asp Arg Leu Met Val Arg Ser Gly Gly Ser Pro Leu Ser Pro	
330 335 340 345	
gtg atc tat gat tcg gac atg gac gat gtc ccc gag cgg ggt ctc atc	1167
Val Ile Tyr Asp Ser Asp Met Asp Asp Val Pro Glu Arg Gly Leu Ile	
350 355 360	
agt gac gcc cag tcc ctc tac gtg gag ctg ctg tca gag aca cct gcc	1215
Ser Asp Ala Gln Ser Leu Tyr Val Glu Leu Leu Ser Glu Thr Pro Ala	
365 370 375	
aat ccc ctg ctg tta agc ctt cga ttt gaa gcc ttt gag gag gat cgc	1263
Asn Pro Leu Leu Leu Ser Leu Arg Phe Glu Ala Phe Glu Glu Asp Arg	
380 385 390	
tgc ttc gcc ccc ttc ctg gca cat gga aat gtc act acc acg gac cct	1311
Cys Phe Ala Pro Phe Leu Ala His Gly Asn Val Thr Thr Thr Asp Pro	
395 400 405	
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Glu Tyr Arg Pro Gly Ala Leu Ala Thr Phe Ser Cys Leu Pro Gly Tyr	
410 415 420 425	
gcc ctg gag ccc cct ggg ccc ccc aat gcc atc gaa tgt gtg gat ccc	1407
Ala Leu Glu Pro Gly Pro Pro Asn Ala Ile Glu Cys Val Asp Pro	
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Thr Glu Pro His Trp Asn Asp Thr Glu Pro Ala Cys Lys Ala Met Cys	
445 450 455	
gga ggg gag ctg tgc gaa cca gct ggc gtg gtc ctc tct ccc gac tgg	1503
Gly Gly Glu Leu Ser Glu Pro Ala Gly Val Val Leu Ser Pro Asp Trp	
460 465 470	
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Pro Gln Ser Tyr Ser Pro Gly Gln Asp Cys Val Trp Gly Val His Val	
475 480 485	
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Glu Gly Asp Met Leu Thr Leu Phe Asp Gly Asp Gly Pro Ser Ala Arg	
510 515 520	
gtc ttg gcc cag ctg cgg gga cct cag ccg cgc cgc cgc ctt ctc tcc	1695
Val Leu Ala Gln Leu Arg Gly Pro Gln Pro Arg Arg Arg Leu Leu Ser	
525 530 535	
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Ser Gly Pro Asp Leu Thr Leu Gln Phe Gln Ala Pro Pro Gly Pro Pro	
540 545 550	
aat cca ggc ctg ggc cag ggc ttc gta ttg cac ttc aaa gag gtc ccg	1791
Asn Pro Gly Leu Gly Gln Gly Phe Val Leu His Phe Lys Glu Val Pro	
555 560 565	
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Arg Asn Asp Thr Cys Pro Glu Leu Pro Pro Pro Glu Trp Gly Trp Arg	
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Thr Ala Ser His Gly Asp Leu Ile Arg Gly Thr Val Leu Thr Tyr Gln	
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Cys Glu Pro Gly Tyr Glu Leu Leu Gly Ser Asp Ile Leu Thr Cys Gln	
605 610 615	
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Trp Asp Leu Ser Trp Ser Ala Ala Pro Pro Ala Cys Gln Lys Ile Met	
620 625 630	
act tgt gct gac cct ggc gag att gcc aac ggg cac cgc acc gcc tcg	2031
Thr Cys Ala Asp Pro Gly Glu Ile Ala Asn Gly His Arg Thr Ala Ser	
635 640 645	
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Asp Ala Gly Phe Pro Val Gly Ser His Val Gln Tyr Arg Cys Leu Pro	
650 655 660 665	
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Gly Tyr Ser Leu Glu Gly Ala Ala Met Leu Thr Cys Tyr Ser Arg Asp	
670 675 680	
aca ggc aca ccc aag tgg agc gat agg gtc ccc aaa tgc gcc ttg aag	2175
Thr Gly Thr Pro Lys Trp Ser Asp Arg Val Pro Lys Cys Ala Leu Lys	
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 Gly His Pro Ser Gln Trp Thr Ser Gln Pro Pro Leu Cys Lys Val Thr
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 Gln Thr Thr Asp Pro Ser Arg Gln Leu Glu Gly Gly Asn Leu Ala Leu
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gcc atc ctg ctg cct cta ggc ttg gtc att gtc ctc ggc agt ggc gtt 2463
 Ala Ile Leu Leu Pro Leu Gly Leu Val Ile Val Leu Gly Ser Gly Val
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 Gly Ser His Ser Tyr Ser Pro Ile Thr Val Glu Ser Asp Phe Ser Asn
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Pro Pro Pro Gln Leu Leu Phe Leu Ile Leu Leu Ser Cys Pro Trp Ile
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cag ggt ctg ccc ctg aag gag gag gag ata ttg cca gag cct gga agt      207
Gln Gly Leu Pro Leu Lys Glu Glu Glu Ile Leu Pro Glu Pro Gly Ser
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Ala Leu Leu Arg Arg Gly Pro Glu Met Gly Tyr Leu Pro Gly Pro Pro
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Leu Gly Pro Glu Gly Gly Glu Glu Glu Thr Thr Thr Thr Ile Ile Thr
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Pro Val Ser Arg Thr Leu Gly Leu Leu Asp Cys Thr Tyr Ser Ile His
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gtc tac cct ggc tac ggc att gag atc cag gtg cag acg ctg aac ctg      543
Val Tyr Pro Gly Tyr Gly Ile Glu Ile Gln Val Gln Thr Leu Asn Leu
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Ser Gln Glu Glu Glu Leu Leu Val Leu Ala Gly Gly Gly Ser Pro Gly
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Leu Ala Pro Arg Leu Leu Ala Asn Ser Ser Met Leu Gly Glu Gly Gln
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Val Leu Arg Ser Pro Thr Asn Arg Leu Leu His Phe Gln Ser Pro
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Tyr Gln Leu Gln Gly Glu Glu Thr Leu Ile Cys Leu Asn Gly Thr Arg	
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Pro Ser Trp Asn Gly Glu Thr Pro Ser Cys Met Ala Ser Cys Gly Gly	
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Thr Ile His Asn Ala Thr Leu Gly Arg Ile Val Ser Pro Glu Pro Gly	
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Val Ile Tyr Asp Ser Asp Met Asp Asp Val Pro Glu Arg Gly Leu Ile	
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Ser Asp Ala Gln Ser Leu Tyr Val Glu Leu Leu Ser Glu Thr Pro Ala	
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Asn Pro Leu Leu Leu Ser Leu Arg Phe Glu Ala Phe Glu Glu Asp Arg	
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Cys Phe Ala Pro Phe Leu Ala His Gly Asn Val Thr Thr Thr Asp Pro	
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Glu Tyr Arg Pro Gly Ala Leu Ala Thr Phe Ser Cys Leu Pro Gly Tyr	
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Glu	Gly	Asp	Met	Leu	Thr	Leu	Phe	Asp	Gly	Asp	Gly	Pro	Ser	Ala	Arg		
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Trp	Asp	Leu	Ser	Trp	Ser	Ala	Ala	Pro	Pro	Ala	Cys	Gln	Lys	Ile	Met		
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Asp	Ala	Gly	Phe	Pro	Val	Gly	Ser	His	Val	Gln	Tyr	Arg	Cys	Leu	Pro		
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Gly His Pro Ser Gln Trp Thr Ser Gln Pro Pro Leu Cys Lys Val Ala
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Asp Pro Ser Arg Gln Leu Glu Gly Gly Asn Leu Ala Leu Ala Ile Leu
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Tyr Thr Lys Leu Gln Gly Lys Ser Leu Phe Gly Phe Ser Gly Ser His
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Ser Tyr Ser Pro Ile Thr Val Glu Ser Asp Phe Ser Asn Pro Leu Tyr
                               830                               835                               840

gaa gct ggg gat acg cgg gag tat gaa gtt tcc atc tga accccaagac      2656
Glu Ala Gly Asp Thr Arg Glu Tyr Glu Val Ser Ile *
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Lys Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg	20 25 30
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Ser Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln	70 75 80
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Leu Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu	85 90 95
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Leu Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp Glu Val Arg Thr Asp	100 105 110
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Leu Lys Gln Gly Leu Asn Gly Val Pro Ile Leu Ser Glu Glu Glu Leu	115 120 125 130
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Ser Thr His Asn His Gln Asn Gly Leu Cys Glu Glu Glu Glu Ala Ala	195 200 205 210
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tgt ttg cca gtg gta agt tca cta gca gat gta tat gcg gga gtg gat Cys Leu Pro Val Val Ser Ser Leu Ala Asp Val Tyr Ala Gly Val Asp 1000 1005 1010	3197
gta caa gct gcc atc tgc ctt ctg gca aac atg gct gtg gat cgg tcc Val Gln Ala Ala Ile Cys Leu Leu Ala Asn Met Ala Val Asp Arg Ser 1015 1020 1025 1030	3245
gtt tca tca agt ctg tca gat gca aga gat gcc tta gtg aat gct gta Val Ser Ser Ser Leu Ser Asp Ala Arg Asp Ala Leu Val Asn Ala Val 1035 1040 1045	3293
gtg gac tca ttg tct gca tat ggc tca act gtc tca aat tta cag cac Val Asp Ser Leu Ser Ala Tyr Gly Ser Thr Val Ser Asn Leu Gln His 1050 1055 1060	3341
tct gca ttg atg gcg ccc agc tcc ctc aag ttg ttt cct ctc tat gtt Ser Ala Leu Met Ala Pro Ser Ser Leu Lys Leu Phe Pro Leu Tyr Val 1065 1070 1075	3389
ttg gcc ctt ctc aaa cag aaa gca ttt aga acg ggt aca agc aca cgg Leu Ala Leu Leu Lys Gln Lys Ala Phe Arg Thr Gly Thr Ser Thr Arg 1080 1085 1090	3437
ctg gat gat cgt gta tat gcc atg tgt cag ata aag tct cag cca ctt Leu Asp Asp Arg Val Tyr Ala Met Cys Gln Ile Lys Ser Gln Pro Leu 1095 1100 1105 1110	3485
gtt cat cta atg aaa atg att cat ccc aac tta tac agg ata gac aga Val His Leu Met Lys Met Ile His Pro Asn Leu Tyr Arg Ile Asp Arg 1115 1120 1125	3533
ttg aca gat gag ggt gca gta cat gtt aat gac agg att gta cca cag Leu Thr Asp Glu Gly Ala Val His Val Asn Asp Arg Ile Val Pro Gln 1130 1135 1140	3581
cca cct ctt caa aaa ttg tct gca gag aag ctg aca aga gaa ggt gct Pro Pro Leu Gln Lys Leu Ser Ala Glu Lys Leu Thr Arg Glu Gly Ala 1145 1150 1155	3629
ttc ctt atg gac tgt ggc tct gtt ttt tac att tgg gtt ggg aaa ggc Phe Leu Met Asp Cys Gly Ser Val Phe Tyr Ile Trp Val Gly Lys Gly 1160 1165 1170	3677
tgt gac aat aac ttc ata gag gat gtg ctt gga tat act aat ttt gca Cys Asp Asn Asn Phe Ile Glu Asp Val Leu Gly Tyr Thr Asn Phe Ala 1175 1180 1185 1190	3725
tca ata cca cag aaa atg aca cat ctt cca gag cta gat aca ctt tca Ser Ile Pro Gln Lys Met Thr His Leu Pro Glu Leu Asp Thr Leu Ser 1195 1200 1205	3773
tca gaa aga gcc aga tcc ttc ata act tgg ctt aga gac agc aga cca Ser Glu Arg Ala Arg Ser Phe Ile Thr Trp Leu Arg Asp Ser Arg Pro 1210 1215 1220	3821
tta agt cca atc ctt cac ata gta aaa gat gag agt cct gcc aaa gca Leu Ser Pro Ile Leu His Ile Val Lys Asp Glu Ser Pro Ala Lys Ala 1225 1230 1235	3869
gaa ttt ttt cag cat ttg att gaa gac cgg aca gag gct gca ttt tct Glu Phe Phe Gln His Leu Ile Glu Asp Arg Thr Glu Ala Ala Phe Ser 1240 1245 1250	3917

tac tat gaa ttt ttg ctt cat gtt cag cag cag att tgt aag tga agt 3965
 Tyr Tyr Glu Phe Leu Leu His Val Gln Gln Gln Ile Cys Lys *
 1255 1260 1265
 agaataaaat tgaataagaa aaagatctat aacctaggta aagcataatc tgtcagagaa 4025
 gcgcgtgaga aatttgaaat gaaggcattt gttaatacaa gatgcaacgc acagcactct 4085
 gtctgaggct ttggtaaaaa gtaaagggga agaaagaact tgacagatct ttttcaactc 4145
 aaattaatgg taacgatgat gctgtttcac caagtatatt ttgaattggt ttctacacat 4205
 ttccagtagt atggcagtac agtgctctgt tcattgcaag ctggcaaatt tatgtagcta 4265
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 acatttctgg acttgaactc tggcaagaga tgccaaaagg cattggtacc gtgttatttg 4385
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 tctctgtaaa aacaatagag tttcagtaca tgaactatag aaaaaaatct atatataatg 4505
 tacataaatg ttacatttgt aaagaaaatg taaaaatgta actatagcat atgaattgct 4565
 taaactgtgc tgcattgttg gatgacaact ctttttgtca cagttagaga atgagggtga 4625
 ctaatgcata ttatgaattg agtcacacaa ggaacacaaa actctttgta attctgttaa 4685
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 <213> Homo sapiens

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 agccagccgt gggccccgcc ccggcgctccg gagcaggaga actccgagct tcttgcccag 180
 gcagagagag caggagcgga ccgcgcgccc gggattgaga gtccttgccg tccagacccc 240
 caccagtggt ccgccagggt ccccgctgtt ccggaccctc gccgcgccc aaggaggcgcg 300
 ccaggggcggg gctgacctgc ccgcgaagtt gcggacagtg cgtgagaaac cagcaccccc 360
 ttccgcccgc tccagctt atg gaa act ggt caa aga act cat gca agt gga 411
 Met Glu Thr Gly Gln Arg Thr His Ala Ser Gly
 1 5 10
 act tac agc ttc ctt gat cgg act cag cat tca gat atc aaa gca gac 459
 Thr Tyr Ser Phe Leu Asp Arg Thr Gln His Ser Asp Ile Lys Ala Asp
 15 20 25

tgc aat acc tgc gtg gaa ata gaa gac aga aag gtt tca aga caa cag	507
Cys Asn Thr Cys Val Glu Ile Glu Asp Arg Lys Val Ser Arg Gln Gln	
30 35 40	
atg aat tgt gaa aga gag cag cta agg ggt aat cag gaa gca gcc gct	555
Met Asn Cys Glu Arg Glu Gln Leu Arg Gly Asn Gln Glu Ala Ala Ala	
45 50 55	
gcc cct gac aca atg gct cag cct tac gct tgc gcc cag ttt gct ccc	603
Ala Pro Asp Thr Met Ala Gln Pro Tyr Ala Ser Ala Gln Phe Ala Pro	
60 65 70 75	
ccg cag aac ggt atc ccc gcg gaa tac acg gcc cct cat ccc cac ccc	651
Pro Gln Asn Gly Ile Pro Ala Glu Tyr Thr Ala Pro His Pro His Pro	
80 85 90	
gcg cca gag tac aca ggc cag acc acg gtt ccc gag cac aca tta aac	699
Ala Pro Glu Tyr Thr Gly Gln Thr Thr Val Pro Glu His Thr Leu Asn	
95 100 105	
ctg tac cct ccc gcc cag acg cac tcc gag cag agc ccg gcg gac acg	747
Leu Tyr Pro Pro Ala Gln Thr His Ser Glu Gln Ser Pro Ala Asp Thr	
110 115 120	
agc gct cag acc gtc tct ggc acc gcc aca cag aca gat gac gca gca	795
Ser Ala Gln Thr Val Ser Gly Thr Ala Thr Gln Thr Asp Asp Ala Ala	
125 130 135	
ccg acg gat ggc cag ccc cag aca caa cct tct gaa aac acg gaa aac	843
Pro Thr Asp Gly Gln Pro Gln Thr Gln Pro Ser Glu Asn Thr Glu Asn	
140 145 150 155	
aag tct cag ccc aag cgg ctg cat gtc tcc aat atc ccc ttc agg ttc	891
Lys Ser Gln Pro Lys Arg Leu His Val Ser Asn Ile Pro Phe Arg Phe	
160 165 170	
cgg gat ccg gac ctc aga caa atg ttt ggt caa ttt ggt aaa atc tta	939
Arg Asp Pro Asp Leu Arg Gln Met Phe Gly Gln Phe Gly Lys Ile Leu	
175 180 185	
gat gtt gaa att att ttt aat gag cga ggc tca aag gga ttt ggt ttc	987
Asp Val Glu Ile Ile Phe Asn Glu Arg Gly Ser Lys Gly Phe Gly Phe	
190 195 200	
gta act ttc gaa aat agt gcc gat gcg gac agg gcg agg gag aaa tta	1035
Val Thr Phe Glu Asn Ser Ala Asp Ala Asp Arg Ala Arg Glu Lys Leu	
205 210 215	
cac ggc acc gtg gta gag ggc cgt aaa atc gag gta aat aat gcc aca	1083
His Gly Thr Val Val Glu Gly Arg Lys Ile Glu Val Asn Asn Ala Thr	
220 225 230 235	
gca cgt gta atg aca aat aaa aag acc gtc aac cct tat aca aat ggc	1131
Ala Arg Val Met Thr Asn Lys Lys Thr Val Asn Pro Tyr Thr Asn Gly	
240 245 250	
tgg aaa ttg aat cca gtt gtg ggt gca gtc tac agt ccc gaa ttc tat	1179
Trp Lys Leu Asn Pro Val Val Gly Ala Val Tyr Ser Pro Glu Phe Tyr	
255 260 265	
gca ggc acg gtc ctg ttg tgc cag gcc aac cag gag gga tct tcc atg	1227
Ala Gly Thr Val Leu Leu Cys Gln Ala Asn Gln Glu Gly Ser Ser Met	
270 275 280	

tac agt gcc ccc agt tca ctt gta tat act tct gca atg cca ggc ttc 1275
 Tyr Ser Ala Pro Ser Ser Leu Val Tyr Thr Ser Ala Met Pro Gly Phe
 285 290 295
 ccg tat cca gca gcc acc gcc gcg gcc gcc tac cga ggg gcg cac ctg 1323
 Pro Tyr Pro Ala Ala Thr Ala Ala Ala Tyr Arg Gly Ala His Leu
 300 305 310 315
 cga ggc cgc ggt cgc acc gtg tac aac acc ttc agg gcc gcg gcg ccc 1371
 Arg Gly Arg Gly Arg Thr Val Tyr Asn Thr Phe Arg Ala Ala Ala Pro
 320 325 330
 ccg ccc ccg atc ccg gcc tac ggc ggt gtt gtt tac cag gat gga ttt 1419
 Pro Pro Pro Ile Pro Ala Tyr Gly Gly Val Val Tyr Gln Asp Gly Phe
 335 340 345
 tat ggt gca gac att tat ggt ggt tat gct gca tac cgc tac gcc cag 1467
 Tyr Gly Ala Asp Ile Tyr Gly Gly Tyr Ala Ala Tyr Arg Tyr Ala Gln
 350 355 360
 cct acc cct gcc act gcc gct gcc tac agt gac agt tac gga cga gtt 1515
 Pro Thr Pro Ala Thr Ala Ala Ala Tyr Ser Asp Ser Tyr Gly Arg Val
 365 370 375
 tat gct gcc gac ccc tac cac cac gca ctt gct cca gcc ccc acc tac 1563
 Tyr Ala Ala Asp Pro Tyr His His Ala Leu Ala Pro Ala Pro Thr Tyr
 380 385 390 395
 ggc gtt ggt gcc atg aat gct ttt gca cct ttg act gat gcc aag act 1611
 Gly Val Gly Ala Met Asn Ala Phe Ala Pro Leu Thr Asp Ala Lys Thr
 400 405 410
 agg agc cat gct gat gat gtg ggt ctc gtt ctt tct tca ttg cag gct 1659
 Arg Ser His Ala Asp Asp Val Gly Leu Val Leu Ser Ser Leu Gln Ala
 415 420 425
 agt ata tac cga ggg gga tac aac cgt ttt gct cca tac taa atgacaa 1708
 Ser Ile Tyr Arg Gly Gly Tyr Asn Arg Phe Ala Pro Tyr *
 430 435 440
 aaccataaaa accttccaat gtggggagaa aggaagcttt ccgaggcctg agtattgcaa 1768
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<220>
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 Met Thr Ile Pro Gly Leu Asp Trp Gly
 1 5

atg gag gaa gtg atg caa aag gat cag aaa aaa gta cct cag aag aaa 101
 Met Glu Glu Val Met Gln Lys Asp Gln Lys Lys Val Pro Gln Lys Lys

10	15	20	25	
gtt cct tat gca aaa ccc att cct gct cag ttc cag cag gct tgg atg				149
Val Pro Tyr Ala Lys Pro Ile Pro Ala Gln Phe Gln Gln Ala Trp Met				
	30	35	40	
caa aat aaa gtt cca att cct gct cca aat gag gtg ctg aat gac aga				197
Gln Asn Lys Val Pro Ile Pro Ala Pro Asn Glu Val Leu Asn Asp Arg				
	45	50	55	
aaa gaa gac att aaa ttg gaa gag aag aaa aaa aca caa gca gaa att				245
Lys Glu Asp Ile Lys Leu Glu Glu Lys Lys Lys Thr Gln Ala Glu Ile				
	60	65	70	
gag caa gaa atg gct aca tta caa tat act aac cca caa ctt ctg gag				293
Glu Gln Glu Met Ala Thr Leu Gln Tyr Thr Asn Pro Gln Leu Leu Glu				
	75	80	85	
caa ctt aaa att gaa aga ctt gca cag aaa caa gtt gag caa att cag				341
Gln Leu Lys Ile Glu Arg Leu Ala Gln Lys Gln Val Glu Gln Ile Gln				
	90	95	100	105
cct cct ccc tca tct ggc acc cct ctc ctc gga ccc cag cct ttt cca				389
Pro Pro Pro Ser Ser Gly Thr Pro Leu Leu Gly Pro Gln Pro Phe Pro				
	110	115	120	
gga caa ggt cca atg tct cag att cct caa ggt ttt caa cag ccc cat				437
Gly Gln Gly Pro Met Ser Gln Ile Pro Gln Gly Phe Gln Gln Pro His				
	125	130	135	
cca tct cag cag atg cca atg aac atg gct caa atg ggg cct cca ggt				485
Pro Ser Gln Gln Met Pro Met Asn Met Ala Gln Met Gly Pro Pro Gly				
	140	145	150	
cca cag gga cag ttt agg cct cct gga ccc cag gga caa atg gga cca				533
Pro Gln Gly Gln Phe Arg Pro Pro Gly Pro Gln Gly Gln Met Gly Pro				
	155	160	165	
caa ggt cct cca ctg cat cag gga ggt ggg ggg cca caa gga ttc atg				581
Gln Gly Pro Pro Leu His Gln Gly Gly Gly Gly Pro Gln Gly Phe Met				
	170	175	180	185
gga cca cag ggg ccc cag ggc ccg ccc cag ggg ttg cca cgg cct cag				629
Gly Pro Gln Gly Pro Gln Gly Pro Pro Gln Gly Leu Pro Arg Pro Gln				
	190	195	200	
gac atg cat ggg ccc caa gga atg cag agg cat cct gga cct cat ggc				677
Asp Met His Gly Pro Gln Gly Met Gln Arg His Pro Gly Pro His Gly				
	205	210	215	
cct ttg gga cct caa ggg cca cct gga cca caa ggt agt tct ggt cct				725
Pro Leu Gly Pro Gln Gly Pro Pro Gly Pro Gln Gly Ser Ser Gly Pro				
	220	225	230	
caa ggt cat atg ggt cct cag ggt cca cct ggc cca cag ggt cac ata				773
Gln Gly His Met Gly Pro Gln Gly Pro Pro Gly Pro Gln Gly His Ile				
	235	240	245	
ggc ccc caa ggc ccg cct ggc cct cag ggt cac ttg ggc cca cag ggg				821
Gly Pro Gln Gly Pro Pro Gly Pro Gln Gly His Leu Gly Pro Gln Gly				
	250	255	260	265
cct ccg ggt act caa ggt atg cag gga cca cct ggt ccc aga gga atg				869
Pro Pro Gly Thr Gln Gly Met Gln Gly Pro Pro Gly Pro Arg Gly Met				

270	275	280	
caa ggg cct cct cat cct cat ggg atc caa ggc gga cca ggg tct caa Gln Gly Pro Pro His Pro His Gly Ile Gln Gly Gly Pro Gly Ser Gln 285 290 295			917
ggg atc caa ggt cct gtg tct cag gga cct ctg atg gga ttg aat cca Gly Ile Gln Gly Pro Val Ser Gln Gly Pro Leu Met Gly Leu Asn Pro 300 305 310			965
aga gga atg cag ggg cct cca ggc ccc cgg gag aac cag ggt cct gct Arg Gly Met Gln Gly Pro Pro Gly Pro Arg Glu Asn Gln Gly Pro Ala 315 320 325			1013
ccc caa ggg atg att atg ggc cac ccg cct caa gag atg aga gga cct Pro Gln Gly Met Ile Met Gly His Pro Pro Gln Glu Met Arg Gly Pro 330 335 340 345			1061
cac cct cca ggt gga cta ctg gga cac ggc cct cag gaa atg aga ggt His Pro Pro Gly Gly Leu Leu Gly His Gly Pro Gln Glu Met Arg Gly 350 355 360			1109
cct cag gag atc cga ggc atg cag ggg cct cca ccc caa gga tca atg Pro Gln Glu Ile Arg Gly Met Gln Gly Pro Pro Pro Gln Gly Ser Met 365 370 375			1157
ctg gga cct ccc cag gaa ttg cga ggg cct cca ggc tca caa agt cag Leu Gly Pro Pro Gln Glu Leu Arg Gly Pro Pro Gly Ser Gln Ser Gln 380 385 390			1205
cag ggg ccg ccc cag ggc tct tta gga cct cca ccc cag ggt ggc atg Gln Gly Pro Pro Gln Gly Ser Leu Gly Pro Pro Pro Gln Gly Gly Met 395 400 405			1253
caa gga ccc ccc gga cct cag gga cag cag aac cca gca aga ggg cca Gln Gly Pro Pro Gly Pro Gln Gly Gln Gln Asn Pro Ala Arg Gly Pro 410 415 420 425			1301
cat cca tct caa ggg cca ata cca ttc cag caa cag aaa acg cct ctg His Pro Ser Gln Gly Pro Ile Pro Phe Gln Gln Gln Lys Thr Pro Leu 430 435 440			1349
cta ggt gat ggg ccc cgg gcc ccc ttc aac cag gaa gga cag agc aca Leu Gly Asp Gly Pro Arg Ala Pro Phe Asn Gln Glu Gly Gln Ser Thr 445 450 455			1397
ggc ccc cca ccc ctg ata cca ggc cta ggg cag cag gga gca caa ggt Gly Pro Pro Pro Leu Ile Pro Gly Leu Gly Gln Gln Gly Ala Gln Gly 460 465 470			1445
cgc att ccc cct ctg aac ccc gga caa gga cct ggc ccc aac aaa gtt Arg Ile Pro Pro Leu Asn Pro Gly Gln Gly Pro Gly Pro Asn Lys Val 475 480 485			1493
tca gaa gag gag ccc cgc cga ggc atg agg gcc gtg ctc ccc cca gag Ser Glu Glu Glu Pro Arg Arg Gly Met Arg Ala Val Leu Pro Pro Glu 490 495 500 505			1541
gaa ggg atg gtt ttc ctg gtc ctg aag act tta gtc cag agg aga att Glu Gly Met Val Phe Leu Val Leu Lys Thr Leu Val Gln Arg Arg Ile 510 515 520			1589
ttg atg ctt atg agg gaa gcg gcc cga gga cga gat ctc aga ggt cga Leu Met Leu Met Arg Glu Ala Ala Arg Gly Arg Asp Leu Arg Gly Arg 520			1637

525	530	535	
ggt cgg ggt acc cca cga gga gga agg aag ggt tta ctt ccc act cct Gly Arg Gly Thr Pro Arg Gly Gly Arg Lys Gly Leu Leu Pro Thr Pro 540 545 550			1685
gac gag ttc cct cgc ttt gaa gga ggg cgg aag cca gat tcc tgg gat Asp Glu Phe Pro Arg Phe Glu Gly Gly Arg Lys Pro Asp Ser Trp Asp 555 560 565			1733
gga aac aga gag cct ggg cca ggt cat gaa cat ttt cgt gat act ccc Gly Asn Arg Glu Pro Gly Pro Gly His Glu His Phe Arg Asp Thr Pro 570 575 580 585			1781
cgc cct gat cat ccc cct cac gac ggt cat tcc cca gcc agc aga gaa Arg Pro Asp His Pro Pro His Asp Gly His Ser Pro Ala Ser Arg Glu 590 595 600			1829
cgc tcc tct tct ctc caa ggc atg gac atg gca tcc cta cct ccc cga Arg Ser Ser Ser Leu Gln Gly Met Asp Met Ala Ser Leu Pro Pro Arg 605 610 615			1877
aag cgc ccc tgg cat gat ggc cca ggc act tct gag cac aga gag atg Lys Arg Pro Trp His Asp Gly Pro Gly Thr Ser Glu His Arg Glu Met 620 625 630			1925
gag gcc cca gga ggc cct tct gaa gac cga gga ggc aaa ggc cga ggg Glu Ala Pro Gly Gly Pro Ser Glu Asp Arg Gly Gly Lys Gly Arg Gly 635 640 645			1973
ggc cca gga cct gct cag aga gtg ccc aaa tct ggg cgt tcc agc tcc Gly Pro Gly Pro Ala Gln Arg Val Pro Lys Ser Gly Arg Ser Ser Ser 650 655 660 665			2021
tta gac gga gag cac cac gat gga tac cac aga gat gaa cct ttt ggg Leu Asp Gly Glu His His Asp Gly Tyr His Arg Asp Glu Pro Phe Gly 670 675 680			2069
ggc cct cca ggc agt ggc acc cct tct cga ggg ggc cgg agt ggc agt Gly Pro Pro Gly Ser Gly Thr Pro Ser Arg Gly Gly Arg Ser Gly Ser 685 690 695			2117
aac tgg ggt aga ggg agt aac atg aac tct ggc ccg ccg agg cga gga Asn Trp Gly Arg Gly Ser Asn Met Asn Ser Gly Pro Pro Arg Arg Gly 700 705 710			2165
gct ttc ctg ggt ggt ggg agg ggt ccg gta aaa cct cga act gag ttc Ala Phe Leu Gly Gly Gly Arg Gly Pro Val Lys Pro Arg Thr Glu Phe 715 720 725			2213
cct gag ggc gtt ttt gga cag att gta aga act ttt ggt gga ctt cac Pro Glu Gly Val Phe Gly Gln Ile Val Arg Thr Phe Gly Gly Leu His 730 735 740 745			2261
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<212> DNA
<213> Homo sapiens

<220>
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<222> (386)..(1147)

<400> 792

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agcgttgcca acgtgtacgg agatagccga agaggcggaa gcggggccac aagagccctt      180
cctgcagggg acctcaggct tcagagagcc gaaaagttgg gaggcgtaac cacttacagg      240
ccggaagtgt ccgggggtgga cgcattcggg tagccgaaga agtcccagga ttgccgaaga      300
agtcccagga tttccgaagc gagccgaagc atcgcgacag ttttcagaga cagctgatcg      360
gttgagctg ttgcgccgag cagtc  atg gcg gcg gcc aga gct act acg ccg      412
                               Met Ala Ala Ala Arg Ala Thr Thr Pro
                               1                               5

gcc gat ggc gag gag ccc gcc ccg gag gct gag gct ctg gcc gca gcc      460
Ala Asp Gly Glu Glu Pro Ala Pro Glu Ala Glu Ala Leu Ala Ala Ala
   10                               15                               20                               25

cgg gag cgg agc agc cgc ttc ttg agc ggc ctg gag ctg gtg aag cag      508
Arg Glu Arg Ser Ser Arg Phe Leu Ser Gly Leu Glu Leu Val Lys Gln
                               30                               35                               40

ggg gcc gag gcg cgc gtg ttc cgt ggc cgc ttc cag ggc cgc gcg gcg      556
Gly Ala Glu Ala Arg Val Phe Arg Gly Arg Phe Gln Gly Arg Ala Ala
   45                               50                               55

gtg atc aag cac cgc ttc ccc aag ggc tac cgg cac ccg gcg ctg gag      604
Val Ile Lys His Arg Phe Pro Lys Gly Tyr Arg His Pro Ala Leu Glu
   60                               65                               70

gcg cgg ctt ggc aga ccg cgg acg gtg cag gag gcc ccg gcg ctc ctc      652
Ala Arg Leu Gly Arg Arg Arg Thr Val Gln Glu Ala Arg Ala Leu Leu
   75                               80                               85

cgc tgt cgc cgc gct gga ata tct gcc cca gtt gtc ttt ttt gtg gac      700
Arg Cys Arg Arg Ala Gly Ile Ser Ala Pro Val Val Phe Phe Val Asp
   90                               95                               100                               105

tat gct tcc aac tgc tta tat atg gaa gaa att gaa ggc tca gtg act      748
Tyr Ala Ser Asn Cys Leu Tyr Met Glu Glu Ile Glu Gly Ser Val Thr
   110                               115                               120

gtt cga gat tat att cag tcc act atg gag act gaa aaa act ccc cag      796
Val Arg Asp Tyr Ile Gln Ser Thr Met Glu Thr Glu Lys Thr Pro Gln
   125                               130                               135

ggg ctc tcc aac tta gcc aag aca att ggg cag gtt ttg gct cga atg      844
Gly Leu Ser Asn Leu Ala Lys Thr Ile Gly Gln Val Leu Ala Arg Met
   140                               145                               150

cac gat gaa gac ctc att cat ggt gat ctc acc acc tcc aac atg ctc      892
His Asp Glu Asp Leu Ile His Gly Asp Leu Thr Thr Ser Asn Met Leu
   155                               160                               165

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ctg aaa ccc ccc ctg gaa cag ctg aac att gtg ctc ata gac ttt ggg      940
Leu Lys Pro Pro Leu Glu Gln Leu Asn Ile Val Leu Ile Asp Phe Gly
170                      175                      180                      185

ctg agt ttc att tca gca ctt cca gag gat aag gga gta gac ctc tat      988
Leu Ser Phe Ile Ser Ala Leu Pro Glu Asp Lys Gly Val Asp Leu Tyr
                      190                      195                      200

gtc ctg gag aag gcc ttc ctc agt acc cat ccc aac act gaa act gtg      1036
Val Leu Glu Lys Ala Phe Leu Ser Thr His Pro Asn Thr Glu Thr Val
                      205                      210                      215

ttt gaa gcc ttt ctg aag agc tac tcc acc tcc tcc aaa aag gcc agg      1084
Phe Glu Ala Phe Leu Lys Ser Tyr Ser Thr Ser Ser Lys Lys Ala Arg
                      220                      225                      230

cca gtg cta aaa aaa tta gat gaa gtg cgc ctg aga gga aga aag agg      1132
Pro Val Leu Lys Lys Leu Asp Glu Val Arg Leu Arg Gly Arg Lys Arg
                      235                      240                      245

tcc atg gtt ggg tag aagaatgtgt atgacaacca cacacagtga agctcttttt      1187
Ser Met Val Gly *
250

tcaaagtaaa tttgaagaaa tgctacaagt atgagatgag atctaagtaa aggtgttaag      1247

atattttttaa aaaaaaaaaa      1267

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 <222> (218)..(1399)

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ggtcaaagac tgggtgcctg ggagctgagg cagccaccgt ttcagcctgg ccagccctct      180
ggaccccgag gttggaccct actgtgacac acctacc atg cgg aca ctc ttc aac      235
                               Met Arg Thr Leu Phe Asn
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ctc ctc tgg ctt gcc ctg gcc tgc agc cct gtt cac act acc ctg tca      283
Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser
                      10                      15                      20

aag tca gat gcc aaa aaa gcc gcc tca aag acg ctg ctg gag aag agt      331
Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser
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cag ttt tca gat aag ccg gtg caa gac cgg ggt ttg gtg gtg acg gac      379
Gln Phe Ser Asp Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp
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ctc aaa gct gag agt gtg gtt ctt gag cat cgc agc tac tgc tcg gca      427

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Leu	Lys	Ala	Glu	Ser	Val	Val	Leu	Glu	His	Arg	Ser	Tyr	Cys	Ser	Ala		
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Lys	Ala	Arg	Asp	Arg	His	Phe	Ala	Gly	Asp	Val	Leu	Gly	Tyr	Val	Thr		
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Pro	Trp	Asn	Ser	His	Gly	Tyr	Tyr	Val	Thr	Lys	Val	Phe	Gly	Ser	Lys		
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Phe	Thr	Gln	Ile	Ser	Pro	Val	Trp	Leu	Gln	Leu	Lys	Arg	Arg	Gly	Arg		
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gag	atg	ttt	gag	gtc	acg	ggc	ctc	cac	gac	gtg	gac	caa	ggg	tgg	atg	619	
Glu	Met	Phe	Glu	Val	Thr	Gly	Leu	His	Asp	Val	Asp	Gln	Gly	Trp	Met		
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Arg	Ala	Val	Arg	Lys	His	Ala	Lys	Gly	Leu	His	Ile	Val	Pro	Arg	Leu		
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Leu	Phe	Glu	Asp	Trp	Thr	Tyr	Asp	Asp	Phe	Arg	Asn	Val	Leu	Tyr	Ser		
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Glu	Asp	Glu	Ile	Glu	Glu	Leu	Ser	Lys	Thr	Val	Val	Gln	Val	Ala	Lys		
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aac	cag	cat	ttc	gat	ggc	ttc	gtg	gtg	gag	gtc	tgg	aac	cag	ctg	cta	811	
Asn	Gln	His	Phe	Asp	Gly	Phe	Val	Val	Glu	Val	Trp	Asn	Gln	Leu	Leu		
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Ser	Gln	Lys	Arg	Val	Gly	Leu	Ile	His	Met	Leu	Thr	His	Leu	Ala	Glu		
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Ala	Leu	His	Gln	Ala	Arg	Leu	Leu	Ala	Leu	Leu	Val	Ile	Pro	Pro	Ala		
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atc	acc	ccc	ggg	acc	gac	cag	ctg	ggc	atg	ttc	acg	cac	aag	gag	ttt	955	
Ile	Thr	Pro	Gly	Thr	Asp	Gln	Leu	Gly	Met	Phe	Thr	His	Lys	Glu	Phe		
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gag	cag	ctg	gcc	ccc	gtg	ctg	gat	ggt	ttc	agc	ctc	atg	acc	tac	gac	1003	
Glu	Gln	Leu	Ala	Pro	Val	Leu	Asp	Gly	Phe	Ser	Leu	Met	Thr	Tyr	Asp		
			250					255					260				
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Tyr	Ser	Thr	Ala	His	Gln	Pro	Gly	Pro	Asn	Ala	Pro	Leu	Ser	Trp	Val		
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cga	gcc	tgc	gtc	cag	gtc	ctg	gac	ccg	aag	tcc	aag	tgg	cga	agc	aaa	1099	
Arg	Ala	Cys	Val	Gln	Val	Leu	Asp	Pro	Lys	Ser	Lys	Trp	Arg	Ser	Lys		
	280					285					290						
atc	ctc	ctg	ggg	ctc	aac	ttc	tat	ggt	atg	gac	tac	gcg	acc	tcc	aag	1147	
Ile	Leu	Leu	Gly	Leu	Asn	Phe	Tyr	Gly	Met	Asp	Tyr	Ala	Thr	Ser	Lys		
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Asp Ala Arg Glu Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys
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Asp His Arg Pro Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe
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Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro
      345                      350                      355

acc ctg aag tcc ctg cag gtg cgg ctg gag ctg gcc cgg gag ctg ggc      1339
Thr Leu Lys Ser Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly
      360                      365                      370

gtt ggg gtc tct atc tgg gag ctg ggc cag ggc ctg gac tac ttc tac      1387
Val Gly Val Ser Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr
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gac ctg ctc tag gtg ggcattgcgg cctccgcggt ggacgtgttc ttttctaagc      1442
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gatgcggcgg ccacctgctg caaagaaccg aagggaaggt tagaagtacg aaggcagttt      240

ggagctgggg ctaagcagct gtcgcacggt cagatc  atg ggc tcc acc aag cac      294
              Met Gly Ser Thr Lys His
              1                      5

tgg ggc gaa tgg ctc ctg aac ttg aag gtg gct cca gcc ggc gtc ttt      342
Trp Gly Glu Trp Leu Leu Asn Leu Lys Val Ala Pro Ala Gly Val Phe
      10                      15                      20

ggt gtg gcc ttt cta gcc aga gtc gcc ctg gtt ttc tat ggc gtc ttc      390
Gly Val Ala Phe Leu Ala Arg Val Ala Leu Val Phe Tyr Gly Val Phe
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cag gac cgg acc ctg cac gtg agg tat acg gac atc gac tac cag gtc      438
Gln Asp Arg Thr Leu His Val Arg Tyr Thr Asp Ile Asp Tyr Gln Val
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aga gcc acg tac cgt tac acc ccg ctg ctg ggt tgg ctc ctc act ccc	534
Arg Ala Thr Tyr Arg Tyr Thr Pro Leu Leu Gly Trp Leu Leu Thr Pro	
75 80 85	
aac atc tac ctc agc gag ctc ttt gga aag ttt ctc ttc atc agc tgc	582
Asn Ile Tyr Leu Ser Glu Leu Phe Gly Lys Phe Leu Phe Ile Ser Cys	
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gac ctc ctc acc gct ttc ctc tta tac cgc ctg ctg ctg ctg aag ggg	630
Asp Leu Leu Thr Ala Phe Leu Tyr Arg Leu Leu Leu Lys Gly	
105 110 115	
ctg ggg cgc cgc cag gct tgt ggc tac tgt gtc ttt tgg ctt ctt aac	678
Leu Gly Arg Arg Gln Ala Cys Gly Tyr Cys Val Phe Trp Leu Leu Asn	
120 125 130	
ccc ctg cct atg gca gta tcc agc cgc ggt aat gcg gac tct att gtc	726
Pro Leu Pro Met Ala Val Ser Ser Arg Gly Asn Ala Asp Ser Ile Val	
135 140 145 150	
gcc tcc ctg gtc ctg atg gtc ctc tac ttg ata aag aaa aga ctc gtc	774
Ala Ser Leu Val Leu Met Val Leu Tyr Leu Ile Lys Lys Arg Leu Val	
155 160 165	
gcg tgt gca gct gta ttc tat ggt ttc gcg gtg cat atg aag ata tat	822
Ala Cys Ala Ala Val Phe Tyr Gly Phe Ala Val His Met Lys Ile Tyr	
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cca gag act tac atc ctt ccc ata acc ctc cac ctg ctt cca gat cgc	870
Pro Glu Thr Tyr Ile Leu Pro Ile Thr Leu His Leu Leu Pro Asp Arg	
185 190 195	
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Asp Asn Asp Lys Ser Leu Arg Gln Phe Arg Thr Arg Leu Cys Asn Arg	
200 205 210	
act gcg ctg atg ttt gta gca gtt gct gga ctc acg ttt ttt gcc ctg	966
Thr Ala Leu Met Phe Val Ala Val Ala Gly Leu Thr Phe Phe Ala Leu	
215 220 225 230	
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Ser Phe Gly Phe Tyr Tyr Glu Tyr Gly Trp Glu Phe Leu Glu His Thr	
235 240 245	
tac ttt tat cac ctg act agg cgg gat atc cgt cac aac ttt tct ccg	1062
Tyr Phe Tyr His Leu Thr Arg Arg Asp Ile Arg His Asn Phe Ser Pro	
250 255 260	
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Tyr Phe Tyr Met Leu Tyr Leu Thr Ala Glu Ser Lys Trp Ser Phe Ser	
265 270 275	
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Leu Gly Ile Ala Ala Phe Leu Pro Gln Leu Ile Leu Leu Ser Ala Val	
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Ser Phe Ala Tyr Tyr Arg Asp Leu Val Phe Cys Cys Phe Leu His Thr	
295 300 305 310	

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 Ser Ile Phe Val Thr Phe Asn Lys Val Cys Thr Ser Gln Tyr Phe Leu
 315 320 325
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 Trp Tyr Leu Cys Leu Leu Pro Leu Val Met Pro Leu Val Arg Met Pro
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 Trp Lys Arg Ala Val Val Leu Leu Met Leu Trp Phe Ile Gly Gln Ala
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 Phe Leu Phe Ile Trp Leu Ala Gly Leu Phe Phe Leu Leu Ile Asn Cys
 375 380 385 390
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 Ser Ile Leu Ile Gln Ile Ile Ser His Tyr Lys Glu Glu Pro Leu Thr
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 Glu Arg Ile Lys Tyr Asp *
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 Met Arg Gly Ala Ala Ser Ala Ser Val Arg Glu Pro Thr
 1 5 10
 ccg ctc ccg ggt aga ggc gcc ccc cgc aca aag ccc ccg gcg ggc cga 158
 Pro Leu Pro Gly Arg Gly Ala Pro Arg Thr Lys Pro Arg Ala Gly Arg
 15 20 25
 ggc ccg act gta ggg act cca gcc acc ttg gcc ctc cct gcc ccg gga 206
 Gly Pro Thr Val Gly Thr Pro Ala Thr Leu Ala Leu Pro Ala Arg Gly
 30 35 40 45
 agg ccg cgc tca agg aat ggc ctc gca tcc aaa ggc cag cga gga gcg 254

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Ala	Pro	Thr	Gly	Pro	Gly	His	Arg	Ala	Leu	Pro	Ser	Arg	Asp	Thr	Ala		
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Leu	Pro	Gln	Glu	Arg	Asn	Lys	Lys	Leu	Glu	Ala	Val	Gly	Thr	Gly	Ile		
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Glu	Pro	Lys	Ala	Met	Ser	Gln	Gly	Leu	Val	Thr	Phe	Gly	Asp	Val	Ala		
	95					100						105					
gta	gat	ttc	tcc	caa	gag	gag	tgg	gag	tgg	ctg	aac	ccc	att	cag	agg	446	
Val	Asp	Phe	Ser	Gln	Glu	Glu	Trp	Glu	Trp	Leu	Asn	Pro	Ile	Gln	Arg		
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Asn	Leu	Tyr	Arg	Lys	Val	Met	Leu	Glu	Asn	Tyr	Arg	Asn	Leu	Ala	Ser		
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Leu	Gly	Leu	Cys	Val	Ser	Lys	Pro	Asp	Val	Ile	Ser	Ser	Leu	Glu	Gln		
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Pro	Asp	Leu	Lys	Ala	Val	Trp	Lys	Ile	Lys	Glu	Leu	Pro	Leu	Lys	Lys		
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Thr	Ser	Tyr	Asn	Leu	Glu	Tyr	Ser	Leu	Leu	Gly	Glu	His	Trp	Asp	Tyr		
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Asp	Ala	Leu	Phe	Glu	Thr	Gln	Pro	Gly	Leu	Val	Thr	Ile	Lys	Asn	Leu		
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Ala	Val	Asp	Phe	Arg	Gln	Gln	Leu	His	Pro	Ala	Gln	Lys	Asn	Phe	Cys		
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Lys	Asn	Gly	Ile	Trp	Glu	Asn	Asn	Ser	Asp	Leu	Gly	Ser	Ala	Gly	His		
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Cys	Val	Ala	Lys	Pro	Asp	Leu	Val	Ser	Leu	Leu	Glu	Gln	Glu	Lys	Glu		
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Pro	Trp	Met	Val	Lys	Arg	Glu	Leu	Thr	Gly	Ser	Leu	Phe	Ser	Gly	Gln		
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Ala	Glu	Gly	Val	Thr	Asp	Arg	Thr	Ser	Asn	Thr	Lys	Leu	Asp	Cys	Ser		
		320					325					330					
agt	ttc	aga	gaa	aat	tgg	gat	tct	gac	tat	gtg	ttc	gga	agg	aag	ctt	1118	
Ser	Phe	Arg	Glu	Asn	Trp	Asp	Ser	Asp	Tyr	Val	Phe	Gly	Arg	Lys	Leu		
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Ala	Val	Gly	Gln	Glu	Thr	Gln	Phe	Arg	Gln	Glu	Pro	Ile	Thr	His	Asn		
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aaa	acc	ctc	tct	aag	gaa	aga	gaa	cgt	aca	tat	aac	aaa	tct	gga	aga	1214	
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Tyr	Ala	Gly	Lys	Lys	Leu	Phe	Lys	Cys	Asn	Glu	Cys	Lys	Lys	Thr	Phe		
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Cys	Ile	Glu	Cys	Gly	Lys	Ala	Phe	Ile	Gln	Asn	Thr	Ser	Leu	Ile	Arg		
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His	Trp	Arg	Tyr	Tyr	His	Thr	Gly	Glu	Lys	Pro	Phe	Asp	Cys	Ile	Asp		
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Cys	Gly	Lys	Ala	Phe	Ser	Asp	His	Ile	Gly	Leu	Asn	Gln	His	Arg	Arg		
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Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Asp	Val	Cys	His	Lys	Ser		
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Phe	Arg	Tyr	Gly	Ser	Ser	Leu	Thr	Val	His	Gln	Arg	Ile	His	Thr	Gly		
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Glu Lys Pro Tyr Glu Cys Asp Val Cys Arg Lys Ala Phe Ser His His	
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Ala Ser Leu Thr Gln His Gln Arg Val His Ser Gly Glu Lys Pro Phe	
575 580 585	
aag tgt aaa gag tgc gga aaa gct ttt agg cag aat ata cac ctt gcc	1886
Lys Cys Lys Glu Cys Gly Lys Ala Phe Arg Gln Asn Ile His Leu Ala	
590 595 600 605	
agt cat tta agg att cat act ggg gag aag cct ttt gaa tgt gcg gag	1934
Ser His Leu Arg Ile His Thr Gly Glu Lys Pro Phe Glu Cys Ala Glu	
610 615 620	
tgt gga aaa tcc ttc agc atc agt tct cag ctt gcc act cat cag aga	1982
Cys Gly Lys Ser Phe Ser Ile Ser Ser Gln Leu Ala Thr His Gln Arg	
625 630 635	
atc cat act gga gag aag ccc tat gaa tgt aag gtt tgt agt aaa gcg	2030
Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Val Cys Ser Lys Ala	
640 645 650	
ttc acc cag aag gct cac ctt gca cag cat cag aaa acc cat aca gga	2078
Phe Thr Gln Lys Ala His Leu Ala Gln His Gln Lys Thr His Thr Gly	
655 660 665	
gag aaa cca tat gag tgc aag gaa tgc ggt aaa gcc ttc agc cag acc	2126
Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Ser Gln Thr	
670 675 680 685	
aca cac ctc att caa cat cag aga gtt cac act ggt gag aaa ccc tat	2174
Thr His Leu Ile Gln His Gln Arg Val His Thr Gly Glu Lys Pro Tyr	
690 695 700	
aaa tgt atg gaa tgt ggg aag gcc ttt ggt gat aac tca tcc tgt act	2222
Lys Cys Met Glu Cys Gly Lys Ala Phe Gly Asp Asn Ser Ser Cys Thr	
705 710 715	
caa cat caa aga ctg cac act ggc caa aga cct tat gaa tgt att gag	2270
Gln His Gln Arg Leu His Thr Gly Gln Arg Pro Tyr Glu Cys Ile Glu	
720 725 730	
tgt gga aag gca ttc aag aca aaa tcc tcc ctt att tgt cat cgc aga	2318
Cys Gly Lys Ala Phe Lys Thr Lys Ser Ser Leu Ile Cys His Arg Arg	
735 740 745	
agt cat act gga gaa aaa cct tat gaa tgc agt gtg tgt ggc aaa gcc	2366
Ser His Thr Gly Glu Lys Pro Tyr Glu Cys Ser Val Cys Gly Lys Ala	
750 755 760 765	
ttt agt cat cgt caa tcc ctt agt gta cat cag aga atc cat tct gga	2414
Phe Ser His Arg Gln Ser Leu Ser Val His Gln Arg Ile His Ser Gly	
770 775 780	
aag aaa cca tat gaa tgt aag gaa tgt agg aaa acc ttc atc caa att	2462
Lys Lys Pro Tyr Glu Cys Lys Glu Cys Arg Lys Thr Phe Ile Gln Ile	
785 790 795	
gga cac ctt aat caa cat aag aga gtt cat act gga gag aga tct tat	2510
Gly His Leu Asn Gln His Lys Arg Val His Thr Gly Glu Arg Ser Tyr	
800 805 810	
aac tat aag aaa agc aga aaa gtc ttc agg caa act gct cac tta gct	2558

Asn Tyr Lys Lys Ser Arg Lys Val Phe Arg Gln Thr Ala His Leu Ala
 815 820 825
 cat cat cag cga att cat act gga gag tcg tca aca tgc ccc tct tta 2606
 His His Gln Arg Ile His Thr Gly Glu Ser Ser Thr Cys Pro Ser Leu
 830 835 840 845
 cct tcc acg tca aat cct gtg gat ctg ttt ccc aaa ttt ctc tgg aat 2654
 Pro Ser Thr Ser Asn Pro Val Asp Leu Phe Pro Lys Phe Leu Trp Asn
 850 855 860
 cca tcc tcc ctc cca tca cca tag cctcgagacg tcatttctgt ttgactactc 2708
 Pro Ser Ser Leu Pro Ser Pro *
 865
 cagcagttta aaaccccatc tcctgcctt tttgttttct ttttgcctt tattagttag 2768
 ttcttcacat aagtgtaaat gtaacttatt cactcctctt gtaaaactta tagtttcttt 2828
 aaattgggta atgtgtgaga tgtgctcagc acagtgcctg gtccatagta agtgctcagt 2888
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 ctttaaaaag atg cag cac ctg gac tgc gac ctt tgg ctc cag ctg gaa 169
 Met Gln His Leu Asp Cys Asp Leu Trp Leu Gln Leu Glu
 1 5 10
 ctt tcc agc cag tgt gtg ctt ctg ggg aac gga gtg gct atg aat ctg 217
 Leu Ser Ser Gln Cys Val Leu Leu Gly Asn Gly Val Ala Met Asn Leu
 15 20 25
 cat gta aag act ttg tcc ctc atg act tgg agg tcc aga ttc ctg gaa 265
 His Val Lys Thr Leu Ser Leu Met Thr Trp Arg Ser Arg Phe Leu Glu
 30 35 40 45
 gag tct ttt tgg tca ctg gag gaa aca gcg gca ttg gca aag caa ctg 313
 Glu Ser Phe Trp Ser Leu Glu Glu Thr Ala Ala Leu Ala Lys Gln Leu
 50 55 60
 ccc ttg aaa tcg cca agc gag aac att ttt ctg cac att gtg gac ttg 361
 Pro Leu Lys Ser Pro Ser Glu Asn Ile Phe Leu His Ile Val Asp Leu
 65 70 75
 tct gat ccc aag caa atc tgg aaa ttt gtt gaa aat ttc aag cag gaa 409
 Ser Asp Pro Lys Gln Ile Trp Lys Phe Val Glu Asn Phe Lys Gln Glu

80	85	90	
cat aaa ctc cat gtt ctg atc aat aat gca ggt tgc atg gtc aat aaa			457
His Lys Leu His Val Leu Ile Asn Asn Ala Gly Cys Met Val Asn Lys			
95	100	105	
aga gag ctc aca gaa gat gga ctt gaa aaa aac ttt gct gcc aat act			505
Arg Glu Leu Thr Glu Asp Gly Leu Glu Lys Asn Phe Ala Ala Asn Thr			
110	115	120	125
ctg ggt gtg tac att ctc acg acc ggc ctg atc cct gtg ctg gag aaa			553
Leu Gly Val Tyr Ile Leu Thr Thr Gly Leu Ile Pro Val Leu Glu Lys			
	130	135	140
gaa cac gac ccc cga gtg ata acc gtc tcc tca gga gga atg ttg gtt			601
Glu His Asp Pro Arg Val Ile Thr Val Ser Ser Gly Gly Met Leu Val			
	145	150	155
cag aaa ctg aac acc aat gat ctc cag tcc gaa aga aca cca ttt gat			649
Gln Lys Leu Asn Thr Asn Asp Leu Gln Ser Glu Arg Thr Pro Phe Asp			
	160	165	170
gga act atg gtc tat gca caa aac aag agg cag caa gtg gtt ctg acg			697
Gly Thr Met Val Tyr Ala Gln Asn Lys Arg Gln Gln Val Val Leu Thr			
	175	180	185
gag cgg tgg gcc caa ggg cac ccg gcc atc cat ttt tct tcc atg cat			745
Glu Arg Trp Ala Gln Gly His Pro Ala Ile His Phe Ser Ser Met His			
	190	195	200
cct ggc tgg gcc gac acc cca ggt gtg agg cag gcg atg ccg ggg ttc			793
Pro Gly Trp Ala Asp Thr Pro Gly Val Arg Gln Ala Met Pro Gly Phe			
	210	215	220
cac gcc agg ttc agg gac cgc ctg cgc tcc gag gcc cag ggc gcg gac			841
His Ala Arg Phe Arg Asp Arg Leu Ser Glu Ala Gln Gly Ala Asp			
	225	230	235
acc atg ctg tgg ctg gcc ctc tcc tct gcc gca gcc gca cag ccc agc			889
Thr Met Leu Trp Leu Ala Leu Ser Ser Ala Ala Ala Ala Gln Pro Ser			
	240	245	250
ggc cgc tct aga gta tcc ctc gag ggg ccc aag ctt acg cgt acc cag			937
Gly Arg Ser Arg Val Ser Leu Glu Gly Pro Lys Leu Thr Arg Thr Gln			
	255	260	265
ctt tct tgt aca aag tgg tcc cta tag tgagt cgtatatgag ctaggcacac			989
Leu Ser Cys Thr Lys Trp Ser Leu *			
	270	275	
agggcaatcc			999

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 <211> 1687
 <212> DNA
 <213> Homo sapiens

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 <222> (129)..(725)

<400> 797

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cgggcgccggc gtctccagg ccctcaccgg ggcggcccg ccctgtgccc gcagtggacc 120

tgctgcag atg ctg gag atg aac atg gcc atc gcc ttc ccc gca gcg ccc 170
Met Leu Glu Met Asn Met Ala Ile Ala Phe Pro Ala Ala Pro
1 5 10

ctg ctg acc gtc atc ctg gcc ctc gtc ggg atg gag gcc atc atg tcg 218
Leu Leu Thr Val Ile Leu Ala Leu Val Gly Met Glu Ala Ile Met Ser
15 20 25 30

gag ttc ttc aac gac acc acc acc gcc ttc tac atc atc ctc atc gtg 266
Glu Phe Phe Asn Asp Thr Thr Thr Ala Phe Tyr Ile Ile Leu Ile Val
35 40 45

tgg ctc gcg gac cag tat gac gcc atc tgc tgc cac acc agc acc agc 314
Trp Leu Ala Asp Gln Tyr Asp Ala Ile Cys Cys His Thr Ser Thr Ser
50 55 60

aag cgg cat tgg ctg cgg ttc ttc tat ctc tac cac ttc gcc ttc tat 362
Lys Arg His Trp Leu Arg Phe Phe Tyr Leu Tyr His Phe Ala Phe Tyr
65 70 75

gcc tat cac tac cgc ttc aat ggg cag tat agc agc ctg gcc ctg gtc 410
Ala Tyr His Tyr Arg Phe Asn Gly Gln Tyr Ser Ser Leu Ala Leu Val
80 85 90

acc tcc tgg ctc ttc atc cag cat tcc atg atc tac ttc ttc cac cac 458
Thr Ser Trp Leu Phe Ile Gln His Ser Met Ile Tyr Phe Phe His His
95 100 105 110

tac gag ctg cct gcc atc ctg cag cag gtc cgc atc cag gag atg ctg 506
Tyr Glu Leu Pro Ala Ile Leu Gln Gln Val Arg Ile Gln Glu Met Leu
115 120 125

ctt cag gcg ccg aca ctg ggc ccc ggg acc ccc acg gcg ctg ccc gat 554
Leu Gln Ala Pro Thr Leu Gly Pro Gly Thr Pro Thr Ala Leu Pro Asp
130 135 140

gac atg aac aac aac tcg ggc gcc ccg gct aca gcc cct gac tct gcc 602
Asp Met Asn Asn Asn Ser Gly Ala Pro Ala Thr Ala Pro Asp Ser Ala
145 150 155

ggc cag ccc ccc gcc ctg ggc ccc gtc tcg cct ggg ggc cag cgg gag 650
Gly Gln Pro Pro Ala Leu Gly Pro Val Ser Pro Gly Gly Gln Arg Glu
160 165 170

tcc cgg gcc tgt ggc agc ggc gcc cag ctc cct ggt ggc cgc ggc agc 698
Ser Arg Ala Cys Gly Ser Gly Ala Gln Leu Pro Gly Gly Arg Gly Ser
175 180 185 190

ctc agt ggc agc agc tgc cgg tgg tga cctgg gttggatggc agagaccgt 750
Leu Ser Gly Ser Ser Cys Arg Trp *
195

gccatcatca cagacgctc ctctctgtcc ggctgagcg cctccctcct ggagcggcgt 810

ccagccagcc cgctggggcc tgctgggggc ctccccacg cccccagga cagtgtcccc 870

ccgagtgact ccgcagcttc tgacacaact ccctggggg ctgcggtagg cgggcctagc 930

ccggcctcca tggccccaac ggaggcgccc tcggaggtgg ggtcctgagc cgcacagctg 990

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tggtccagtc ccactcgggg atggagtggg ccggcggcc aaccagtcac tcggggagga 1590
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cttgcacttt cttaagcagg atattcctgc tctgagctgg gagttctttg tcaatagatt 180
tgagacgctt tctttggaag ccagctaca tttggattgt aacaaggaat ttccttttcc 240
tacaaccatc actgctgtga ggaccaatgt tgctaacctc agcgatgcag ccttatggaa 300
gatcaagaga gctcgctttg caagaaaccg ccagaagagt gtacgttccc tgagggacag 360
cgtgaaaggg cctgtggaat ccaagagggc gctctccctc cctgagacct tgacctcaa 420
aattcct atg agg ttg acc agg cat gag cag tct gct cca gct ctc ggt 469
      Met Arg Leu Thr Arg His Glu Gln Ser Ala Pro Ala Leu Gly
        1             5             10

ggg aca ccc gaa cag acg cca gga caa caa tct cct gag aat gac aac 517
Gly Thr Pro Glu Gln Thr Pro Gly Gln Gln Ser Pro Glu Asn Asp Asn
  15             20             25             30

acc atc aag gac ctg ctc cca gaa gac gct ggg atc gac cac cag aca 565
Thr Ile Lys Asp Leu Leu Pro Glu Asp Ala Gly Ile Asp His Gln Thr
      35             40             45

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ggt cac cag ctg att aca gtg ctc atg aag ttc atg gcc aag gat gaa	613
Val His Gln Leu Ile Thr Val Leu Met Lys Phe Met Ala Lys Asp Glu	
50 55 60	
agc agc gct gag tca gac atc agc agt gca aag gcc ttc aac acg gtc	661
Ser Ser Ala Glu Ser Asp Ile Ser Ser Ala Lys Ala Phe Asn Thr Val	
65 70 75	
aag cga cac ctg tac gtc tta ctc ggc tat gac cag cag gaa ggt tgc	709
Lys Arg His Leu Tyr Val Leu Leu Gly Tyr Asp Gln Gln Glu Gly Cys	
80 85 90	
ttc atg att gca cct caa aaa atg cgc ctg tca act tgc ttt aat gca	757
Phe Met Ile Ala Pro Gln Lys Met Arg Leu Ser Thr Cys Phe Asn Ala	
95 100 105 110	
ttc att gca gga att gcc caa gtt atg gac tat aac att aac ttg gga	805
Phe Ile Ala Gly Ile Ala Gln Val Met Asp Tyr Asn Ile Asn Leu Gly	
115 120 125	
aaa cac ctt ctc ccc tta gtg gtt cag gtg ctc aaa tac tgc tct tgt	853
Lys His Leu Leu Pro Leu Val Val Gln Val Leu Lys Tyr Cys Ser Cys	
130 135 140	
cct caa ctc cgg cat tat ttc caa cag ccg cct cgt tgc tcc ctc tgg	901
Pro Gln Leu Arg His Tyr Phe Gln Gln Pro Pro Arg Cys Ser Leu Trp	
145 150 155	
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Ser Leu Lys Pro His Ile Arg Gln Met Trp Leu Lys Ala Leu Leu Val	
160 165 170	
atc ctt tac aag tat cca tac cga gac tgt gat atc agc aag atc ctg	997
Ile Leu Tyr Lys Tyr Pro Tyr Arg Asp Cys Asp Ile Ser Lys Ile Leu	
175 180 185 190	
ctg cat ctg att cac ata aca gtc aat aca ctc aat gcg cag tat cat	1045
Leu His Leu Ile His Ile Thr Val Asn Thr Leu Asn Ala Gln Tyr His	
195 200 205	
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Ser Cys Lys Pro His Ala Thr Ala Gly Pro Leu Tyr Ser Asp Asn Ser	
210 215 220	
aac ata agc aga tac agc gaa aaa gaa aaa gaa gaa gat agt gtt ttt	1141
Asn Ile Ser Arg Tyr Ser Glu Lys Glu Lys Glu Glu Asp Ser Val Phe	
225 230 235	
gat gaa tct gat att cat gat aca cct act gga ccc tgc aat aaa gag	1189
Asp Glu Ser Asp Ile His Asp Thr Pro Thr Gly Pro Cys Asn Lys Glu	
240 245 250	
tct caa act ttt ttt gca aga ttg aaa aga ata ggc ggc agc aaa atg	1237
Ser Gln Thr Phe Phe Ala Arg Leu Lys Arg Ile Gly Gly Ser Lys Met	
255 260 265 270	
gtg aaa tat cag ccg gtt gag atg aat gtt cag aga agt gaa ata gaa	1285
Val Lys Tyr Gln Pro Val Glu Met Asn Val Gln Arg Ser Glu Ile Glu	
275 280 285	
ctg gct gaa tat aga gag acg ggt gca tta caa gac agc ctt ctc cac	1333
Leu Ala Glu Tyr Arg Glu Thr Gly Ala Leu Gln Asp Ser Leu Leu His	
290 295 300	

tgt gtg aga gaa gaa agc att ccg aaa aaa aag cta cgc tct ttc aaa	1381
Cys Val Arg Glu Glu Ser Ile Pro Lys Lys Lys Leu Arg Ser Phe Lys	
305 310 315	
caa aaa tct ctt gat ata ggg aat gca gac tcg ctt ttg ttt aca tta	1429
Gln Lys Ser Leu Asp Ile Gly Asn Ala Asp Ser Leu Leu Phe Thr Leu	
320 325 330	
gac gaa cat cgt agg aag tcg tgc ata gat cgg tgt gac ata gag aag	1477
Asp Glu His Arg Arg Lys Ser Cys Ile Asp Arg Cys Asp Ile Glu Lys	
335 340 345 350	
cct ccg acc caa gct gcg tat atc gca caa aga cca aac gac cct gga	1525
Pro Pro Thr Gln Ala Ala Tyr Ile Ala Gln Arg Pro Asn Asp Pro Gly	
355 360 365	
cgt tct aga cag aac tct gct acg agg cct gac aat agt gaa atc ccc	1573
Arg Ser Arg Gln Asn Ser Ala Thr Arg Pro Asp Asn Ser Glu Ile Pro	
370 375 380	
gag aac cca gct atg gaa ggg ttt cca gat gct cga agg cct gtc ata	1621
Glu Asn Pro Ala Met Glu Gly Phe Pro Asp Ala Arg Arg Pro Val Ile	
385 390 395	
cca gag gtt agg tta aac tgt atg gag act ttc gag gtg aaa gtt gac	1669
Pro Glu Val Arg Leu Asn Cys Met Glu Thr Phe Glu Val Lys Val Asp	
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Ser Pro Val Lys Pro Ala Pro Lys Glu Asp Leu Asp Leu Ile Asp Leu	
415 420 425 430	
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Ser Ser Asp Ser Thr Ser Gly Pro Glu Lys His Ser Ile Leu Ser Thr	
435 440 445	
tcc gac agc gac tct ctt gta ttt gag cct ctt ccc cct ctc aga ata	1813
Ser Asp Ser Asp Ser Leu Val Phe Glu Pro Leu Pro Pro Leu Arg Ile	
450 455 460	
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Val Glu Ser Asp Glu Glu Glu Glu Thr Met Asn Gln Gly Asp Asp Gly	
465 470 475	
ccc tcc ggt aaa aat gct gcc tct tct ccc tcc atc ccc agc cat ccc	1909
Pro Ser Gly Lys Asn Ala Ala Ser Ser Pro Ser Ile Pro Ser His Pro	
480 485 490	
tcc gtc ctc agc ctg agc aca gct ccg ctt gta caa gta agt gtg gag	1957
Ser Val Leu Ser Leu Ser Thr Ala Pro Leu Val Gln Val Ser Val Glu	
495 500 505 510	
gat tgt tcc aaa gac ttt tct tct aag gac tca gga aat aat cag tca	2005
Asp Cys Ser Lys Asp Phe Ser Ser Lys Asp Ser Gly Asn Asn Gln Ser	
515 520 525	
gca ggg aac act gac tct gcc ctc atc act ctg gaa gac cct atg gac	2053
Ala Gly Asn Thr Asp Ser Ala Leu Ile Thr Leu Glu Asp Pro Met Asp	
530 535 540	
gcc gaa gga tcc tca aag cca gag gag ctg cca gag ttc tcc tgc ggt	2101
Ala Glu Gly Ser Ser Lys Pro Glu Glu Leu Pro Glu Phe Ser Cys Gly	
545 550 555	

agc cca ctg acg ctg aag caa aaa cga gac ctc ctt cag aag tcg ttt Ser Pro Leu Thr Leu Lys Gln Lys Arg Asp Leu Leu Gln Lys Ser Phe 560 565 570	2149
gct ctc ccc gag atg tcg ctg gat gat cac cct gac ccg ggc act gag Ala Leu Pro Glu Met Ser Leu Asp Asp His Pro Asp Pro Gly Thr Glu 575 580 585 590	2197
ggg gag aag cct ggg gag ctg atg cca agt tca ggg gca aaa acc gtc Gly Glu Lys Pro Gly Glu Leu Met Pro Ser Ser Gly Ala Lys Thr Val 595 600 605	2245
ctc ctc aaa gtt ccc gaa gat gca gag aac ccc aca gaa agt gag aag Leu Leu Lys Val Pro Glu Asp Ala Glu Asn Pro Thr Glu Ser Glu Lys 610 615 620	2293
cct gat acc agt gca gaa tct gat aca gaa cag aat cct gaa agg aag Pro Asp Thr Ser Ala Glu Ser Asp Thr Glu Gln Asn Pro Glu Arg Lys 625 630 635	2341
gtg gaa gag gat gga gct gag gaa tcc gaa ttt aag att cag att gtt Val Glu Glu Asp Gly Ala Glu Glu Ser Glu Phe Lys Ile Gln Ile Val 640 645 650	2389
ccc agg cag agg aag cag agg aag att gct gtc agt gct atc cag aga Pro Arg Gln Arg Lys Gln Arg Lys Ile Ala Val Ser Ala Ile Gln Arg 655 660 665 670	2437
gag tac ctc gac atc tcc ttc aac att ctg gac aaa ctg gga gaa cag Glu Tyr Leu Asp Ile Ser Phe Asn Ile Leu Asp Lys Leu Gly Glu Gln 675 680 685	2485
aaa gat cca gat cct tct act aaa gga ctt tca act ttg gaa atg cca Lys Asp Pro Asp Pro Ser Thr Lys Gly Leu Ser Thr Leu Glu Met Pro 690 695 700	2533
cga gaa tct tca tct gcc cct acg tta gat gca ggt gtg ccg gaa aca Arg Glu Ser Ser Ser Ala Pro Thr Leu Asp Ala Gly Val Pro Glu Thr 705 710 715	2581
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tcc ctg gga gtt ctg aca atg agc cag tta atg aag cgg cag ctg gag Ser Leu Gly Val Leu Thr Met Ser Gln Leu Met Lys Arg Gln Leu Glu 735 740 745 750	2677
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ata cag cct ggg aaa cgc cag tgt aac gtg cca aca tgc cta aac cct Ile Gln Pro Gly Lys Arg Gln Cys Asn Val Pro Thr Cys Leu Asn Pro 770 775 780	2773
gac ctg gag gga cag cca ttg agg atg aga ggt gcc acc aaa tcc agc Asp Leu Glu Gly Gln Pro Leu Arg Met Arg Gly Ala Thr Lys Ser Ser 785 790 795	2821
ctg cta tca gca cca agc ata gtc agt atg ttt gtg cct gca cct gaa Leu Leu Ser Ala Pro Ser Ile Val Ser Met Phe Val Pro Ala Pro Glu 800 805 810	2869

gag ttc act gac gag cag ccg acg gtg atg acg gac aaa tgc cat gac	2917
Glu Phe Thr Asp Glu Gln Pro Thr Val Met Thr Asp Lys Cys His Asp	
815 820 825 830	
tgt ggg gcc att ctt gaa gaa tac gat gaa gag aca ctt ggg cta gcc	2965
Cys Gly Ala Ile Leu Glu Glu Tyr Asp Glu Glu Thr Leu Gly Leu Ala	
835 840 845	
atc gtg gtc ctc tcc aca ttc att cac tta agc cca gac ctg gca gcc	3013
Ile Val Val Leu Ser Thr Phe Ile His Leu Ser Pro Asp Leu Ala Ala	
850 855 860	
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Pro Leu Leu Leu Asp Ile Met Gln Ser Val Gly Arg Leu Ala Ser Ser	
865 870 875	
act acc ttt tct aat caa gca gaa agc atg atg gtt ccc ggc aat gcg	3109
Thr Thr Phe Ser Asn Gln Ala Glu Ser Met Met Val Pro Gly Asn Ala	
880 885 890	
gcg ggg gtg gcc aag cag ttc ctg cgc tgc atc ttc cat cag ttg gcc	3157
Ala Gly Val Ala Lys Gln Phe Leu Arg Cys Ile Phe His Gln Leu Ala	
895 900 905 910	
ccc aac ggc atc ttc ccg cag ctg ttc caa agc acg atc aaa gat ggg	3205
Pro Asn Gly Ile Phe Pro Gln Leu Phe Gln Ser Thr Ile Lys Asp Gly	
915 920 925	
act ttt tta cgg acc tta gcc tcg tct ctg atg gac ttc aat gag ctg	3253
Thr Phe Leu Arg Thr Leu Ala Ser Ser Leu Met Asp Phe Asn Glu Leu	
930 935 940	
agc tcc atc gca gct ctc agt cag ctc cta gag ggt cta aat aac aaa	3301
Ser Ser Ile Ala Ala Leu Ser Gln Leu Leu Glu Gly Leu Asn Asn Lys	
945 950 955	
aag aat tta cca gca ggg ggt gct atg att cgc tgt ttg gaa aac att	3349
Lys Asn Leu Pro Ala Gly Gly Ala Met Ile Arg Cys Leu Glu Asn Ile	
960 965 970	
gca acc ttc atg gaa gct ttg cct atg gat tct cct agt agc ctc tgg	3397
Ala Thr Phe Met Glu Ala Leu Pro Met Asp Ser Pro Ser Ser Leu Trp	
975 980 985 990	
acc aca att agc aac cag ttt cag aca ttt ttt gcc aag ctg cct tgt	3445
Thr Thr Ile Ser Asn Gln Phe Gln Thr Phe Phe Ala Lys Leu Pro Cys	
995 1000 1005	
gtt tta cct ctg aag tgt tct tta gat tcc agt tta aga att atg att	3493
Val Leu Pro Leu Lys Cys Ser Leu Asp Ser Ser Leu Arg Ile Met Ile	
1010 1015 1020	
tgc ctc ttg aag atc cct tct acc aat gct aca agg agt ttg ttg gaa	3541
Cys Leu Leu Lys Ile Pro Ser Thr Asn Ala Thr Arg Ser Leu Leu Glu	
1025 1030 1035	
cca ttt tca aaa ctg ctc agc ttt gta att cag aat gcc gtc ttc act	3589
Pro Phe Ser Lys Leu Leu Ser Phe Val Ile Gln Asn Ala Val Phe Thr	
1040 1045 1050	
ctg gcc tac ctg gtg gag ctg tgt ggc tta tgt tac cga gct ttc act	3637
Leu Ala Tyr Leu Val Glu Leu Cys Gly Leu Cys Tyr Arg Ala Phe Thr	
1055 1060 1065 1070	

aag gaa cga gat aaa ttc tac ttg tct cgt agt gtt gtt cta gaa ctt Lys Glu Arg Asp Lys Phe Tyr Leu Ser Arg Ser Val Val Leu Glu Leu	3685
1075 1080 1085	
ctg cag gcc cta aag ctc aaa tct cct tta cca gat aca aac ctt ctt Leu Gln Ala Leu Lys Leu Lys Ser Pro Leu Pro Asp Thr Asn Leu Leu	3733
1090 1095 1100	
ctg ctt gtt cag ttt att tgt gca gat gct gga acc aaa cta gct gag Leu Leu Val Gln Phe Ile Cys Ala Asp Ala Gly Thr Lys Leu Ala Glu	3781
1105 1110 1115	
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1120 1125 1130	
act gca gcg atg gag tgt gtg agg cag tac atc aac gaa gtg ctg gat Thr Ala Ala Met Glu Cys Val Arg Gln Tyr Ile Asn Glu Val Leu Asp	3877
1135 1140 1145 1150	
ttc atg gca gac atg cac acg ctg acc aaa ctg aag agc cac atg aag Phe Met Ala Asp Met His Thr Leu Thr Lys Leu Lys Ser His Met Lys	3925
1155 1160 1165	
aca tgt tcc cag cct ctg cat gaa gat acc ttt ggg gga cat ctc aaa Thr Cys Ser Gln Pro Leu His Glu Asp Thr Phe Gly Gly His Leu Lys	3973
1170 1175 1180	
gtg ggg ctg gcc cag att gca gcc atg gac atc tca cgg ggc aac cac Val Gly Leu Ala Gln Ile Ala Ala Met Asp Ile Ser Arg Gly Asn His	4021
1185 1190 1195	
aga gat aac aaa gct gtg atc cgc tat ctg cct tgg ctt tat cat ccc Arg Asp Asn Lys Ala Val Ile Arg Tyr Leu Pro Trp Leu Tyr His Pro	4069
1200 1205 1210	
ccc tct gca atg cag caa gga cct aaa gaa ttc att gag tgt gtc tcc Pro Ser Ala Met Gln Gln Gly Pro Lys Glu Phe Ile Glu Cys Val Ser	4117
1215 1220 1225 1230	
cat atc cga ctg ttg tcc tgg ctg ctg ctg ggt tcc ctc act cac aat His Ile Arg Leu Leu Ser Trp Leu Leu Leu Gly Ser Leu Thr His Asn	4165
1235 1240 1245	
gca gtg tgc cca aat gcc tcc tct ccc tgc ctg ccc att cct ctg gat Ala Val Cys Pro Asn Ala Ser Ser Pro Cys Leu Pro Ile Pro Leu Asp	4213
1250 1255 1260	
gca ggc tcc cac gtt gca gac cat ctt att gtt atc ctg att gga ttt Ala Gly Ser His Val Ala Asp His Leu Ile Val Ile Leu Ile Gly Phe	4261
1265 1270 1275	
cca gag caa tca aag acc tcc gtg ctg cac atg tgc tcc ctc ttc cac Pro Glu Gln Ser Lys Thr Ser Val Leu His Met Cys Ser Leu Phe His	4309
1280 1285 1290	
gcg ttc atc ttt gct cag ctg tgg aca gtt tat tgc gag caa agt gcc Ala Phe Ile Phe Ala Gln Leu Trp Thr Val Tyr Cys Glu Gln Ser Ala	4357
1295 1300 1305 1310	
gtc gct aca aat ctc caa aat cag aat gaa ttc agc ttc acg gcg ata Val Ala Thr Asn Leu Gln Asn Gln Asn Glu Phe Ser Phe Thr Ala Ile	4405
1315 1320 1325	

ctg aca gca cta gaa ttt tgg agt agg gtg aca ccc agc atc ctt cag 4453
 Leu Thr Ala Leu Glu Phe Trp Ser Arg Val Thr Pro Ser Ile Leu Gln
 1330 1335 1340

cta atg gcc cat aac aaa gtg atg gta gaa atg gtg tgt ctc cat gtg 4501
 Leu Met Ala His Asn Lys Val Met Val Glu Met Val Cys Leu His Val
 1345 1350 1355

att agt tta atg gag gca ttg cag gaa tgc aat tcg acc att ttt gtc 4549
 Ile Ser Leu Met Glu Ala Leu Gln Glu Cys Asn Ser Thr Ile Phe Val
 1360 1365 1370

aag ctg ata cct atg tgg ttg cca atg att cag tca aat atc aag cac 4597
 Lys Leu Ile Pro Met Trp Leu Pro Met Ile Gln Ser Asn Ile Lys His
 1375 1380 1385 1390

tta tct gcg gga ctc cag ctt cgc ctc cag gct att cag aac cac gtg 4645
 Leu Ser Ala Gly Leu Gln Leu Arg Leu Gln Ala Ile Gln Asn His Val
 1395 1400 1405

aac cac cac agc cta agg acg ctg ccg ggc tgc ggc cag agc agt gct 4693
 Asn His His Ser Leu Arg Thr Leu Pro Gly Ser Gly Gln Ser Ser Ala
 1410 1415 1420

ggc ctg gca gcc ctc cga aag tgg ttg cag tgc act cag ttc aaa atg 4741
 Gly Leu Ala Ala Leu Arg Lys Trp Leu Gln Cys Thr Gln Phe Lys Met
 1425 1430 1435

gcc cag gtg gag atc cag tcc tcg gaa gca gcc tct caa ttt tat cct 4789
 Ala Gln Val Glu Ile Gln Ser Ser Glu Ala Ala Ser Gln Phe Tyr Pro
 1440 1445 1450

cta tga gtggactcct cggcgctcag tgtcaacact ctggtttagc aataatgggt 4845
 Leu *
 1455

ttaaaaacaa acaatttgat ccaagcaggt tggggaacat attggtactg tacattctct 4905

ttctagtttta gtaaaagatg tgcaaaggcc agagagggcc gaaaatgaag ctttcttgct 4965

acacatatatt ctgatgactc cttgggctat ctgattaagt gtttccttac attatttttt 5025

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 tgcctcgctt cccggcgcgg tcgcagccct cagcccaact aggata atg gcg aca 175
 Met Ala Thr

gct gag gta ctg aac att ggt aaa aaa tta tat gag ggt aaa aca aaa	223
Ala Glu Val Leu Asn Ile Gly Lys Lys Leu Tyr Glu Gly Lys Thr Lys	
5 10 15	
gaa gtc tac gaa ttg tta gac agt cca gga aaa gtc ctc ctg cag tcc	271
Glu Val Tyr Glu Leu Leu Asp Ser Pro Gly Lys Val Leu Leu Gln Ser	
20 25 30 35	
aag gac cag att aca gca gga aat gca gct aga aaa aac cac ctg gaa	319
Lys Asp Gln Ile Thr Ala Gly Asn Ala Ala Arg Lys Asn His Leu Glu	
40 45 50	
gga aaa gct gca atc tca aat aaa atc acc agt tgt att ttt cag tta	367
Gly Lys Ala Ala Ile Ser Asn Lys Ile Thr Ser Cys Ile Phe Gln Leu	
55 60 65	
tta cag gaa gca ggt att aaa act gcc ttc acc aga aaa tgt ggg gag	415
Leu Gln Glu Ala Gly Ile Lys Thr Ala Phe Thr Arg Lys Cys Gly Glu	
70 75 80	
aca gct ttc att gca ccg cag tgt gaa atg att cca att gaa tgg gtt	463
Thr Ala Phe Ile Ala Pro Gln Cys Glu Met Ile Pro Ile Glu Trp Val	
85 90 95	
tgc aga aga ata gca act ggt tct ttt ctc aaa aga aat cct ggt gtc	511
Cys Arg Arg Ile Ala Thr Gly Ser Phe Leu Lys Arg Asn Pro Gly Val	
100 105 110 115	
aag gaa gga tat aag ttt tac cca cct aaa gtg gag ttg ttt ttc aag	559
Lys Glu Gly Tyr Lys Phe Tyr Pro Pro Lys Val Glu Leu Phe Phe Lys	
120 125 130	
gat gat gcc aat aat gac cca cag tgg tct gag gaa cag ctg att gct	607
Asp Asp Ala Asn Asn Asp Pro Gln Trp Ser Glu Glu Gln Leu Ile Ala	
135 140 145	
gca aaa ttt tgc ttt gct gga ctt ctt ata ggc cag act gaa gtg gat	655
Ala Lys Phe Cys Phe Ala Gly Leu Leu Ile Gly Gln Thr Glu Val Asp	
150 155 160	
atc atg agt cat gct aca cag gct ata ttt gaa ata ctg gag aaa tcc	703
Ile Met Ser His Ala Thr Gln Ala Ile Phe Glu Ile Leu Glu Lys Ser	
165 170 175	
tgg ttg ccc cag aat tgt aca ctg gtt gat atg aag att gaa ttt ggt	751
Trp Leu Pro Gln Asn Cys Thr Leu Val Asp Met Lys Ile Glu Phe Gly	
180 185 190 195	
gtt gat gta acc acc aaa gaa att gtt ctt gct gat gtt att gac aat	799
Val Asp Val Thr Thr Lys Glu Ile Val Leu Ala Asp Val Ile Asp Asn	
200 205 210	
gat tcc tgg aga ctc tgg cca tca gga gat cga agc caa cag aaa gac	847
Asp Ser Trp Arg Leu Trp Pro Ser Gly Asp Arg Ser Gln Gln Lys Asp	
215 220 225	
aaa cag tct tat cgg gac ctc aaa gaa gta act cct gaa ggg ctc caa	895
Lys Gln Ser Tyr Arg Asp Leu Lys Glu Val Thr Pro Glu Gly Leu Gln	
230 235 240	
atg gta aag aaa aac ttt gag tgg gtt gca gag aga gta gag ttg ctt	943
Met Val Lys Lys Asn Phe Glu Trp Val Ala Glu Arg Val Glu Leu Leu	
245 250 255	

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Leu Lys Ser Glu Ser Gln Cys Arg Val Val Val Leu Met Gly Ser Thr
260                      265                      270                      275

tct gat ctt ggt cac tgt gaa aaa atc aag aag gcc tgt gga aat ttt      1039
Ser Asp Leu Gly His Cys Glu Lys Ile Lys Lys Ala Cys Gly Asn Phe
                280                      285                      290

ggc att cca tgt gaa ctt cga gta aca tct gcg cat aaa gga cca gat      1087
Gly Ile Pro Cys Glu Leu Arg Val Thr Ser Ala His Lys Gly Pro Asp
                295                      300                      305

gaa act ctg agg att aaa gct gag tat gaa ggg gat ggc att cct act      1135
Glu Thr Leu Arg Ile Lys Ala Glu Tyr Glu Gly Asp Gly Ile Pro Thr
                310                      315                      320

gta ttt gtg gca gtg gca ggc aga agt aat ggt ttg gga cca gtg atg      1183
Val Phe Val Ala Val Ala Gly Arg Ser Asn Gly Leu Gly Pro Val Met
    325                      330                      335

tct ggg aac act gca tat cca gtt atc agc tgt cct ccc ctc aca cca      1231
Ser Gly Asn Thr Ala Tyr Pro Val Ile Ser Cys Pro Pro Leu Thr Pro
340                      345                      350                      355

gac tgg gga gtt cag gat gtg tgg tct tct ctt cga cta ccc agt ggt      1279
Asp Trp Gly Val Gln Asp Val Trp Ser Ser Leu Arg Leu Pro Ser Gly
                360                      365                      370

ctt ggc tgt tca acc gta ctt tct cca gaa gga tca gct caa ttt gct      1327
Leu Gly Cys Ser Thr Val Leu Ser Pro Glu Gly Ser Ala Gln Phe Ala
                375                      380                      385

gct cag ata ttt ggg tta agc aac cat ttg gta tgg agc aaa ctg cga      1375
Ala Gln Ile Phe Gly Leu Ser Asn His Leu Val Trp Ser Lys Leu Arg
                390                      395                      400

gca agc att ttg aac aca tgg att tcc ttg aag cag gct gac aag aaa      1423
Ala Ser Ile Leu Asn Thr Trp Ile Ser Leu Lys Gln Ala Asp Lys Lys
    405                      410                      415

atc aga gaa tgt aat tta taa ga aagaatgccca ttgaattttt taggggaaaa      1476
Ile Arg Glu Cys Asn Leu *
420                      425

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agcctggagc gggtctgggc ttttggttct ctgcatcaac acagccagc atg cct	235
Met Pro	
1	
atg att tct gtg ctg ggc aaa atg ttt ctg tgg cag cgt gaa ggg cct	283
Met Ile Ser Val Leu Gly Lys Met Phe Leu Trp Gln Arg Glu Gly Pro	
5 10 15	
gga gga cga tgg act tgt cag aca agt cgc aga gtg tcc tcg gac ccc	331
Gly Gly Arg Trp Thr Cys Gln Thr Ser Arg Arg Val Ser Ser Asp Pro	
20 25 30	
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Ala Trp Ala Val Glu Trp Ile Glu Leu Pro Arg Gly Leu Ser Leu Ser	
35 40 45 50	
tct ttg gga tct gct cga acc ctc cga ggc tgg agc agg tcc tcc cgc	427
Ser Leu Gly Ser Ala Arg Thr Leu Arg Gly Trp Ser Arg Ser Ser Arg	
55 60 65	
cct tcc tcg gtg gac agt cag gac ttg cca gag gtg aat gtt gga gac	475
Pro Ser Ser Val Asp Ser Gln Asp Leu Pro Glu Val Asn Val Gly Asp	
70 75 80	
aca gtc gcg atg ctg ccc aag tcc cgg cga gcc cta act atc cag gag	523
Thr Val Ala Met Leu Pro Lys Ser Arg Arg Ala Leu Thr Ile Gln Glu	
85 90 95	
atc gct gcg ctg gcc agg tcc tcc ctg cat ggt att tcc cag gtg gtg	571
Ile Ala Ala Leu Ala Arg Ser Ser Leu His Gly Ile Ser Gln Val Val	
100 105 110	
aag gac cac gtg acc aag cct acc gcc atg gcc cag ggc cga gtg gct	619
Lys Asp His Val Thr Lys Pro Thr Ala Met Ala Gln Gly Arg Val Ala	
115 120 125 130	
cac ctc att gag tgg aag ggc tgg agc aag ccg agt gac tca cct gct	667
His Leu Ile Glu Trp Lys Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala	
135 140 145	
gcc ctg gaa tca gcc ttt tcc tcc tat tca gac ctc agc gag ggc gaa	715
Ala Leu Glu Ser Ala Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu	
150 155 160	
caa gag gct cgc ttt gca gca gga gtg gct gag cag ttt gcc atc gcg	763
Gln Glu Ala Arg Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala	
165 170 175	
gaa gcc aag ctc cga gca tgg tct tcg gtg gat ggc gag gac tcc act	811
Glu Ala Lys Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr	
180 185 190	
gat gac tcc tat gat gag gac ttt gct ggg gga atg gac aca gac atg	859
Asp Asp Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met	
195 200 205 210	
gct ggg cag ctg ccc ctg ggg ccg cac ctc cag gac ctg ttc acc ggc	907
Ala Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly	
215 220 225	

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cac cgg ttc tcc cgg cct gtg cgc cag ggc tcc gtg gag cct gag agc      955
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu Ser
      230                      235                      240

gac tgc tca cag acc gtg tcc cca gac acc ctg tgc tct agt ctg tgc      1003
Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser Leu Cys
      245                      250                      255

agc ctg gag gat ggg ttg ttg ggc tcc ccg gcc cgg ctg gcc tcc cag      1051
Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu Ala Ser Gln
      260                      265                      270

ctg ctg ggc gat gag ctg ctt ctc gcc aaa ctg ccc ccc agc cgg gaa      1099
Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro Pro Ser Arg Glu
      275                      280                      285                      290

agt gcc ttc cgc agc ctg ggc cca ctg gag gcc cag gac tca ctc tac      1147
Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala Gln Asp Ser Leu Tyr
      295                      300                      305

aac tcg ccc ctc aca gag tcc tgc ctt tcc ccc gcg gag gag gag cca      1195
Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser Pro Ala Glu Glu Glu Pro
      310                      315                      320

gcc ccc tgc aag gac tgc cag cca ctc tgc cca cca cta acg ggc agc      1243
Ala Pro Cys Lys Asp Cys Gln Pro Leu Cys Pro Pro Leu Thr Gly Ser
      325                      330                      335

tgg gaa cgg cag cgg caa gcc tct gac ctg gcc tct tct ggg gtg gtg      1291
Trp Glu Arg Gln Arg Gln Ala Ser Asp Leu Ala Ser Ser Gly Val Val
      340                      345                      350

tcc tta gat gag gat gag gca gag cca gag gaa cag tga cccacatcat      1340
Ser Leu Asp Glu Asp Glu Ala Glu Pro Glu Glu Gln *
      355                      360                      365

gcctggcagt ggcatgcac ccccggtgc tgccaggggc agagccttct gtgcccaagt      1400

gtgggctcaa ggctcccagc agagctccac agcctagagg gctcctggga gcgctcgctt      1460

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catgtcctgc ccccaactccc ggggcttgcc gggggttgcc cgggggcctc tggggcatgg      1580

ctacagctgt ggcagacagt gatgttcacg ttcttaaaat gccacacaca catttctcc      1640

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<210> 801
 <211> 3065
 <212> DNA
 <213> Homo sapiens

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 <222> (72)..(1958)

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Met	Ser	Pro	Gly	Gly	Lys	Phe	Asp	Phe	Asp	Asp	Gly	Gly	
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Cys Tyr Val Gly Gly Trp Glu Ala Gly Arg Ala His Gly Tyr Gly Val				20				25					
15													
tgc acg ggc ccc ggc gcc cag ggc gag tac agc ggc tgc tgg gca cac	206												
Cys Thr Gly Pro Gly Ala Gln Gly Glu Tyr Ser Gly Cys Trp Ala His				35			40					45	
30													
ggc ttc gag tca ctg ggc gtc ttc acg ggg ccc ggc gga cac agc tac	254												
Gly Phe Glu Ser Leu Gly Val Phe Thr Gly Pro Gly Gly His Ser Tyr				50			55					60	
cag ggc cac tgg cag cag ggc aag cgc gaa ggg ctg ggc gtg gag cgc	302												
Gln Gly His Trp Gln Gln Gly Lys Arg Glu Gly Leu Gly Val Glu Arg				65			70				75		
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Lys Ser Arg Trp Thr Tyr Arg Gly Glu Trp Leu Gly Gly Leu Lys Gly							85			90			
cgc agc ggc gtg tgg gaa agc gtg tcc ggc ctg cgc tac gcc ggg ctc	398												
Arg Ser Gly Val Trp Glu Ser Val Ser Gly Leu Arg Tyr Ala Gly Leu							100			105			
95													
tgg aag gac ggt ttc cag gac ggc tac ggc act gag acc tac tcc gac	446												
Trp Lys Asp Gly Phe Gln Asp Gly Tyr Gly Thr Glu Thr Tyr Ser Asp							115			120		125	
110													
gga ggc acc tac cag ggc cag tgg cag gcc ggg aag cgc cac ggc tac	494												
Gly Gly Thr Tyr Gln Gly Gln Trp Gln Ala Gly Lys Arg His Gly Tyr							130			135		140	
ggg gta cgc cag agt gtg ccc tac cat cag gcg gcg ctg ctg cgc tcg	542												
Gly Val Arg Gln Ser Val Pro Tyr His Gln Ala Ala Leu Leu Arg Ser							145			150		155	
ccc cgc cgc acc tcc ctg gat tcc ggc cac agc gac ccc ccg acg cca	590												
Pro Arg Arg Thr Ser Leu Asp Ser Gly His Ser Asp Pro Pro Thr Pro							160			165		170	
ccc ccg ccc ctg ccc ttg ccg ggc gac gag gga ggc agc ccc gcc tcg	638												
Pro Pro Pro Leu Pro Leu Pro Gly Asp Glu Gly Gly Ser Pro Ala Ser							175			180		185	
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Ser Thr Gly Pro Pro Gly Ser Glu Ala Ser Gly Pro Pro Ala Ala Ala	
255 260 265	
cgc ccc gcc ctc atc gag ggc tcg gcc aca gag gtg tac gcg ggc gag	926
Pro Pro Ala Leu Ile Glu Gly Ser Ala Thr Glu Val Tyr Ala Gly Glu	
270 275 280 285	
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Trp Arg Ala Asp Arg Ser Gly Phe Gly Val Ser Gln Arg Ser Asn	
290 295 300	
ggg ctg cgc tac gag ggc gag tgg ctg ggc aac cgg cgg cac ggc tac	1022
Gly Leu Arg Tyr Glu Gly Glu Trp Leu Gly Asn Arg Arg His Gly Tyr	
305 310 315	
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Gly Arg Thr Thr Arg Pro Asp Gly Ser Arg Glu Glu Gly Lys Tyr Lys	
320 325 330	
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Arg Asn Arg Leu Val His Gly Gly Arg Val Arg Ser Leu Leu Pro Leu	
335 340 345	
gcc ctt cgg cgg ggc aag gtt aag gag aag gtg gac agg gct gtc gag	1166
Ala Leu Arg Arg Gly Lys Val Lys Glu Lys Val Asp Arg Ala Val Glu	
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Gly Ala Arg Arg Ala Val Ser Ala Ala Arg Gln Arg Gln Glu Ile Ala	
370 375 380	
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Ala Ala Arg Ala Ala Asp Ala Leu Leu Lys Ala Val Ala Ala Ser Ser	
385 390 395	
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Gln Asp Leu Gln Pro Met Leu Glu Ala Pro Gly Arg Arg Pro Arg Gln	
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Asp Ser Glu Gly Ser Asp Thr Glu Pro Leu Asp Glu Asp Ser Pro Gly	
430 435 440 445	
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Val Tyr Glu Asn Gly Leu Thr Pro Ser Glu Gly Ser Pro Glu Leu Pro	
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 Thr Ser Ser Asp Lys Asp Phe Arg Phe Met Ala Thr Ser Asp Leu Met
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 Ser Glu Leu Gln Lys Asp Ser Ile Gln Leu Asp Glu Asp Ser Glu Arg
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 His Ala Ser Leu Leu His Cys Leu Leu Pro Gln Leu Ser Ser Pro Arg
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Thr Ser Leu Cys Leu Gln Tyr Ile Lys His Asp Pro Asn Tyr Asn Tyr				
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Trp Leu Glu Ala Met Glu Glu Pro Thr Gln Thr Gly Ser Asn Leu His				
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Val Leu Val Ser Gly Ile Ile Phe Ser Leu Ala Asp Arg Ser Ser Ser				
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Ser Thr Ile Arg Met Asp Ala Leu Ala Phe Leu Gln Gly Leu Leu Gly				
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Thr Glu Pro Ala Glu Ala Phe His Pro His Leu Pro Ile Leu Leu Pro				
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Pro Val Met Ala Cys Val Ala Asp Ser Phe Tyr Lys Ile Ala Ala Glu				

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cgg ctt ggg gat gac ctg gag ccc acg tta ctg ctc ctc ctg gac cgc Arg Leu Gly Asp Asp Leu Glu Pro Thr Leu Leu Leu Leu Leu Asp Arg 515 520 525			1642
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Val Thr Leu Ala Arg Leu Arg Ala Thr Asp Leu Asp Gln Glu Val Lys	
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Glu Arg Ala Ile Ser Cys Met Gly His Leu Val Gly His Leu Gly Asp	
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Arg Leu Gly Asp Asp Leu Glu Pro Thr Leu Leu Leu Leu Asp Arg	
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Val Gly Thr Arg Pro Pro Cys Val Asp Tyr Ala Lys Leu Ile Ser Leu	
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Met Ile Thr Leu Ile Thr Glu Gln Leu Gln Lys Gln Thr
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Leu Asp Glu Leu Lys Cys Thr Arg Phe Ser Ile Ser Leu Pro Leu Pro
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gat cat gca gac atc tcc aac tgt ggg aac tct ttc cag ctt gtg tct 324
Asp His Ala Asp Ile Ser Asn Cys Gly Asn Ser Phe Gln Leu Val Ser
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gaa ggt gct tcc tgg agg ggc ctg ccc cac tgt tcc tgt gct gag ttc 372
Glu Gly Ala Ser Trp Arg Gly Leu Pro His Cys Ser Cys Ala Glu Phe
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cag gac agc ctc aac ttc agc tac cat ccc tca ggc ctg agc ctg cac 420
Gln Asp Ser Leu Asn Phe Ser Tyr His Pro Ser Gly Leu Ser Leu His
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Leu Arg Pro Pro Ser Arg Gly Asn Ser Pro Lys Glu Gln Pro Phe Ser
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Gln Val Leu Arg Pro Glu Pro Pro Asp Pro Glu Lys Leu Pro Val Pro
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Trp Thr Pro Ile Lys His Arg Gly Ser Gly Gly Gly Gly Gly Pro Gln	
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Val Pro His Gln Ser Pro Pro Lys Arg Val Ser Ser Leu Arg Phe Leu	
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Cys Ala Ala Ser Pro Gln Ser Gly Ser Trp Glu Ser Asp Ala Glu Ser	
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Lys Arg Arg His Glu Glu Asp Pro Arg Arg Leu Arg Pro Ser Leu Asp	
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Cys Ser Pro Pro Pro Leu Ser Ala Ser Cys Ser Pro Thr Gly Gly Ser	
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Ser Gln Val Leu Ser Glu Ser Glu Glu Glu Glu Glu Gly Ala Val Arg	
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 Met Glu Pro Asp Ser Val Ile Glu Asp Lys Thr
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 atc gag ctc atg tgt tct gtg cca agg tct ttg tgg cta ggc tgc gcc 220
 Ile Glu Leu Met Cys Ser Val Pro Arg Ser Leu Trp Leu Gly Cys Ala
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 aac ctg gta gag agc atg tgc gca ctg agt tgc ctg cag agc atg ccc 268
 Asn Leu Val Glu Ser Met Cys Ala Leu Ser Cys Leu Gln Ser Met Pro
 30 35 40
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 Ser Val Arg Cys Leu Gln Ile Ser Asn Gly Thr Ser Ser Val Ile Val
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 Ser Arg Lys Arg Pro Ser Glu Gly Asn Tyr Gln Lys Glu Lys Asp Leu
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 Cys Ile Lys Tyr Phe Asp Gln Trp Ser Glu Ser Asp Gln Val Glu Phe
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 Val Glu His Leu Ile Ser Arg Met Cys His Tyr Gln His Gly His Ile
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 aac tct tac ctg aag ccc atg ttg cag cgg gac ttt att acc gct tta 508
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 Pro Glu Gln Gly Leu Asp His Ile Ala Glu Asn Ile Leu Ser Tyr Leu
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 Met Asp Gly Ser Thr Glu Arg Leu Glu Ala Arg Arg
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 Pro Ala Gly Arg Leu Pro Trp Ser Ser Arg Gln Glu Met Thr Arg Arg
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 ccc tcc ctg atg gcg ggc aga cag cac gga tgg agc gcc cag cag agt 207
 Pro Ser Leu Met Ala Gly Arg Gln His Gly Trp Ser Ala Gln Gln Ser
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 gcc acc gtg gcc aac cca gtg cct ggt gcc aac ccg gac ctg ctt ccc 255
 Ala Thr Val Ala Asn Pro Val Pro Gly Ala Asn Pro Asp Leu Leu Pro
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 His Phe Leu Val Glu Pro Glu Asp Val Tyr Ile Val Lys Asn Lys Pro
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 Val Leu Leu Val Cys Lys Ala Val Pro Ala Thr Gln Ile Phe Phe Lys
 80 85 90
 tgc aac ggg gag tgg gtg cgc cag gtg gac cac gtg atc gag cgc agc 399
 Cys Asn Gly Glu Trp Val Arg Gln Val Asp His Val Ile Glu Arg Ser
 95 100 105
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 Thr Asp Gly Ser Ser Gly Leu Pro Thr Met Glu Val Arg Ile Asn Val
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 tca agg cag cag gtc gag aag gtg ttc ggg ctg gag gaa tac tgg tgc 495
 Ser Arg Gln Gln Val Glu Lys Val Phe Gly Leu Glu Glu Tyr Trp Cys
 125 130 135 140
 cag tgc gtg gca tgg agc tcc tcg ggc acc acc aag agt cag aag gcc 543
 Gln Cys Val Ala Trp Ser Ser Ser Gly Thr Thr Lys Ser Gln Lys Ala
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 Tyr Ile Arg Ile Ala Tyr Leu Arg Lys Asn Phe Glu Gln Glu Pro Leu
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 Ala Lys Glu Val Ser Leu Glu Gln Gly Ile Val Leu Pro Cys Arg Pro
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 ccg gag ggc atc cct cca gcc gag gtg gag tgg ctc cgg aac gag gac 687
 Pro Glu Gly Ile Pro Pro Ala Glu Val Glu Trp Leu Arg Asn Glu Asp
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Leu Val Asp Pro Ser Leu Asp Pro Asn Val Tyr Ile Thr Arg Glu His	
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Ser Leu Val Val Arg Gln Ala Arg Leu Ala Asp Thr Ala Asn Tyr Thr	
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Cys Val Ala Lys Asn Ile Val Ala Arg Arg Arg Ser Ala Ser Ala Ala	
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Ala Ser Cys Gly Arg Gly Trp Gln Lys Arg Ser Arg Ser Cys Thr Asn	
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Pro Ala Pro Leu Asn Gly Gly Ala Phe Cys Glu Gly Gln Asn Val Gln	
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aaa aca gcc tgc gcc acc ctg tgc cca gtg gac ggc agc tgg agc ccg	1119
Lys Thr Ala Cys Ala Thr Leu Cys Pro Val Asp Gly Ser Trp Ser Pro	
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Trp Ser Lys Trp Ser Ala Cys Gly Leu Asp Cys Thr His Trp Arg Ser	
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Arg Glu Cys Ser Asp Pro Ala Pro Arg Asn Gly Gly Glu Glu Cys Gln	
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ggc act gac ctg gac acc cgc aac tgt acc agt gac ctc tgt gta cac	1263
Gly Thr Asp Leu Asp Thr Arg Asn Cys Thr Ser Asp Leu Cys Val His	
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Ala Val Cys Leu Val Leu Leu Leu Leu Val Leu Ile Leu Val Tyr Cys	
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Thr Ser Gly Phe Gln Pro Val Ser Ile Lys Pro Ser Lys Ala Asp Asn	
465 470 475	
ccc cat ctg ctc acc atc cag ccg gac ctc agc acc acc acc acc	1551
Pro His Leu Leu Thr Ile Gln Pro Asp Leu Ser Thr Thr Thr Thr	
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495 500 505	
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Gln Leu Thr Asn Gly His Leu Leu Ser Pro Leu Gly Gly Gly Arg His	
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Asn Met Thr Tyr Gly Thr Phe Asn Phe Leu Gly Gly Arg Leu Met Ile	
560 565 570	
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575 580 585	
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Cys Tyr Val Phe Thr Glu Gln Leu Gly Arg Phe Ala Leu Val Gly Glu	
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Pro Val Ala Cys Thr Ser Leu Glu Tyr Asn Ile Arg Val Tyr Cys Leu	
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ctg ggg gga cag ctg atc cag gag cca cgg gtc ctg cac ttc aag gac Leu Gly Gly Gln Leu Ile Gln Glu Pro Arg Val Leu His Phe Lys Asp 735 740 745	2319
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aag gac aca agg ttt gct gag ctg ctg gct ctg gag agt gaa gcg ggg Lys Asp Thr Arg Phe Ala Glu Leu Leu Ala Leu Glu Ser Glu Ala Gly 830 835 840	2607
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ttc ttt gcc tcc aag ccc agc ccc aca gcc atg atc ctc aac ctg tgg Phe Phe Ala Ser Lys Pro Ser Pro Thr Ala Met Ile Leu Asn Leu Trp 895 900 905	2799
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 ctteggcccc ggggtggtctc ccccgcccgg ggacccctg tgctccctt cccgggctcc 180
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 Met Arg Lys Phe Asn Ile Arg Lys Val Leu Asp Gly Leu Thr
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 Ala Gly Ser Ser Ser Ala Ser Gln Gln Gln Gln Gln Gln His Pro Pro
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 Gly Asn Arg Glu Pro Glu Ile Gln Glu Thr Leu Gln Ser Glu His Phe
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 cag ctc tgc aag act gtt cgc cat gga ttt ccc tat caa ccc tca gcc 372
 Gln Leu Cys Lys Thr Val Arg His Gly Phe Pro Tyr Gln Pro Ser Ala
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 115 120 125
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 Leu Arg Gln Lys Arg Pro Ala Ile Leu His Ser Leu Lys Phe Cys Arg
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Asp Thr Val Gly Arg Arg Pro Cys Leu Thr Val Met His Gly Lys Ser	
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Glu Glu Gln His Lys Thr Leu Gln Ser Glu Asn Ile Leu Tyr Asp Ile	
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785 790 795	
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Ile Glu Leu Ser Ser Lys Ser His Pro Gly Pro Val Val His Ile Ser	
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gat aat cca atg gac gag gga aag ctt ttg att ggc ttt gaa tct gga	2676
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835 840 845	
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850 855 860	
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Gln Phe Ile Cys Ser His Ser Asp Gly Thr Leu Thr Ile Trp Asn Val	
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Arg Ser Pro Ala Lys Pro Val Gln Thr Ile Thr Pro His Gly Lys Gln	
880 885 890	
tta aag gat ggg aag aag cca gaa cca tgc aaa cct atc ctc aag gtg	2916
Leu Lys Asp Gly Lys Lys Pro Glu Pro Cys Lys Pro Ile Leu Lys Val	
895 900 905 910	
gaa ttc aaa acg act aga tct ggg gag cct ttt att att tta tca gga	2964
Glu Phe Lys Thr Thr Arg Ser Gly Glu Pro Phe Ile Ile Leu Ser Gly	
915 920 925	
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Gly Leu Ser Tyr Asp Thr Val Gly Arg Arg Pro Cys Leu Thr Val Met	
930 935 940	
cat ggg aaa agc act gct gtg cta gaa atg gac tat tca att gtt gat	3060
His Gly Lys Ser Thr Ala Val Leu Glu Met Asp Tyr Ser Ile Val Asp	
945 950 955	


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Phe Leu Thr Leu Cys Glu Thr Pro Tyr Pro Asn Asp Phe Gln Glu Pro
    960                      965                      970

tat gct gtg gtt gtt ctt cta gaa aag gat tta gta ctt ata gac ctt      3156
Tyr Ala Val Val Val Leu Leu Glu Lys Asp Leu Val Leu Ile Asp Leu
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gca caa aat gga tat cct ata ttt gaa atc cct acc ctt tga gtaacat      3205
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His Leu Lys His Leu Arg Thr Leu Leu Ser Pro Gln Asp Gly Ala Ala
    5                      10                      15

aag gtg acc tgc atg gct tgg tcc cag aac aat gcc aaa ttt gct gtc      151
Lys Val Thr Cys Met Ala Trp Ser Gln Asn Asn Ala Lys Phe Ala Val
    20                      25                      30

tgc aca gtg gac cga gtg gtc ttg ctg tat gat gaa cat gga gaa cgg      199
Cys Thr Val Asp Arg Val Val Leu Leu Tyr Asp Glu His Gly Glu Arg
    35                      40                      45

aga gat aaa ttc tcc acc aaa cca gct gac atg aag tat ggc agg aag      247
Arg Asp Lys Phe Ser Thr Lys Pro Ala Asp Met Lys Tyr Gly Arg Lys
    50                      55                      60                      65

agc tat atg gtg aag ggc atg gct ttt tct cct gat tcc act aaa att      295
Ser Tyr Met Val Lys Gly Met Ala Phe Ser Pro Asp Ser Thr Lys Ile
    70                      75                      80

gcc ata gga cag act gac aac atc atc tat gtc tac aag att gga gaa      343
Ala Ile Gly Gln Thr Asp Asn Ile Ile Tyr Val Tyr Lys Ile Gly Glu
    85                      90                      95

gat tgg ggt gac aag aaa gtc atc tgc aac aag ttc atc cag acg agt      391
Asp Trp Gly Asp Lys Lys Val Ile Cys Asn Lys Phe Ile Gln Thr Ser
    100                      105                      110

gct gtc act tgt ctg caa tgg ccg gca gaa tac atc att gtc ttt gga      439
Ala Val Thr Cys Leu Gln Trp Pro Ala Glu Tyr Ile Ile Val Phe Gly
    115                      120                      125

ctg gct gaa ggg aag gtt cgt tta gca aac acc aaa act aat aaa tca      487

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Ser	Thr	Ile	Tyr	Gly	Thr	Glu	Ser	Tyr	Val	Val	Ser	Leu	Thr	Thr	Asn		
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Cys	Ser	Gly	Lys	Gly	Ile	Leu	Ser	Gly	His	Ala	Asp	Gly	Thr	Ile	Val		
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Arg	Tyr	Phe	Phe	Asp	Asp	Glu	Gly	Ser	Gly	Glu	Ser	Gln	Glu	Lys	Leu		
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gtt	aac	cac	ccg	tgt	cca	ccc	tat	gcc	ttg	gca	tgg	gca	acc	aat	agc	679	
Val	Asn	His	Pro	Cys	Pro	Tyr	Ala	Leu	Ala	Trp	Ala	Thr	Asn	Ser			
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Gly	His	Met	Leu	Gln	Thr	Phe	Asp	Tyr	Ser	Arg	Asp	Pro	Gln	Glu	Arg		
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Glu	Phe	Thr	Thr	Ala	Val	Ser	Ser	Pro	Gly	Gly	Gln	Ser	Val	Val	Leu		
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Gly	Ser	Tyr	Asp	Arg	Leu	Arg	Val	Phe	Asn	Trp	Ile	Pro	Arg	Arg	Ser		
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Ile	Trp	Glu	Glu	Ala	Lys	Pro	Lys	Glu	Ile	Thr	Asn	Leu	Tyr	Thr	Ile		
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act	gcc	ttg	gcc	tgg	aag	cgg	gat	ggc	tca	cgg	ctc	tgt	gtg	ggc	aca	967	
Thr	Ala	Leu	Ala	Trp	Lys	Arg	Asp	Gly	Ser	Arg	Leu	Cys	Val	Gly	Thr		
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Leu	Cys	Gly	Gly	Val	Glu	Gln	Phe	Asp	Cys	Cys	Leu	Arg	Arg	Ser	Ile		
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tac	aag	aac	aag	ttt	gag	ttg	acg	tat	gtg	gga	cct	agc	cag	gtg	att	1063	
Tyr	Lys	Asn	Lys	Phe	Glu	Leu	Thr	Tyr	Val	Gly	Pro	Ser	Gln	Val	Ile		
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Val	Lys	Asn	Leu	Ser	Ser	Gly	Thr	Arg	Val	Val	Leu	Lys	Ser	His	Tyr		
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ggc	tat	gag	gtg	gaa	gag	gtg	aaa	atc	cta	gga	aag	gaa	cgt	tac	ttg	1159	
Gly	Tyr	Glu	Val	Glu	Glu	Val	Lys	Ile	Leu	Gly	Lys	Glu	Arg	Tyr	Leu		
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Val	Ala	His	Thr	Ser	Glu	Thr	Leu	Leu	Leu	Gly	Asp	Leu	Asn	Thr	Asn		
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Phe	Phe	Glu	Asn	Glu	Asn	Val	Cys	Met	Ile	Phe	Asn	Ala	Gly	Glu	Leu		
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Thr	Leu	Val	Glu	Tyr	Gly	Asn	Asn	Asp	Thr	Leu	Gly	Ser	Val	Arg	Thr		
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Glu	Phe	Met	Asn	Pro	His	Leu	Ile	Ser	Val	Arg	Ile	Asn	Glu	Arg	Cys		
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cag	cga	gga	aca	gaa	gat	aat	aag	aaa	ttg	gct	tat	ctt	att	gat	att	1447	
Gln	Arg	Gly	Thr	Glu	Asp	Asn	Lys	Lys	Leu	Ala	Tyr	Leu	Ile	Asp	Ile		
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Lys	Thr	Ile	Ala	Ile	Val	Asp	Leu	Ile	Gly	Gly	Tyr	Asn	Ile	Gly	Thr		
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Val	Ser	His	Glu	Ser	Arg	Val	Asp	Trp	Leu	Glu	Leu	Asn	Glu	Thr	Gly		
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His	Lys	Leu	Leu	Phe	Arg	Asp	Arg	Lys	Leu	Arg	Leu	His	Leu	Tyr	Asp		
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Ile	Glu	Ser	Cys	Ser	Lys	Thr	Met	Ile	Leu	Asn	Phe	Cys	Ser	Tyr	Met		
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Gln	Trp	Val	Pro	Gly	Ser	Asp	Val	Leu	Val	Ala	Gln	Asn	Arg	Asn	Ser		
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Thr	Ile	Arg	Gly	Asp	Val	Ile	Gly	Leu	Glu	Arg	Gly	Gly	Gly	Lys	Thr		
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Glu	Val	Met	Val	Met	Glu	Gly	Val	Thr	Thr	Val	Ala	Tyr	Thr	Leu	Asp		
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Glu	Gly	Leu	Ile	Glu	Phe	Gly	Thr	Ala	Ile	Asp	Asp	Gly	Asn	Tyr	Ile		
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Arg	Ala	Thr	Ala	Phe	Leu	Glu	Thr	Leu	Glu	Met	Thr	Pro	Glu	Thr	Glu		
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Ala	Met	Trp	Lys	Thr	Leu	Ser	Lys	Leu	Ala	Leu	Glu	Ala	Arg	Gln	Leu		
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cac	att	gcg	gag	agg	tgc	ttt	tct	gct	ttg	ggc	caa	gta	gca	aaa	gct	2023	

His Ile Ala	Glu Arg Cys Phe Ser	Ala Leu Gly Gln Val	Ala Lys Ala	
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tat ggc gga gaa gga aca gac ttt tat cag gtc cga gca cgt cta gcc	2119			
Tyr Gly Gly Glu Gly Thr Asp Phe Tyr Gln Val Arg Ala Arg Leu Ala		675	680	685
atg ctg gaa aag aac tac aaa ctg gct gaa atg atc ttt ttg gaa cag	2167			
Met Leu Glu Lys Asn Tyr Lys Leu Ala Glu Met Ile Phe Leu Glu Gln		690	695	700
705				
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Asn Ala Val Glu Ala Met Gly Met Tyr Gln Glu Leu His Arg Trp		710	715	720
gat gag tgt atc gct gtg gct gaa gcc aag ggg cac cca gcc ctg gag	2263			
Asp Glu Cys Ile Ala Val Ala Glu Ala Lys Gly His Pro Ala Leu Glu		725	730	735
aag cta cgt cgt agt tac tac cag tgg ctg atg gac aca cag caa gag	2311			
Lys Leu Arg Arg Ser Tyr Tyr Gln Trp Leu Met Asp Thr Gln Gln Glu		740	745	750
gag cga gca ggt gaa cta cag gag agc caa ggg gat ggg cta gca gcc	2359			
Glu Arg Ala Gly Glu Leu Gln Glu Ser Gln Gly Asp Gly Leu Ala Ala		755	760	765
atc agc ctc tac ctc aaa gct ggg ctc cct gcc aaa gct gct cgg ctg	2407			
Ile Ser Leu Tyr Leu Lys Ala Gly Leu Pro Ala Lys Ala Ala Arg Leu		770	775	780
785				
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Ile Thr Ala Ala Leu Ile Lys Gly Glu Leu Tyr Glu Arg Ala Gly Asp		805	810	815
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Leu Phe Glu Lys Ile His Asn Pro Gln Lys Ala Leu Glu Cys Tyr Arg		820	825	830
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Lys Gly Asn Ala Phe Met Lys Ala Val Glu Leu Ala Arg Leu Ala Phe		835	840	845
cca gtg gag gtg gtg aaa cta gag gag gca tgg ggg gac cac ctg gtg	2647			
Pro Val Glu Val Val Lys Leu Glu Glu Ala Trp Gly Asp His Leu Val		850	855	860
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cag cag aag cag ctt gat gca gcc att aat cac tac atc gaa gcc agg	2695			
Gln Gln Lys Gln Leu Asp Ala Ala Ile Asn His Tyr Ile Glu Ala Arg		870	875	880
tgc tcc att aag gca att gag gcc gcc ctg ggt gcc cgc cag tgg aag	2743			
Cys Ser Ile Lys Ala Ile Glu Ala Ala Leu Gly Ala Arg Gln Trp Lys		885	890	895
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Lys Ala Ile Tyr Ile Leu Asp Leu Gln Asp Arg Asn Thr Ala Ser Lys	
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Tyr Tyr Pro Leu Val Ala Gln His Tyr Ala Ser Leu Gln Glu Tyr Glu	
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Ile Ala Glu Glu Leu Tyr Thr Lys Gly Asp Arg Thr Lys Asp Ala Ile	
930 935 940 945	
gac atg tac acc cag gct ggt cgt tgg gaa caa gcc cac aag ctg gcg	2935
Asp Met Tyr Thr Gln Ala Gly Arg Trp Glu Gln Ala His Lys Leu Ala	
950 955 960	
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Met Lys Cys Met Arg Pro Glu Asp Val Ser Val Leu Tyr Ile Thr Gln	
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Ala Gln Glu Met Glu Lys Gln Gly Lys Tyr Arg Glu Ala Glu Arg Leu	
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Tyr Val Thr Val Gln Glu Pro Asp Leu Ala Ile Thr Met Tyr Lys Lys	
995 1000 1005	
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Ala Tyr Arg Val Ala Arg Thr Gln Gly Gly Ala Asn Ala His Lys His	
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Val Ala Tyr Leu Trp Ala Lys Ser Leu Gly Glu Ala Ala Val Arg	
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Lys His Lys Thr Pro Glu Val His Leu Lys Tyr Ala Met Phe Leu Glu	
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Gln His Tyr Lys Glu Phe Leu Lys Asn Gln Gly Lys Val Asp Ser Leu	
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Leu His Lys Tyr Val Ala Leu Tyr Ala Thr His Leu Ile Arg Glu Gly	
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Ala His Tyr Tyr Ala Thr Arg Ser Ala Ala Gln Ser Val Lys Gln Leu	
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Leu Leu Pro Val Asp Lys Ala Phe Tyr Glu Ala Gly Ile Ala Ala Lys	
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Ala Val Gly Trp Asp Asn Met Ala Phe Ile Phe Leu Asn Arg Phe Leu	
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gac ctg acc gat gca atc gag gaa ggg act cta gat ggc ctt gac cac	4903
Asp Leu Thr Asp Ala Ile Glu Glu Gly Thr Leu Asp Gly Leu Asp His	
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Ser Asp Phe Gln Asp Thr Asp Ile Pro Phe Glu Val Pro Leu Pro Ala	
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Lys Gln His Val Pro Glu Ala Glu Arg Glu Glu Val Arg Asp Trp Val	
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Leu Thr Val Ser Met Asp Gln Arg Leu Glu Gln Val Leu Pro Arg Asp	
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Glu Arg Gly Ala Tyr Glu Ala Ser Leu Val Ala Ala Ser Thr Gly Val	
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Arg Ala Leu Pro Cys Leu Ile Thr Gly Tyr Pro Ile Leu Arg Asn Lys	
1685 1690 1695	
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Ile Glu Phe Lys Arg Pro Gly Lys Ala Ala Asn Lys Asp Asn Trp Asn	
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Lys Phe Leu Met Ala Ile Lys Thr Ser His Ser Pro Val Cys Gln Asp	
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Val Leu Lys Phe Ile Ser Gln Trp Cys Gly Gly Leu Pro Ser Thr Ser	
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Phe Ser Phe Gln *	
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Val Lys Glu Thr Leu Arg Arg Cys Gly Ala Ser Gly Asp Glu Cys Gly		
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Arg Leu Gln Tyr Ala Leu Thr Cys Leu Arg Lys Val Thr Gly Leu Gly		
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Gly Glu His Lys Glu Asp Ser Ser Trp Ser Ser Leu Asp Ala Arg Arg		
40 45 50		
gaa agt ggc tca ggg cct tcc acg gac acc ctc tca gca gcc agc ctg	246	
Glu Ser Gly Ser Gly Pro Ser Thr Asp Thr Leu Ser Ala Ala Ser Leu		
55 60 65		
ccc tgg ccc cca ggg agc tcc cag ctg ggc aga gca ggc aac agc gcc	294	
Pro Trp Pro Pro Gly Ser Ser Gln Leu Gly Arg Ala Gly Asn Ser Ala		
70 75 80 85		
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Gln Gly Pro Arg Ser Ile Ser Val Ser Ala Leu Pro Ala Ser Asp Ser		

90	95	100	
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cac gcc agc ggc cgg ctg acc ccc cgt gcc ctg cac agc ttc atc acc His Ala Ser Gly Arg Leu Thr Pro Arg Ala Leu His Ser Phe Ile Thr 120 125 130			438
ccg ccc acc aca ccc cag ctg cga cgg cac acc aag ctg aag cca cca Pro Pro Thr Thr Pro Gln Leu Arg Arg His Thr Lys Leu Lys Pro Pro 135 140 145			486
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cgc att gat gac gtc tcc tcg atg agg ttt gat ctc tcg cat gga tcc Arg Ile Asp Asp Val Ser Ser Met Arg Phe Asp Leu Ser His Gly Ser 185 190 195			630
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atg ata ttt gga gtg aag tgc aag cat tgc agg ttg aag tgt cac aac Met Ile Phe Gly Val Lys Cys Lys His Cys Arg Leu Lys Cys His Asn 230 235 240 245			774
aaa tgt acc aaa gaa gcc cct gcc tgt aga ata tcc ttc ctg cca cta Lys Cys Thr Lys Glu Ala Pro Ala Cys Arg Ile Ser Phe Leu Pro Leu 250 255 260			822
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aca aag aag gag cac cct ccg gcc atg aat cac ctg gac tcc agc agc Thr Lys Lys Glu His Pro Pro Ala Met Asn His Leu Asp Ser Ser Ser 295 300 305			966
aac cct tcc tcc acc acc tcc tcc aca ccc tcc tca ccg gcg ccc ttc Asn Pro Ser Ser Thr Thr Ser Ser Thr Pro Ser Ser Pro Ala Pro Phe 310 315 320 325			1014
ccg aca tca tcc aac cca tcc agc gcc acc acg ccc ccc aac ccc tca Pro Thr Ser Ser Asn Pro Ser Ser Ala Thr Thr Pro Pro Asn Pro Ser 330 335 340			1062
cct ggc cag cgg gac agc agg ttc aac ttc cca gct gcc tac ttc att Pro Gly Gln Arg Asp Ser Arg Phe Asn Phe Pro Ala Ala Tyr Phe Ile			1110

345	350	355	
cat cat aga cag cag ttt atc ttt cca gac att tca gcc ttt gca cac His His Arg Gln Gln Phe Ile Phe Pro Asp Ile Ser Ala Phe Ala His 360 365 370			1158
gca gcc ccg ctc cct gaa gct gcc gac ggt acc cgg ctc gat gac cag Ala Ala Pro Leu Pro Glu Ala Ala Asp Gly Thr Arg Leu Asp Asp Gln 375 380 385			1206
ccg aaa gca gat gtg ttg gaa gct cac gaa gcg gag gct gag gag cca Pro Lys Ala Asp Val Leu Glu Ala His Glu Ala Glu Ala Glu Glu Pro 390 395 400 405			1254
gag gct ggc aag tca gag gca gaa gac gat gag gac gag gtg gac gac Glu Ala Gly Lys Ser Glu Ala Glu Asp Asp Glu Asp Glu Val Asp Asp 410 415 420			1302
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ggc cac aac cag gac cac ctg aag ctc ttc aag aaa gag gtg atg aac Gly His Asn Gln Asp His Leu Lys Leu Phe Lys Lys Glu Val Met Asn 490 495 500			1542
tac cgg cag acg cgg cat gag aac gtg gtg ctc ttc atg ggg gcc tgc Tyr Arg Gln Thr Arg His Glu Asn Val Val Leu Phe Met Gly Ala Cys 505 510 515			1590
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aag acg agg caa atc gct cag gag atc atc aag ggc atg gga tat ctt Lys Thr Arg Gln Ile Ala Gln Glu Ile Ile Lys Gly Met Gly Tyr Leu 550 555 560 565			1734
cat gcc aag ggc atc gta cac aaa gat ctc aaa tct aag aac gtc ttc His Ala Lys Gly Ile Val His Lys Asp Leu Lys Ser Lys Asn Val Phe 570 575 580			1782
tat gac aac ggc aag gtg gtc atc aca gac ttc ggg ctg ttt ggg atc Tyr Asp Asn Gly Lys Val Val Ile Thr Asp Phe Gly Leu Phe Gly Ile 585 590 595			1830
tca ggc gtg gtc cga gag gga cgg cgt gag aac cag cta aag ctg tcc Ser Gly Val Val Arg Glu Gly Arg Arg Glu Asn Gln Leu Lys Leu Ser			1878

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ccc ggg aag gac gag gat cag ctg cca ttc tcc aaa gct gct gat gtc Pro Gly Lys Asp Glu Asp Gln Leu Pro Phe Ser Lys Ala Ala Asp Val 630 635 640 645			1974
tat gca ttt ggg act gtt tgg tat gag ctg caa gca aga gac tgg ccc Tyr Ala Phe Gly Thr Val Trp Tyr Glu Leu Gln Ala Arg Asp Trp Pro 650 655 660			2022
ttg aag aac cag gct gca gag gca tcc atc tgg cag att gga agc ggg Leu Lys Asn Gln Ala Ala Glu Ala Ser Ile Trp Gln Ile Gly Ser Gly 665 670 675			2070
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agt gag atc ctg tgc gcc tgc tgg gct ttc gac ctg cag gag aga ccc Ser Glu Ile Leu Ser Ala Cys Trp Ala Phe Asp Leu Gln Glu Arg Pro 695 700 705			2166
agc ttc agc ctg ctg atg gac atg ctg gag aaa ctt ccc aag ctg aac Ser Phe Ser Leu Leu Met Asp Met Leu Glu Lys Leu Pro Lys Leu Asn 710 715 720 725			2214
cgg cgg ctc tcc cac cct gga cac ttc tgg aag tca gct gac att aac Arg Arg Leu Ser His Pro Gly His Phe Trp Lys Ser Ala Asp Ile Asn 730 735 740			2262
agc agc aaa gtt gta ccc cgg ttt gaa agg ttt ggc ttg ggc gtc ctg Ser Ser Lys Val Val Pro Arg Phe Glu Arg Phe Gly Leu Gly Val Leu 745 750 755			2310
gag tcc agt aat cca aag atg tag ccagccatat gggttttctgc tgctgatctc Glu Ser Ser Asn Pro Lys Met * 760 765			2364
tttcttttta aaatgtgttt ctgaaacatc ccaacaacca ccacgacaaa aaaacactgc			2424
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2226

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Lys	Val	Lys	Lys	Arg	Ile	Gln	Leu	Ser	Pro	Lys	Lys	Ile	Lys	Gly	Tyr		
			245				250						255				
gaa	gta	aca	tca	aaa	gtt	gat	tta	tca	gaa	ctc	aca	agc	aat	gtt	ttc		933
Glu	Val	Thr	Ser	Lys	Val	Asp	Leu	Ser	Glu	Leu	Thr	Ser	Asn	Val	Phe		
			260				265					270					
cca	gaa	ggt	ctt	cct	cca	tca	tat	gta	ttt	gtg	tct	act	caa	aga	ttt		981
Pro	Glu	Gly	Leu	Pro	Pro	Ser	Tyr	Val	Phe	Val	Ser	Thr	Gln	Arg	Phe		
		275				280					285						
aaa	gtc	aag	aaa	att	tgg	gat	tta	tgg	aga	ata	tta	act	att	gat	gga		1029
Lys	Val	Lys	Lys	Ile	Trp	Asp	Leu	Trp	Arg	Ile	Leu	Thr	Ile	Asp	Gly		
				295					300					305			
tgc	cac	aaa	tag	cag	ttaccttaaa	tggtgtggac	aaaatcttat	tatttacaac									1084
Cys	His	Lys	*														
aaccagcgta	attaatggct	cacaagtgg	tacctttgct	aaccctcaag	ttaagacgtt												1144
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tgggcaaacc	caaattggaa	aatattctgg	aaaagaagaa	actgttcagt	ttgatgtcca												1324
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tggattttgc	cttaatggtc	ccagtgatgt	aggttcaact	ccagctccct	gtatttgtcc												1444
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cggatatatct	gggattacag	gatatcaggg	aattgcaggg	acaccaggtg	ttccaggatc												1624
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1				5				10					15				
agc	atg	ttt	ttg	aac	aca	tta	aca	ccg	aag	ttc	tac	gtg	gcc	cta	aca		96
Ser	Met	Phe	Leu	Asn	Thr	Leu	Thr	Pro	Lys	Phe	Tyr	Val	Ala	Leu	Thr		

20	25	30	
ggc act tcc tca cta ata tca ggg ctt att ttg ata ttt gaa tgg tgg			144
Gly Thr Ser Ser Leu Ile Ser Gly Leu Ile Leu Ile Phe Glu Trp Trp			
35	40	45	
tat ttt cgc aaa tac gga act tca ttc att gaa caa gtc tca gta agc			192
Tyr Phe Arg Lys Tyr Gly Thr Ser Phe Ile Glu Gln Val Ser Val Ser			
50	55	60	
cac ttg cgc ccc ctt ctg gga ggg gtt gac aac aac tct tcc aac aat			240
His Leu Arg Pro Leu Leu Gly Gly Val Asp Asn Asn Ser Ser Asn Asn			
65	70	75	80
tct aat tcc agt aac ggg gac tca gat tcc aat agg caa agt gtc tca			288
Ser Asn Ser Ser Asn Gly Asp Ser Asp Ser Asn Arg Gln Ser Val Ser			
85	90	95	
gaa tgc aaa gta tgg cga aat cca cta aat tta ttt agg ggt gct gaa			336
Glu Cys Lys Val Trp Arg Asn Pro Leu Asn Leu Phe Arg Gly Ala Glu			
100	105	110	
tac aat cgg tat act tgg gtg aca gga cga gag cct ctt act tac tat			384
Tyr Asn Arg Tyr Thr Trp Val Thr Gly Arg Glu Pro Leu Thr Tyr Tyr			
115	120	125	
gac atg aat ctc tct gcc caa gac cac cag aca ttc ttt act tgt gac			432
Asp Met Ash Leu Ser Ala Gln Asp His Gln Thr Phe Phe Thr Cys Asp			
130	135	140	
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Ser Asp His Leu Arg Pro Ala Asp Ala Ile Met Gln Lys Ala Trp Arg			
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gag aga aac ccc caa gct agg att tct gca gct cat gaa gcc ttg gag			528
Glu Arg Asn Pro Gln Ala Arg Ile Ser Ala Ala His Glu Ala Leu Glu			
165	170	175	
ata aat gag acg aga cac caa tgt ctt ggt gta cat caa aag aag gct			576
Ile Asn Glu Thr Arg His Gln Cys Leu Gly Val His Gln Lys Lys Ala			
180	185	190	
agc aat gtg tgc cag aag act cgg gag gac cag gga agc aaa gcc ctt			624
Ser Asn Val Cys Gln Lys Thr Arg Glu Asp Gln Gly Ser Lys Ala Leu			
195	200	205	
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Leu Glu Leu Gln Ala Tyr Ala Asp Val Gln Ala Val Leu Ala Lys Tyr			
210	215	220	
gat gat ata agc tta cca aag tca gca aca ata tgc tac aca gct gct			720
Asp Asp Ile Ser Leu Pro Lys Ser Ala Thr Ile Cys Tyr Thr Ala Ala			
225	230	235	240
ttg ctc aaa gca aga gct gtc tct gac aaa ttc tct cct gag gct gca			768
Leu Leu Lys Ala Arg Ala Val Ser Asp Lys Phe Ser Pro Glu Ala Ala			
245	250	255	
tct cgg cgg ggg ctg agc aca gca gag atg aat gca gta gag gcc att			816
Ser Arg Arg Gly Leu Ser Thr Ala Glu Met Asn Ala Val Glu Ala Ile			
260	265	270	
cat aga gct gtg gaa ttc aat cct cat gtg cca aaa tac cta cta gaa			864
His Arg Ala Val Glu Phe Asn Pro His Val Pro Lys Tyr Leu Leu Glu			

275	280	285	
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Met Lys Ser Leu Ile Leu Pro Pro Glu His Ile Leu Lys Arg Gly Asp			
290	295	300	
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Ser Glu Ala Ile Ala Tyr Ala Phe Phe His Leu Ala His Trp Lys Arg			
305	310	315	320
gtg gaa ggg gct ttg aat ctt ttg cat tgt acg tgg gaa ggc act ttt			1008
Val Glu Gly Ala Leu Asn Leu Leu His Cys Thr Trp Glu Gly Thr Phe			
325	330	335	
cgg atg atc cct tat ccc ttg gaa aag ggg cac cta ttt tat cct tac			1056
Arg Met Ile Pro Tyr Pro Leu Glu Lys Gly His Leu Phe Tyr Pro Tyr			
340	345	350	
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Pro Ile Cys Thr Glu Thr Ala Asp Arg Glu Leu Leu Pro Ser Phe His			
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gaa gtc tca gtt tac cca aag aag gag ctt ccc ttc ttt att ctc ttt			1152
Glu Val Ser Val Tyr Pro Lys Lys Glu Leu Pro Phe Phe Ile Leu Phe			
370	375	380	
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Thr Ala Gly Leu Cys Ser Phe Thr Ala Met Leu Ala Leu Leu Thr His			
385	390	395	400
cag ttc ccg gaa ctt atg ggg gtc ttc gca aaa gct gtg agt gtt tgc			1248
Gln Phe Pro Glu Leu Met Gly Val Phe Ala Lys Ala Val Ser Val Cys			
405	410	415	
cta gag gga ggc ctt ggg gaa tgg atg ggg aaa gcc aag ggc ata aaa			1296
Leu Glu Gly Gly Leu Gly Glu Trp Met Gly Lys Ala Lys Gly Ile Lys			
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Ala Ala *			
435			

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taaaccgaa aaagaaaatg aagaaaaaga aatacgtgaa ttctggcaca gaccagatc	180
aacttcactg tggccattga ttctactgcc tccaatggga acccctcaca gtccacatcc	240

ctgcactac	atg agc ccc tac cag ctg aac gcc tac gcg ctg gcg ctg	288
	Met Ser Pro Tyr Gln Leu Asn Ala Tyr Ala Leu Ala Leu	
	1 5 10	
act gcc gtc gga gag atc atc cag cac tac gac agt gac aag atg ttc	336	
Thr Ala Val Gly Glu Ile Ile Gln His Tyr Asp Ser Asp Lys Met Phe		
15 20 25		
cct gcc ctg ggc ttc ggg gcc aag ctg ccc ccg gat ggc aga gtg tcc	384	
Pro Ala Leu Gly Phe Gly Ala Lys Leu Pro Pro Asp Gly Arg Val Ser		
30 35 40 45		
cac gag ttc cca ctg aat ggc aac cag gag aac ccc tca tgc tgc ggc	432	
His Glu Phe Pro Leu Asn Gly Asn Gln Glu Asn Pro Ser Cys Cys Gly		
50 55 60		
atc gac ggc atc ctg gag gcc tac cac cgc agc ctg cgc act gtg cag	480	
Ile Asp Gly Ile Leu Glu Ala Tyr His Arg Ser Leu Arg Thr Val Gln		
65 70 75		
ctg tac ggc ccc acc aac ttt gcc ccc gtg gtc acc cac gtg gcc agg	528	
Leu Tyr Gly Pro Thr Asn Phe Ala Pro Val Val Thr His Val Ala Arg		
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Asn Ala Ala Ala Val Gln Asp Gly Ser Gln Tyr Ser Val Leu Leu Ile		
95 100 105		
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Ile Thr Asp Gly Val Ile Ser Asp Met Ala Gln Thr Lys Glu Ala Ile		
110 115 120 125		
gtc aac gct gcc aag ctc ccc atg tcc atc att atc gtc ggc gtg ggc	672	
Val Asn Ala Ala Lys Leu Pro Met Ser Ile Ile Ile Val Gly Val Gly		
130 135 140		
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Gln Ala Glu Phe Asp Ala Met Val Glu Leu Asp Gly Asp Asp Val Arg		
145 150 155		
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Ile Ser Ser Arg Gly Lys Leu Ala Glu Arg Asp Ile Val Gln Phe Val		
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Pro Phe Arg Asp Tyr Val Asp Arg Thr Gly Asn His Val Leu Ser Met		
175 180 185		
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Ala Arg Leu Ala Arg Asp Val Leu Ala Glu Ile Pro Asp Gln Leu Val		
190 195 200 205		
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Ser Tyr Met Lys Ala Gln Gly Ile Arg Pro Arg Ser Pro Pro Ala Ala		
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Pro Thr His Ser Pro Ser Gln Ser Pro Ala Arg Thr Pro Pro Ala Cys		
225 230 235		
ccc ctg cac acg cac atc tga ac ctggtctcag caggcaggtg gctggggcct	1013	
Pro Leu His Thr His Ile *		
240		


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gggagaggcc aggtgaatgg gaggccaggg cccagactc cccgaagttg gcctgcccgg 1073
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<210> 813
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<220>
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 <222> (217) .. (3495)

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gtaccaagaa ggggagtgcc cgcggcaggg ttcattgaaa aaatccttag tgatattgac 180
atgtctcaag tgacataaat tagccaatga ctcgga atg atg gat tct ccg aag 234
Met Met Asp Ser Pro Lys
1 5
att gga aat ggt ttg cca gtg att gga cca ggg act gat ata ggg ata 282
Ile Gly Asn Gly Leu Pro Val Ile Gly Pro Gly Thr Asp Ile Gly Ile
10 15 20
tct tca ctc cac atg gtg ggg tat ttg gga aaa aat ttt gat tca gct 330
Ser Ser Leu His Met Val Gly Tyr Leu Gly Lys Asn Phe Asp Ser Ala
25 30 35

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aaa gtt cca tca gat gag tat tgc cct gct tgt aga gag aag gga aag	378
Lys Val Pro Ser Asp Glu Tyr Cys Pro Ala Cys Arg Glu Lys Gly Lys	
40 45 50	
tta aaa gcc tta aag act tac cga att agt ttt caa gaa tct atc ttt	426
Leu Lys Ala Leu Lys Thr Tyr Arg Ile Ser Phe Gln Glu Ser Ile Phe	
55 60 65 70	
ttg tgt gag gat ctg cag tgc atc tat cct ttg ggc tct aaa tca ctt	474
Leu Cys Glu Asp Leu Gln Cys Ile Tyr Pro Leu Gly Ser Lys Ser Leu	
75 80 85	
aat aac cta att tct cct gat ttg gaa gaa tgt cac act cca cat aag	522
Asn Asn Leu Ile Ser Pro Asp Leu Glu Glu Cys His Thr Pro His Lys	
90 95 100	
cct cag aaa agg aag agc tta gaa agc agc tat aag gat tca ctc ctt	570
Pro Gln Lys Arg Lys Ser Leu Glu Ser Ser Tyr Lys Asp Ser Leu Leu	
105 110 115	
tta gca aat tcc aaa aag act aga aat tat att gct att gac ggt gga	618
Leu Ala Asn Ser Lys Lys Thr Arg Asn Tyr Ile Ala Ile Asp Gly Gly	
120 125 130	
aaa gtt ttg aac agc aaa cat aat gga gaa gta tat gac gaa acc tcg	666
Lys Val Leu Asn Ser Lys His Asn Gly Glu Val Tyr Asp Glu Thr Ser	
135 140 145 150	
tca aac tta cct gat agt agt ggt caa cag aat cca att agg aca gct	714
Ser Asn Leu Pro Asp Ser Ser Gly Gln Gln Asn Pro Ile Arg Thr Ala	
155 160 165	
gat tcc ttg gag cgg aat gag att ttg gaa gct gat act gtt gac atg	762
Asp Ser Leu Glu Arg Asn Glu Ile Leu Glu Ala Asp Thr Val Asp Met	
170 175 180	
gct act aca aaa gat cct gct aca gtt gat gtc tct gga act ggc aga	810
Ala Thr Thr Lys Asp Pro Ala Thr Val Asp Val Ser Gly Thr Gly Arg	
185 190 195	
cct tcc cct caa aat gaa gga tgt aca tct aaa ctg gaa atg cca ctg	858
Pro Ser Pro Gln Asn Glu Gly Cys Thr Ser Lys Leu Glu Met Pro Leu	
200 205 210	
gag agc aaa tgt aca tca ttt ccc cag gct tta tgt gtc cag tgg aaa	906
Glu Ser Lys Cys Thr Ser Phe Pro Gln Ala Leu Cys Val Gln Trp Lys	
215 220 225 230	
aat gct tat gct ctc tgt tgg tta gac tgt atc ctg tca gct ttg gtg	954
Asn Ala Tyr Ala Leu Cys Trp Leu Asp Cys Ile Leu Ser Ala Leu Val	
235 240 245	
cac tcg gaa gag tta aag aac acc gtg act gga ctg tgc tcg aag gag	1002
His Ser Glu Glu Leu Lys Asn Thr Val Thr Gly Leu Cys Ser Lys Glu	
250 255 260	
gaa tct ata ttc tgg cgg ttg ctt aca aaa tat aat caa gca aat aca	1050
Glu Ser Ile Phe Trp Arg Leu Leu Thr Lys Tyr Asn Gln Ala Asn Thr	
265 270 275	
ctt cta tat acc agt caa ttg agt ggt gtt aaa gat gga gat tgt aaa	1098
Leu Leu Tyr Thr Ser Gln Leu Ser Gly Val Lys Asp Gly Asp Cys Lys	
280 285 290	

aaa ctt acc tca gaa ata ttt gca gag ata gag acc tgt ctg aat gaa	1146
Lys Leu Thr Ser Glu Ile Phe Ala Glu Ile Glu Thr Cys Leu Asn Glu	
295 300 305 310	
gtt aga gat gaa att ttt att agc ctt cag ccc cag ctt aga tgc aca	1194
Val Arg Asp Glu Ile Phe Ile Ser Leu Gln Pro Gln Leu Arg Cys Thr	
315 320 325	
tta ggt gat atg gaa agc cct gtg ttt gca ttt ccc ctg ctc tta aaa	1242
Leu Gly Asp Met Glu Ser Pro Val Phe Ala Phe Pro Leu Leu Leu Lys	
330 335 340	
cta gaa acc cac att gaa aag ctc ttc cta tat tct ttt tct tgg gac	1290
Leu Glu Thr His Ile Glu Lys Leu Phe Leu Tyr Ser Phe Ser Trp Asp	
345 350 355	
ttt gaa tgt tcg cag tgt gga cac caa tat caa aac agg cat atg aag	1338
Phe Glu Cys Ser Gln Cys Gly His Gln Tyr Gln Asn Arg His Met Lys	
360 365 370	
agt ctg gtc acc ttt aca aat gtc atc cct gag tgg cac cca ctt aat	1386
Ser Leu Val Thr Phe Thr Asn Val Ile Pro Glu Trp His Pro Leu Asn	
375 380 385 390	
gct gcc cat ttt ggc cca tgt aac aat tgc aac agt aaa tca caa ata	1434
Ala Ala His Phe Gly Pro Cys Asn Asn Cys Asn Ser Lys Ser Gln Ile	
395 400 405	
aga aaa atg gta tta gaa aaa gta tct ccc ata ttc atg ttg cac ttt	1482
Arg Lys Met Val Leu Glu Lys Val Ser Pro Ile Phe Met Leu His Phe	
410 415 420	
gta gaa ggc tta cca cag aat gac ttg cag cac tat gca ttt cat ttt	1530
Val Glu Gly Leu Pro Gln Asn Asp Leu Gln His Tyr Ala Phe His Phe	
425 430 435	
gaa ggc tgt ctt tat cag ata act tct gta att cag tat cga gca aat	1578
Glu Gly Cys Leu Tyr Gln Ile Thr Ser Val Ile Gln Tyr Arg Ala Asn	
440 445 450	
aat cat ttt ata aca tgg att tta gat gct gat gga agt tgg ctg gaa	1626
Asn His Phe Ile Thr Trp Ile Leu Asp Ala Asp Gly Ser Trp Leu Glu	
455 460 465 470	
tgt gat gac tta aaa ggc cca tgt tct gaa agg cac aag aaa ttt gaa	1674
Cys Asp Asp Leu Lys Gly Pro Cys Ser Glu Arg His Lys Lys Phe Glu	
475 480 485	
gtt cct gct tca gag ata cat att gtt att tgg gaa aga aaa ata tcc	1722
Val Pro Ala Ser Glu Ile His Ile Val Ile Trp Glu Arg Lys Ile Ser	
490 495 500	
caa gtg aca gat aaa gaa gct gcc tgc ctt cca ctt aaa aag act aat	1770
Gln Val Thr Asp Lys Glu Ala Ala Cys Leu Pro Leu Lys Lys Thr Asn	
505 510 515	
gac caa cac gct ctc agt aat gag aaa cca gta tct tta aca tcg tgt	1818
Asp Gln His Ala Leu Ser Asn Glu Lys Pro Val Ser Leu Thr Ser Cys	
520 525 530	
tct gtg ggt gat gct gcc tca gct gaa aca gcc tca gta act cac cct	1866
Ser Val Gly Asp Ala Ala Ser Ala Glu Thr Ala Ser Val Thr His Pro	
535 540 545 550	

aaa gat ata tca gtt gcc cct cgt act ctt tca cag gac aca gct gta	1914
Lys Asp Ile Ser Val Ala Pro Arg Thr Leu Ser Gln Asp Thr Ala Val	
555 560 565	
act cat gga gat cat tta ctt tca ggt cca aaa ggt ttg gtt gac aat	1962
Thr His Gly Asp His Leu Leu Ser Gly Pro Lys Gly Leu Val Asp Asn	
570 575 580	
att tta cct ctg aca ctt gaa gaa act atc cag aaa aca gcc tca gtt	2010
Ile Leu Pro Leu Thr Leu Glu Glu Thr Ile Gln Lys Thr Ala Ser Val	
585 590 595	
tca cag tta aat tct gaa gct ttc ctg tta gaa aat aaa cct gta gca	2058
Ser Gln Leu Asn Ser Glu Ala Phe Leu Leu Glu Asn Lys Pro Val Ala	
600 605 610	
gaa aat aca gga att ctc aaa acc aat act ttg cta tca caa gaa tca	2106
Glu Asn Thr Gly Ile Leu Lys Thr Asn Thr Leu Leu Ser Gln Glu Ser	
615 620 625 630	
cta atg gct tct tca gta tca gct cca tgt aat gaa aag ctt att caa	2154
Leu Met Ala Ser Ser Val Ser Ala Pro Cys Asn Glu Lys Leu Ile Gln	
635 640 645	
gac caa ttt gtg gac ata agt ttt cca tcc caa gtt gta aat aca aac	2202
Asp Gln Phe Val Asp Ile Ser Phe Pro Ser Gln Val Val Asn Thr Asn	
650 655 660	
atg cag tca gta cag ctg aat aca gaa gat act gta aat act aaa tct	2250
Met Gln Ser Val Gln Leu Asn Thr Glu Asp Thr Val Asn Thr Lys Ser	
665 670 675	
gtg aat aat act gat gct act ggt ctt ata cag gga gtg aag tca gta	2298
Val Asn Asn Thr Asp Ala Thr Gly Leu Ile Gln Gly Val Lys Ser Val	
680 685 690	
gaa att gag aag gac gct cag tta aaa caa ttc ctt aca cca aaa act	2346
Glu Ile Glu Lys Asp Ala Gln Leu Lys Gln Phe Leu Thr Pro Lys Thr	
695 700 705 710	
gaa caa tta aaa cca gaa cgt gtc aca tct cag gta tct aat ttg aag	2394
Glu Gln Leu Lys Pro Glu Arg Val Thr Ser Gln Val Ser Asn Leu Lys	
715 720 725	
aaa aaa gaa act aca gca gat tct caa acc aca aca tct aag tca tta	2442
Lys Lys Glu Thr Thr Ala Asp Ser Gln Thr Thr Thr Ser Lys Ser Leu	
730 735 740	
cag aat cag tct ctg aaa gaa aat cag aag aag cca ttt gtg gga agt	2490
Gln Asn Gln Ser Leu Lys Glu Asn Gln Lys Lys Pro Phe Val Gly Ser	
745 750 755	
tgg gtt aaa ggc tta ata agc agg ggt gct tct ttt atg cca ctc tgt	2538
Trp Val Lys Gly Leu Ile Ser Arg Gly Ala Ser Phe Met Pro Leu Cys	
760 765 770	
gtt tca gct cat aat aga aac act ata act gat tta caa cct tca gtt	2586
Val Ser Ala His Asn Arg Asn Thr Ile Thr Asp Leu Gln Pro Ser Val	
775 780 785 790	
aaa ggg gta aat aat ttt ggt ggc ttt aaa act aaa ggt ata aac cag	2634
Lys Gly Val Asn Asn Phe Gly Gly Phe Lys Thr Lys Gly Ile Asn Gln	
795 800 805	

aag gcc agc cac gta.tcc aag aaa gct cgt aag agt gca agt aag cct Lys Ala Ser His Val Ser Lys Lys Ala Arg Lys Ser Ala Ser Lys Pro 810 815 820	2682
dct ccc atc agt aag cca cca gca ggc cct cca tcg tct aat ggc aca Pro Pro Ile Ser Lys Pro Pro Ala Gly Pro Pro Ser Ser Asn Gly Thr 825 830 835	2730
gct gcc cac cca cat gct cat gct gct tca gaa gtt ttg gaa aag tct Ala Ala His Pro His Ala His Ala Ala Ser Glu Val Leu Glu Lys Ser 840 845 850	2778
gga agc acc tca tgt gga gct caa ctc aac cac agt tct tat ggg aat Gly Ser Thr Ser Cys Gly Ala Gln Leu Asn His Ser Ser Tyr Gly Asn 855 860 865 870	2826
ggg att tct tca gca aac cat gaa gac ttg gtg gaa ggt cag att cat Gly Ile Ser Ser Ala Asn His Glu Asp Leu Val Glu Gly Gln Ile His 875 880 885	2874
aaa ctt cgt cta aaa ctt cgt aaa aag cta aag gca gaa aag aag aaa Lys Leu Arg Leu Lys Leu Arg Lys Lys Leu Lys Ala Glu Lys Lys Lys 890 895 900	2922
tta gct gct ctt atg tct tcc ccg caa agc aga aca gtt cga agt gaa Leu Ala Ala Leu Met Ser Ser Pro Gln Ser Arg Thr Val Arg Ser Glu 905 910 915	2970
aat cta gaa cag gtg ccc cag gat ggg tct cca aat gat tgt gaa tca Asn Leu Glu Gln Val Pro Gln Asp Gly Ser Pro Asn Asp Cys Glu Ser 920 925 930	3018
ata gag gac ttg tta aat gag cta cca tat cca att gat att gcc aat Ile Glu Asp Leu Leu Asn Glu Leu Pro Tyr Pro Ile Asp Ile Ala Asn 935 940 945 950	3066
gag tct gca tgc acc act gtt cct ggt gtt tcc ctg tac agt agt caa Glu Ser Ala Cys Thr Thr Val Pro Gly Val Ser Leu Tyr Ser Ser Gln 955 960 965	3114
act cat gaa gaa att tta gcg gaa tta ttg tct cct aca cct gtt tca Thr His Glu Glu Ile Leu Ala Glu Leu Ser Pro Thr Pro Val Ser 970 975 980	3162
aca gag ctg tca gaa aat ggg gaa ggt gac ttt agg tat ttg gga atg Thr Glu Leu Ser Glu Asn Gly Glu Gly Asp Phe Arg Tyr Leu Gly Met 985 990 995	3210
gga gat agt cat atc cca cca cca gta cca agt gaa ttc aat gat gtt Gly Asp Ser His Ile Pro Pro Pro Val Pro Ser Glu Phe Asn Asp Val 1000 1005 1010	3258
tcc cag aac aca cat ctg aga cag gac cat aat tat tgt agc ccc acc Ser Gln Asn Thr His Leu Arg Gln Asp His Asn Tyr Cys Ser Pro Thr 1015 1020 1025 1030	3306
aag aaa aat cca tgt gaa gtt cag cca gac tct ctg aca aat aat gcc Lys Lys Asn Pro Cys Glu Val Gln Pro Asp Ser Leu Thr Asn Asn Ala 1035 1040 1045	3354
tgc gtt aga aca tta aac ttg gag agt ccg atg aag act gat att ttc Cys Val Arg Thr Leu Asn Leu Glu Ser Pro Met Lys Thr Asp Ile Phe 1050 1055 1060	3402

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gat gag ttt ttt tcc tcc tca gca tta aat gct tta gca aat gac aca      3450
Asp Glu Phe Phe Ser Ser Ser Ala Leu Asn Ala Leu Ala Asn Asp Thr
      1065              1070              1075

tta gac cta cct cat ttc gat gaa tat ctg ttt gag aat tat tga att      3498
Leu Asp Leu Pro His Phe Asp Glu Tyr Leu Phe Glu Asn Tyr *
      1080              1085              1090

aatgcttggt aacttttttc atataatatt tattattatt agaagaactt acaatgtggt      3558

caggtagtgt ttatacactg gacttggtga attacttggt taataacccat gaacaaaatg      3618

caagggtttaa cctttggttc tgcccatgaa gcatgtaatc tttcttacac attaaaaatca      3678

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<210> 814
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<213> Homo sapiens

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<222> (71)..(1789)

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caaggagggc   atg gat gct aag tca cta act gcc tgg tcc cgg aca ctg      109
              Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu
              1              5              10

gtg acc ttc aag gat gta ttt gtg gac ttc acc agg gag gag tgg aag      157
Val Thr Phe Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys
      15              20              25

ctg ctg gac act gct cag cag atc gtg tac aga aat gtg atg ctg gag      205
Leu Leu Asp Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu
      30              35              40              45

aac tat aag aac ctg gtt tcc ttg ggt tat cag ctt act aag cca gat      253
Asn Tyr Lys Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp
              50              55              60

gtg atc ctc cgg ttg gag aag gga gaa gag ccc tgg ctg gtg gag aga      301
Val Ile Leu Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg
              65              70              75

gaa att cac caa gag acc cat cct gat tca gag act gca ttt gaa atc      349
Glu Ile His Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile
              80              85              90

aaa tca tca gtt tcc agc agg agc att ttt aaa gat aag caa tcc tgt      397
Lys Ser Ser Val Ser Ser Arg Ser Ile Phe Lys Asp Lys Gln Ser Cys
      95              100              105

gac att aaa atg gaa gga atg gca agg aat gat ctc tgg tat ttg tca      445
Asp Ile Lys Met Glu Gly Met Ala Arg Asn Asp Leu Trp Tyr Leu Ser
      110              115              120              125

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tta gaa gaa gtc tgg aaa tgt aga gac cag tta gac aag tat cag gaa	493
Leu Glu Glu Val Trp Lys Cys Arg Asp Gln Leu Asp Lys Tyr Gln Glu	
130 135 140	
aac cca gag aga cat ttg agg caa gtg gca ttc acc caa aag aaa gta	541
Asn Pro Glu Arg His Leu Arg Gln Val Ala Phe Thr Gln Lys Lys Val	
145 150 155	
ctt act cag gag aga gtc tct gaa agt ggt aaa tat ggg gga aac tgt	589
Leu Thr Gln Glu Arg Val Ser Glu Ser Gly Lys Tyr Gly Gly Asn Cys	
160 165 170	
ctt ctt cct gct cag cta gta ctg aga gag tat ttc cat aaa cgt gac	637
Leu Leu Pro Ala Gln Leu Val Leu Arg Glu Tyr Phe His Lys Arg Asp	
175 180 185	
tca cat act aaa agt tta aaa cat gat tta gtt ctt aat ggt cat cag	685
Ser His Thr Lys Ser Leu Lys His Asp Leu Val Leu Asn Gly His Gln	
190 195 200 205	
gac agt tgt gca agt aac agt aat gaa tgt ggt caa act ttc tgt caa	733
Asp Ser Cys Ala Ser Asn Ser Asn Glu Cys Gly Gln Thr Phe Cys Gln	
210 215 220	
aac att cac ctt att cag ttt gca aga act cac aca ggt gat aaa tcc	781
Asn Ile His Leu Ile Gln Phe Ala Arg Thr His Thr Gly Asp Lys Ser	
225 230 235	
tac aaa tgc cct gat aat gac aac tct ctt act cat ggt tca tct ctt	829
Tyr Lys Cys Pro Asp Asn Asp Asn Ser Leu Thr His Gly Ser Ser Leu	
240 245 250	
ggt ata tca aag ggc ata cat aga gag aaa ccc tat gaa tgt aag gaa	877
Gly Ile Ser Lys Gly Ile His Arg Glu Lys Pro Tyr Glu Cys Lys Glu	
255 260 265	
tgt gga aaa ttc ttc agc tgg cgc tct aat ctt act agg cat cag ctt	925
Cys Gly Lys Phe Phe Ser Trp Arg Ser Asn Leu Thr Arg His Gln Leu	
270 275 280 285	
att cat act gga gaa aaa ccc tat gag tgt aaa gaa tgt gga aag tct	973
Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ser	
290 295 300	
ttc agc egg agt tct cac ctc att gga cat caa aag acc cat act ggt	1021
Phe Ser Arg Ser Ser His Leu Ile Gly His Gln Lys Thr His Thr Gly	
305 310 315	
gag gaa ccc tat gaa tgt aaa gaa tgt gga aaa tcc ttc agc tgg ttc	1069
Glu Glu Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ser Phe Ser Trp Phe	
320 325 330	
tct cac ctt gtt act cat cag aga act cat aca gga gac aaa ctg tac	1117
Ser His Leu Val Thr His Gln Arg Thr His Thr Gly Asp Lys Leu Tyr	
335 340 345	
aca tgt aat cag tgt ggg aaa tct ttt gtt cat agc tct agg ctt att	1165
Thr Cys Asn Gln Cys Gly Lys Ser Phe Val His Ser Ser Arg Leu Ile	
350 355 360 365	
aga cac cag agg aca cat act gga gag aaa ccc tat gaa tgt cct gaa	1213
Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Pro Glu	
370 375 380	

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tgt ggg aaa tct ttc aga cag agc aca cat ctc att ctg cat cag aga      1261
Cys Gly Lys Ser Phe Arg Gln Ser Thr His Leu Ile Leu His Gln Arg
          385                      390                      395

acc cat gtg aga gtg agg ccc tat gaa tgc aat gaa tgt gga aag tct      1309
Thr His Val Arg Val Arg Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ser
          400                      405                      410

tac agc cag aga tct cac ctt gtt gtg cat cat aga att cac act gga      1357
Tyr Ser Gln Arg Ser His Leu Val Val His His Arg Ile His Thr Gly
          415                      420                      425

cta aaa cct ttt gag tgt aag gat tgt gga aaa tgt ttt agt cga agc      1405
Leu Lys Pro Phe Glu Cys Lys Asp Cys Gly Lys Cys Phe Ser Arg Ser
          430                      435                      440                      445

tct cac ctt tat tca cat caa aga acc cac act gga gag aaa cca tat      1453
Ser His Leu Tyr Ser His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
          450                      455                      460

gag tgt cat gat tgt gga aaa tct ttc agc cag agt tct gcc ctt att      1501
Glu Cys His Asp Cys Gly Lys Ser Phe Ser Gln Ser Ser Ala Leu Ile
          465                      470                      475

gtg cat cag agg ata cac act gga gag aaa cca tat gaa tgc tgt cag      1549
Val His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Cys Gln
          480                      485                      490

tgt ggg aaa gcc ttc atc cgg aag aat gac ctc att aag cac cag aga      1597
Cys Gly Lys Ala Phe Ile Arg Lys Asn Asp Leu Ile Lys His Gln Arg
          495                      500                      505

att cat gtt gga gaa gag acc tat aaa tgt aat caa tgt ggc att atc      1645
Ile His Val Gly Glu Glu Thr Tyr Lys Cys Asn Gln Cys Gly Ile Ile
          510                      515                      520                      525

ttc agc cag aac tct cca ttt ata gtt cat caa ata gct cac act gga      1693
Phe Ser Gln Asn Ser Pro Phe Ile Val His Gln Ile Ala His Thr Gly
          530                      535                      540

gag cag ttc tta aca tgc aat caa tgt ggg aca gcg ctt gtt aat acc      1741
Glu Gln Phe Leu Thr Cys Asn Gln Cys Gly Thr Ala Leu Val Asn Thr
          545                      550                      555

tct aac ctt att gga tac cag aca aat cat att aga gaa aat gct tac      1789
Ser Asn Leu Ile Gly Tyr Gln Thr Asn His Ile Arg Glu Asn Ala Tyr
          560                      565                      570

taataaatat gggaattttt cacaaagaaa aaaaaaaaaa      1828

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<210> 815
<211> 1426
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<220>
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<222> (71)..(1390)

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	Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu	
	1 5 10	
gtg acc ttc aag gat gta ttt gtg gac ttc acc agg gag gag tgg aag	157	
Val Thr Phe Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys		
15 20 25		
ctg ctg gac act gct cag cag atc gtg tac aga aat gtg atg ctg gag	205	
Leu Leu Asp Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu		
30 35 40 45		
aac tat aag aac ctg gtt tcc ttg ggt tat cag ctt act aag cca gat	253	
Asn Tyr Lys Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp		
50 55 60		
gtg atc ctc cgg ttg gag aag gga gaa gag ccc tgg ctg gtg gag aga	301	
Val Ile Leu Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg		
65 70 75		
gaa att cac caa gag acc cat cct gat tca gag act gca ttt gaa atc	349	
Glu Ile His Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile		
80 85 90		
aaa tca tca gtt tcc agc agg agc att ttt aaa gat aag caa tcc tgt	397	
Lys Ser Ser Val Ser Ser Arg Ser Ile Phe Lys Asp Lys Gln Ser Cys		
95 100 105		
gac att aaa atg gaa gga atg gca agg aat gat ctc tgg tat ttg tca	445	
Asp Ile Lys Met Glu Gly Met Ala Arg Asn Asp Leu Trp Tyr Leu Ser		
110 115 120 125		
tta gaa gaa gtc tgg aaa tgt aga gac cag tta gac aag tat cag gaa	493	
Leu Glu Glu Val Trp Lys Cys Arg Asp Gln Leu Asp Lys Tyr Gln Glu		
130 135 140		
aac cca gag aga cat ttg agg cat cag ctt att cat act gga gaa aaa	541	
Asn Pro Glu Arg His Leu Arg His Gln Leu Ile His Thr Gly Glu Lys		
145 150 155		
ccc tat gag tgt aaa gaa tgt gga aag tct ttc agc cgg agt tct cac	589	
Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ser Phe Ser Arg Ser Ser His		
160 165 170		
ctc att gga cat caa aag acc cat act ggt gag gaa ccc tat gaa tgt	637	
Leu Ile Gly His Gln Lys Thr His Thr Gly Glu Glu Pro Tyr Glu Cys		
175 180 185		
aaa gaa tgt gga aaa tcc ttc agc tgg ttc tct cac ctt gtt act cat	685	
Lys Glu Cys Gly Lys Ser Phe Ser Trp Phe Ser His Leu Val Thr His		
190 195 200 205		
cag aga act cat aca gga gac aaa ctg tac aca tgt aat cag tgt ggg	733	
Gln Arg Thr His Thr Gly Asp Lys Leu Tyr Thr Cys Asn Gln Cys Gly		
210 215 220		
aaa tct ttt gtt cat agc tct agg ctt att aga cac cag agg aca cat	781	
Lys Ser Phe Val His Ser Ser Arg Leu Ile Arg His Gln Arg Thr His		
225 230 235		
act gga gag aaa ccc tat gaa tgt cct gaa tgt ggg aaa tct ttc aga	829	
Thr Gly Glu Lys Pro Tyr Glu Cys Pro Glu Cys Gly Lys Ser Phe Arg		
240 245 250		

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cag agc aca cat ctc att ctg cat cag aga acc cat gtg aga gtg agg      877
Gln Ser Thr His Leu Ile Leu His Gln Arg Thr His Val Arg Val Arg
      255                      260                      265

ccc tat gaa tgc aat gaa tgt gga aag tct tac agc cag aga tct cac      925
Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ser Tyr Ser Gln Arg Ser His
      270                      275                      280                      285

ctt gtt gtg cat cat aga att cac act gga cta aaa cct ttt gag tgt      973
Leu Val Val His His Arg Ile His Thr Gly Leu Lys Pro Phe Glu Cys
                      290                      295                      300

aag gat tgt gga aaa tgt ttt agt cga agc tct cac ctt tat tca cat      1021
Lys Asp Cys Gly Lys Cys Phe Ser Arg Ser Ser His Leu Tyr Ser His
                      305                      310                      315

caa aga acc cac act gga gag aaa cca tat gag tgt cat gat tgt gga      1069
Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys His Asp Cys Gly
                      320                      325                      330

aaa tct ttc agc cag agt tct gcc ctt att gtg cat cag agg ata cac      1117
Lys Ser Phe Ser Gln Ser Ser Ala Leu Ile Val His Gln Arg Ile His
                      335                      340                      345

act gga gag aaa cca tat gaa tgc tgt cag tgt ggg aaa gcc ttc atc      1165
Thr Gly Glu Lys Pro Tyr Glu Cys Cys Gln Cys Gly Lys Ala Phe Ile
      350                      355                      360                      365

cgg aag aat gac ctc att aag cac cag aga att cat gtt gga gaa gag      1213
Arg Lys Asn Asp Leu Ile Lys His Gln Arg Ile His Val Gly Glu Glu
                      370                      375                      380

acc tat aaa tgt aat caa tgt ggc att atc ttc agc cag aac tct cca      1261
Thr Tyr Lys Cys Asn Gln Cys Gly Ile Ile Phe Ser Gln Asn Ser Pro
                      385                      390                      395

ttt ata gtt cat caa ata gct cac act gga gag cag ttc tta aca tgc      1309
Phe Ile Val His Gln Ile Ala His Thr Gly Glu Gln Phe Leu Thr Cys
                      400                      405                      410

aat caa tgt ggg aca gcg ctt gtt aat acc tct aac ctt att gga tac      1357
Asn Gln Cys Gly Thr Ala Leu Val Asn Thr Ser Asn Leu Ile Gly Tyr
                      415                      420                      425

cag aca aat cat att aga gaa aat gct tac taa taaatatg ggaatttttc      1408
Gln Thr Asn His Ile Arg Glu Asn Ala Tyr *
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<210> 816
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<213> Homo sapiens

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<222> (289)..(2127)

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<220>

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<400> 816

2241

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tta agt aca aac aaa aac caa ctg aag cag ctg aca gag aca tat gag Leu Ser Thr Asn Lys Asn Gln Leu Lys Gln Leu Thr Glu Thr Tyr Glu 215 220 225	969
gaa gat cga aaa aac tac tct gaa gtt caa att aga tgt caa cgt ttg Glu Asp Arg Lys Asn Tyr Ser Glu Val Gln Ile Arg Cys Gln Arg Leu 230 235 240	1017
gcc tta gaa tta gca gac aca aaa cag tta att cag caa ggt gac tac Ala Leu Glu Leu Ala Asp Thr Lys Gln Leu Ile Gln Gln Gly Asp Tyr 245 250 255	1065
cgt caa gag aac tat gat aaa gtc aag agt gaa cgt gat gca ctt gaa Arg Gln Glu Asn Tyr Asp Lys Val Lys Ser Glu Arg Asp Ala Leu Glu 260 265 270 275	1113
cag gaa gta att gag ctt agg aga aaa cat gaa ata ctt gaa gcc tct Gln Glu Val Ile Glu Leu Arg Arg Lys His Glu Ile Leu Glu Ala Ser 280 285 290	1161
cac atg att caa aca aaa gaa cga agt gaa tta tca aaa gag gta gtc His Met Ile Gln Thr Lys Glu Arg Ser Glu Leu Ser Lys Glu Val Val 295 300 305	1209
acc tta gag caa act gtt act tta ctg caa aag gat aaa gaa tat ctt Thr Leu Glu Gln Thr Val Thr Leu Leu Gln Lys Asp Lys Glu Tyr Leu 310 315 320	1257
aat cgc caa aac atg gag ctt agt gtt cgc tgt gct cat gaa gag gat Asn Arg Gln Asn Met Glu Leu Ser Val Arg Cys Ala His Glu Glu Asp 325 330 335	1305
cgc ctt gaa aga ctt caa gct caa ctg gaa gaa agc aaa aag gct aga Arg Leu Glu Arg Leu Gln Ala Gln Leu Glu Glu Ser Lys Lys Ala Arg 340 345 350 355	1353
gaa gag atg tat gaa aaa tat gta gca tcc aga gac cat tat aaa aca Glu Glu Met Tyr Glu Lys Tyr Val Ala Ser Arg Asp His Tyr Lys Thr 360 365 370	1401
gaa tat gaa aat aaa cta cat gat gaa cta gaa caa atc aga ttg aaa Glu Tyr Glu Asn Lys Leu His Asp Glu Leu Glu Gln Ile Arg Leu Lys 375 380 385	1449
acc aac caa gaa att gat caa ctt cga aat gcc tct agg gaa atg tat Thr Asn Gln Glu Ile Asp Gln Leu Arg Asn Ala Ser Arg Glu Met Tyr 390 395 400	1497
gaa cga gaa aac aga aat ctc cga gaa gca agg gat aat gct gtg gct Glu Arg Glu Asn Arg Asn Leu Arg Glu Ala Arg Asp Asn Ala Val Ala 405 410 415	1545
gaa aag gaa cga gca gtg atg gct gaa aag gat gct tta gaa aaa cac Glu Lys Glu Arg Ala Val Met Ala Glu Lys Asp Ala Leu Glu Lys His 420 425 430 435	1593
gat cag ctc tta gac agg tac aga gaa cta caa ctt agt aca gaa agc Asp Gln Leu Leu Asp Arg Tyr Arg Glu Leu Gln Leu Ser Thr Glu Ser 440 445 450	1641

aaa gta aca gaa ttt ctc cat caa agt aaa tta aaa tct ttt gaa agt	1689
Lys Val Thr Glu Phe Leu His Gln Ser Lys Leu Lys Ser Phe Glu Ser	
455 460 465	
gag cgt gtt caa ctt ctg caa gag gaa aca gca aga aat ctc aca cag	1737
Glu Arg Val Gln Leu Leu Gln Glu Glu Thr Ala Arg Asn Leu Thr Gln	
470 475 480	
tgt caa ttg gaa tgt gaa aaa tat cag aaa aaa ttg gag gtt tta acc	1785
Cys Gln Leu Glu Cys Glu Lys Tyr Gln Lys Lys Leu Glu Val Leu Thr	
485 490 495	
aaa gaa ttt tat agt ctc caa gcc tct tct gaa aaa cgc att act gaa	1833
Lys Glu Phe Tyr Ser Leu Gln Ala Ser Ser Glu Lys Arg Ile Thr Glu	
500 505 510 515	
ctt caa gca cag aac tca gag cat caa gca agg cta gac att tat gag	1881
Leu Gln Ala Gln Asn Ser Glu His Gln Ala Arg Leu Asp Ile Tyr Glu	
520 525 530	
aaa ctg gaa aaa gag ctt gat gaa ata ata atg caa act gca gaa att	1929
Lys Leu Glu Lys Glu Leu Asp Glu Ile Ile Met Gln Thr Ala Glu Ile	
535 540 545	
gaa aat gaa gat gag gct gaa agg gtt ctt ttt tcc tac ggc tat ggt	1977
Glu Asn Glu Asp Glu Ala Glu Arg Val Leu Phe Ser Tyr Gly Tyr Gly	
550 555 560	
gct aat gtt ccc aca aca gcc aaa aga cga cta aag caa agt gtt cac	2025
Ala Asn Val Pro Thr Thr Ala Lys Arg Arg Leu Lys Gln Ser Val His	
565 570 575	
ttg gca aga aga gtg ctt caa tta gaa aaa caa aac tcg ctg att tta	2073
Leu Ala Arg Arg Val Leu Gln Leu Glu Lys Gln Asn Ser Leu Ile Leu	
580 585 590 595	
aaa gat ctg gaa cat cga aag gac caa gta aca cag ctt tca cca gga	2121
Lys Asp Leu Glu His Arg Lys Asp Gln Val Thr Gln Leu Ser Pro Gly	
600 605 610	
gct tga cagaggccaa ttgcgtatta aaccagactc aacagcetta caggatatctc	2177
Ala *	
attgaatcag tgcgtcagag agattctaag attgattcac tgacggaatc tattgcacaa	2237
cttggagaaa ggatgtcagc aacttaaata aagaaaagtc agctttacta cagacggang	2297
gaatcaaaat ggcattagga tttaggacca acttctaaat catcgtgagg aattggcagc	2357
aatgaaacag attctcgtta agatgcatag taaacattct gagaacagct tactttctac	2417
taaaacagaa ccaaaacatg tgacagaaaa tcagaaatca aagactttga atgtgcctaa	2477
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<212> DNA
<213> Homo sapiens

<220>
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<222> (93) .. (2354)

<400> 817

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                                   Met Lys Val Ile Gly Phe Lys
                                   1               5

cct gag gag atc caa aca gtg tat aag att ttg gct gct att ctg cac      161
Pro Glu Glu Ile Gln Thr Val Tyr Lys Ile Leu Ala Ala Ile Leu His
      10               15               20

ttg gga aat tta aaa ttt gta gta gat ggt gac acg cct ctt att gag      209
Leu Gly Asn Leu Lys Phe Val Val Asp Gly Asp Thr Pro Leu Ile Glu
      25               30               35

aat ggc aaa gta gta tct atc ata gca gaa ttg ctc tct act aag aca      257
Asn Gly Lys Val Val Ser Ile Ile Ala Glu Leu Leu Ser Thr Lys Thr
      40               45               50               55

gat atg gtt gag aaa gcc ctt ctt tac cgg act ggg gcc aca ggc cgt      305
Asp Met Val Glu Lys Ala Leu Leu Tyr Arg Thr Gly Ala Thr Gly Arg
      60               65               70

gac atc att gac aag cag cac aca gaa caa gag gcc agc tac ggc aga      353
Asp Ile Ile Asp Lys Gln His Thr Glu Gln Glu Ala Ser Tyr Gly Arg
      75               80               85

gac gcc ttt gcc aag gca ata tat gag cgc ctt ttt tgt tgg atc gtt      401
Asp Ala Phe Ala Lys Ala Ile Tyr Glu Arg Leu Phe Cys Trp Ile Val
      90               95               100

act cgc atc aat gat att att gag gtc aag aac tat gac acc aca atc      449
Thr Arg Ile Asn Asp Ile Ile Glu Val Lys Asn Tyr Asp Thr Thr Ile
      105               110               115

cat ggg aaa aac act gtt att ggt gtc ttg gat atc tat ggc ttt gaa      497
His Gly Lys Asn Thr Val Ile Gly Val Leu Asp Ile Tyr Gly Phe Glu
      120               125               130               135

atc ttt gac aac aac agt ttt gaa caa ttc tgt atc aat tac tgc aat      545
Ile Phe Asp Asn Asn Ser Phe Glu Gln Phe Cys Ile Asn Tyr Cys Asn
      140               145               150

gag aaa ctg cag cag cta ttt att cag ctg gtt ctg aag caa gaa caa      593
Glu Lys Leu Gln Gln Leu Phe Ile Gln Leu Val Leu Lys Gln Glu Gln
      155               160               165

gag gaa tac cag cgg gaa ggg atc ccc tgg aaa cat att gac tac ttc      641
Glu Glu Tyr Gln Arg Glu Gly Ile Pro Trp Lys His Ile Asp Tyr Phe
      170               175               180

aac aat cag atc att gtt gac ctc gtg gag caa cag cac aaa ggg atc      689
Asn Asn Gln Ile Ile Val Asp Leu Val Glu Gln Gln His Lys Gly Ile
      185               190               195

att gca atc ctt gat gat gct tgc atg aat gtc ggc aaa gtc acc gat      737
Ile Ala Ile Leu Asp Asp Ala Cys Met Asn Val Gly Lys Val Thr Asp

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200	205	210	215	
gaa atg ttt ctt gaa gca ctt aac agt aaa ttg ggc aaa cac gcc cat				785
Glu Met Phe Leu Glu Ala Leu Asn Ser Lys Leu Gly Lys His Ala His				
220	225	230		
ttt tcc agc cga aag ctc tgt gcc tca gac aaa att ctg gag ttt gat				833
Phe Ser Ser Arg Lys Leu Cys Ala Ser Asp Lys Ile Leu Glu Phe Asp				
235	240	245		
cga gat ttt cga att cga cat tat gca ggc gat gta gtc tat tct gtc				881
Arg Asp Phe Arg Ile Arg His Tyr Ala Gly Asp Val Val Tyr Ser Val				
250	255	260		
att ggt ttt att gac aaa aat aaa gat act tta ttt caa gat ttc aag				929
Ile Gly Phe Ile Asp Lys Asn Lys Asp Thr Leu Phe Gln Asp Phe Lys				
265	270	275		
cgc ctt atg tat aac agt tca aat cct gtg ctc aag aat atg tgg cct				977
Arg Leu Met Tyr Asn Ser Ser Asn Pro Val Leu Lys Asn Met Trp Pro				
280	285	290	295	
gaa ggc aaa ctg agc att aca gag gtg acc aag cga cct ctg act gct				1025
Glu Gly Lys Leu Ser Ile Thr Glu Val Thr Lys Arg Pro Leu Thr Ala				
300	305	310		
gct acc ttg ttt aag aat tct atg att gct cta gta gac aac ctt gca				1073
Ala Thr Leu Phe Lys Asn Ser Met Ile Ala Leu Val Asp Asn Leu Ala				
315	320	325		
tca aag gaa cca tat tac gtt cgt tgc atc aaa ccc aat gac aag aaa				1121
Ser Lys Glu Pro Tyr Tyr Val Arg Cys Ile Lys Pro Asn Asp Lys Lys				
330	335	340		
tct cca cag ata ttt gat gat gaa cgc tgc cgg cac caa gta gaa tat				1169
Ser Pro Gln Ile Phe Asp Asp Glu Arg Cys Arg His Gln Val Glu Tyr				
345	350	355		
ctt gga cta ctg gaa aat gtg aga gtg cgt cgg gca gga ttt gcc ttc				1217
Leu Gly Leu Leu Glu Asn Val Arg Val Arg Arg Ala Gly Phe Ala Phe				
360	365	370	375	
cgc cag aca tac gag aag ttt ctt cac agg tat aag atg atc tct gaa				1265
Arg Gln Thr Tyr Glu Lys Phe Leu His Arg Tyr Lys Met Ile Ser Glu				
380	385	390		
ttc acc tgg ccc aac cat gac ctt cct tca gac aaa gag gct gtc aag				1313
Phe Thr Trp Pro Asn His Asp Leu Pro Ser Asp Lys Glu Ala Val Lys				
395	400	405		
aaa cta att gaa cgg tgt ggt ttt cag gat gat gta gct tat ggg aag				1361
Lys Leu Ile Glu Arg Cys Gly Phe Gln Asp Asp Val Ala Tyr Gly Lys				
410	415	420		
acc aaa att ttc att cga aca ccc cga aca ttg ttt acc ttg gaa gaa				1409
Thr Lys Ile Phe Ile Arg Thr Pro Arg Thr Leu Phe Thr Leu Glu Glu				
425	430	435		
ctc cgt gcc cag atg ctc ata agg att gtc ctc ttt cta caa aag gtg				1457
Leu Arg Ala Gln Met Leu Ile Arg Ile Val Leu Phe Leu Gln Lys Val				
440	445	450	455	
tgg cgg ggc acc ctg gcc cgc atg cgg tac aaa aga acc aag gca gct				1505
Trp Arg Gly Thr Leu Ala Arg Met Arg Tyr Lys Arg Thr Lys Ala Ala				

2246

715	720	725	
gtg gag acg cgg ctc aac cag ccc cag ccc gac ttc acc aag aat cgc			2321
Val Glu Thr Arg Leu Asn Gln Pro Gln Pro Asp Phe Thr Lys Asn Arg			
730	735	740	
tcg ggc ttc atc ctc agc gtg ccc ggg aac tga cgccccgc ggaggcctgg			2372
Ser Gly Phe Ile Leu Ser Val Pro Gly Asn *			
745	750		
cccgagcccc ggccacactc cgagtcctgg gtcccagtc agctgctgcc tcccaaccca			2432
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cactagtggg accatctaac tggaaacttcc tctctccttc cacttatcttc ctcaaacttg 4052
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 gcgggcatga ttgtagacaa tgaggggggt ctcttgatgt aatgaaatgc aattttatgg 4412
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 Met Gln Ile Glu Gln Leu Glu Arg Tyr
 1 5
 att cag cga tat ctg gtt tat gcc ata ctc tgg tcc ctg tct gga gac 159
 Ile Gln Arg Tyr Leu Val Tyr Ala Ile Leu Trp Ser Leu Ser Gly Asp
 10 15 20 25
 agc cgg cta aaa atg aga gca gag ctg ggt gaa tac atc aga aga atc 207
 Ser Arg Leu Lys Met Arg Ala Glu Leu Gly Glu Tyr Ile Arg Arg Ile
 30 35 40
 acg acc gtg cct ctg ccc act gcg ccc aac ata ccc att atc gat tat 255
 Thr Thr Val Pro Leu Pro Thr Ala Pro Asn Ile Pro Ile Ile Asp Tyr
 45 50 55
 gag gtg tcc atc agc gga gaa tgg tct ccg tgg cag gcc aag gtg cct 303
 Glu Val Ser Ile Ser Gly Glu Trp Ser Pro Trp Gln Ala Lys Val Pro
 60 65 70
 cag att gaa gtg gag acg cac aag gtg gca gcc cct gat gtc gtc gtg 351
 Gln Ile Glu Val Glu Thr His Lys Val Ala Ala Pro Asp Val Val Val
 75 80 85
 cca acg ctg gac aca gtc cgc cac gaa gcc ctc ttg tac act tgg ctg 399
 Pro Thr Leu Asp Thr Val Arg His Glu Ala Leu Leu Tyr Thr Trp Leu
 90 95 100 105
 gcc gaa cac aag ccc ctg gtc ttg tgt gcc cct cct ggg tct gcc aag 447
 Ala Glu His Lys Pro Leu Val Leu Cys Gly Pro Pro Gly Ser Gly Lys
 110 115 120

acc atg aca ctc ttc agc gcc ctc cgg gcc ttg cct gac atg gag gtg	495
Thr Met Thr Leu Phe Ser Ala Leu Arg Ala Leu Pro Asp Met Glu Val	
125 130 135	
gtg ggt ctc aac ttc tcc agt gct act act cca gag ctg ctt ctg aag	543
Val Gly Leu Asn Phe Ser Ser Ala Thr Thr Pro Glu Leu Leu Lys	
140 145 150	
act ttt gat cac tac tgc gag tac agg cgc aca cct aat ggg gtg gtt	591
Thr Phe Asp His Tyr Cys Glu Tyr Arg Arg Thr Pro Asn Gly Val Val	
155 160 165	
ttg gct cct gtt caa ctt gga aag tgg ctg gtg ttg ttc tgt gat gaa	639
Leu Ala Pro Val Gln Leu Gly Lys Trp Leu Val Leu Phe Cys Asp Glu	
170 175 180 185	
atc aac ttg cca gat atg gat aaa tat ggg acc cag agg gtc ata tcc	687
Ile Asn Leu Pro Asp Met Asp Lys Tyr Gly Thr Gln Arg Val Ile Ser	
190 195 200	
ttc atc aga cag atg gtg gag cac gga ggc ttt tac cgt acc tca gat	735
Phe Ile Arg Gln Met Val Glu His Gly Gly Phe Tyr Arg Thr Ser Asp	
205 210 215	
caa aca tgg gtg aag ctg gag aga atc cag ttt gtt ggg gct tgt aat	783
Gln Thr Trp Val Lys Leu Glu Arg Ile Gln Phe Val Gly Ala Cys Asn	
220 225 230	
ccc ccc aca gac cct gga aga aag ccc ctc tca cac agg ttc ctg cgc	831
Pro Pro Thr Asp Pro Gly Arg Lys Pro Leu Ser His Arg Phe Leu Arg	
235 240 245	
cac gtg cct gtc gtg tat gtg gat tac ccg ggc ccc gcc tcc ctc aca	879
His Val Pro Val Val Tyr Val Asp Tyr Pro Gly Pro Ala Ser Leu Thr	
250 255 260 265	
cag atc tac ggc acc ttc aac cgc gcc atg ctg agg ctc att cca tcc	927
Gln Ile Tyr Gly Thr Phe Asn Arg Ala Met Leu Arg Leu Ile Pro Ser	
270 275 280	
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Leu Arg Thr Tyr Ala Glu Pro Leu Thr Ala Ala Met Val Glu Phe Tyr	
285 290 295	
acc atg tct cag gag aga ttc acc cag gat aca caa cct cac tat atc	1023
Thr Met Ser Gln Glu Arg Phe Thr Gln Asp Thr Gln Pro His Tyr Ile	
300 305 310	
tat tca ccc cgt gaa atg act agg tgg gtg aga ggc atc ttt gaa gcg	1071
Tyr Ser Pro Arg Glu Met Thr Arg Trp Val Arg Gly Ile Phe Glu Ala	
315 320 325	
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Leu Arg Pro Leu Glu Thr Leu Pro Val Glu Gly Leu Ile Arg Ile Trp	
330 335 340 345	
gca cat gaa gct ctg cgt ctc ttc caa gat aga ctc gta gag gat gag	1167
Ala His Glu Ala Leu Arg Leu Phe Gln Asp Arg Leu Val Glu Asp Glu	
350 355 360	
gag agg cgt tgg act gat gag aac atc gac acg gtt gct ctg aag cac	1215
Glu Arg Arg Trp Thr Asp Glu Asn Ile Asp Thr Val Ala Leu Lys His	
365 370 375	

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Phe Pro Asn Ile Asp Arg Glu Lys Ala Met Ser Arg Pro Ile Leu Tyr	
380 385 390	
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Ser Asn Trp Leu Ser Lys Asp Tyr Ile Pro Val Asp Gln Glu Glu Leu	
395 400 405	
aga gat tat gtc aaa gct agg ctg aag gtc ttt tat gaa gaa gaa ctt	1359
Arg Asp Tyr Val Lys Ala Arg Leu Lys Val Phe Tyr Glu Glu Glu Leu	
410 415 420 425	
gat gtt ccg ctg gtg ctg ttt aat gaa gtc cta gac cac gtg ctg agg	1407
Asp Val Pro Leu Val Leu Phe Asn Glu Val Leu Asp His Val Leu Arg	
430 435 440	
att gac aga ata ttc cgt caa cct caa ggc cac ttg ctt ctg att ggt	1455
Ile Asp Arg Ile Phe Arg Gln Pro Gln Gly His Leu Leu Leu Ile Gly	
445 450 455	
gtt agt gga gca gga aaa act acc ctg tct cgt ttc gtc gcc tgg atg	1503
Val Ser Gly Ala Gly Lys Thr Leu Ser Arg Phe Val Ala Trp Met	
460 465 470	
aac ggt ttg agt gtg tac cag att aag gtc cat agg aag tac aca ggg	1551
Asn Gly Leu Ser Val Tyr Gln Ile Lys Val His Arg Lys Tyr Thr Gly	
475 480 485	
gaa gac ttt gat gaa gat cta cgg aca gtg ttg aga cgt tct ggc tgt	1599
Glu Asp Phe Asp Glu Asp Leu Arg Thr Val Leu Arg Arg Ser Gly Cys	
490 495 500 505	
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Lys Asn Glu Lys Ile Ala Phe Ile Met Asp Glu Ser Asn Val Leu Asp	
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Ser Gly Phe Leu Glu Arg Met Asn Thr Leu Leu Ala Asn Gly Glu Val	
525 530 535	
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Pro Gly Leu Phe Glu Gly Asp Glu Tyr Ala Thr Leu Met Thr Gln Cys	
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Lys Glu Gly Ala Gln Lys Glu Gly Leu Met Leu Asp Ser His Glu Glu	
555 560 565	
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Leu Tyr Lys Trp Phe Thr Ser Gln Val Ile Arg Asn Leu His Val Val	
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Phe Thr Met Asn Pro Ser Ser Glu Gly Leu Lys Asp Arg Ala Ala Thr	
590 595 600	
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Ser Pro Ala Leu Phe Asn Arg Cys Val Leu Asn Trp Phe Gly Asp Trp	
605 610 615	
tcc acc gaa gca ctg tat cag gtt ggc aaa gaa ttc aca agt aag atg	1983
Ser Thr Glu Ala Leu Tyr Gln Val Gly Lys Glu Phe Thr Ser Lys Met	
620 625 630	

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tat gat aag ctg ccg cag cca cca tcc cat cgg gaa gcc att gtg aac Tyr Asp Lys Leu Pro Gln Pro Pro Ser His Arg Glu Ala Ile Val Asn 650 655 660 665	2079
agc tgt gtg ttt gtt cat cag act ctt cac cag gcg aat gct cgg cta Ser Cys Val Phe Val His Gln Thr Leu His Gln Ala Asn Ala Arg Leu 670 675 680	2127
gca aag cga ggc ggc aga acg atg gcc atc acc cct cgc cac tac ctg Ala Lys Arg Gly Gly Arg Thr Met Ala Ile Thr Pro Arg His Tyr Leu 685 690 695	2175
gac ttc atc aat cac tat gcc aac ctg ttc cac gag aag cgg agc gag Asp Phe Ile Asn His Tyr Ala Asn Leu Phe His Glu Lys Arg Ser Glu 700 705 710	2223
ctg gag gag cag cag atg cac ttg aac gtg ggg ctc agg aag atc aaa Leu Glu Glu Gln Gln Met His Leu Asn Val Gly Leu Arg Lys Ile Lys 715 720 725	2271
gag aca gtc gac cag gta gaa gaa ctg cgt cgt gac ttg agg ata aag Glu Thr Val Asp Gln Val Glu Glu Leu Arg Arg Asp Leu Arg Ile Lys 730 735 740 745	2319
agc caa gag ctg gag gtg aag aat gca gca gcc aat gac aag ctg aaa Ser Gln Glu Leu Glu Val Lys Asn Ala Ala Asn Asp Lys Leu Lys 750 755 760	2367
aag atg gtg aaa gac cag cag gag gct gaa aag aag aag gtt atg agc Lys Met Val Lys Asp Gln Gln Glu Ala Glu Lys Lys Lys Val Met Ser 765 770 775	2415
caa gaa atc cag gaa cag ctg cat aag cag cag gag gta att gca gac Gln Glu Ile Gln Glu Gln Leu His Lys Gln Gln Glu Val Ile Ala Asp 780 785 790	2463
aaa cag atg agt gtc aaa gaa gat ctt gat aag gtg gaa cct gcc gtc Lys Gln Met Ser Val Lys Glu Asp Leu Asp Lys Val Glu Pro Ala Val 795 800 805	2511
att gag gcc cag aat gct gtg aag tcg atc aag aag cag cac ctg gtg Ile Glu Ala Gln Asn Ala Val Lys Ser Ile Lys Lys Gln His Leu Val 810 815 820 825	2559
gag gtg agg tcc atg gcc aac cct cct gct gct gtg aag ctg gcg ctg Glu Val Arg Ser Met Ala Asn Pro Pro Ala Ala Val Lys Leu Ala Leu 830 835 840	2607
gag tcc atc tgc ctg ctg ctg ggg gaa agc acc aca gac tgg aag cag Glu Ser Ile Cys Leu Leu Leu Gly Glu Ser Thr Thr Asp Trp Lys Gln 845 850 855	2655
atc cgc tcc atc atc atg cgg gag aac ttc atc ccc acc atc gtc aac Ile Arg Ser Ile Ile Met Arg Glu Asn Phe Ile Pro Thr Ile Val Asn 860 865 870	2703
ttc tct gca gag gag atc agt gac gcc ata agg gag aag atg aag aaa Phe Ser Ala Glu Glu Ile Ser Asp Ala Ile Arg Glu Lys Met Lys Lys 875 880 885	2751

aat tac atg tcc aat cca agt tac aat tat gaa att gtg aat cgg gct Asn Tyr Met Ser Asn Pro Ser Tyr Asn Tyr Glu Ile Val Asn Arg Ala 890 895 900 905	2799
tcc ctg gct tgc ggc cct atg gtg aaa tgg gca att gca cag ctt aac Ser Leu Ala Cys Gly Pro Met Val Lys Trp Ala Ile Ala Gln Leu Asn 910 915 920	2847
tat gca gac atg tta aag aga gtg gag ccc cta cgc aat gag ctg cag Tyr Ala Asp Met Leu Lys Arg Val Glu Pro Leu Arg Asn Glu Leu Gln 925 930 935	2895
aag ctg gaa gat gac gcc aag gac aac cag cag aag gcc aac gag gtg Lys Leu Glu Asp Asp Ala Lys Asp Asn Gln Gln Lys Ala Asn Glu Val 940 945 950	2943
gag cag atg atc cga gac ctg gaa gcc agc atc gcc cgc tac aag gag Glu Gln Met Ile Arg Asp Leu Glu Ala Ser Ile Ala Arg Tyr Lys Glu 955 960 965	2991
gaa tac gcc gtc ctg atc tca gag gcc cag gcc atc aag gca gac ctg Glu Tyr Ala Val Leu Ile Ser Glu Ala Gln Ala Ile Lys Ala Asp Leu 970 975 980 985	3039
gca gct gtc gag gca aaa gta aac cgg agc act gct ctt ctg aag agc Ala Ala Val Glu Ala Lys Val Asn Arg Ser Thr Ala Leu Leu Lys Ser 990 995 1000	3087
ttg tct gct gaa cgt gaa cga tgg gaa aaa aca agt gaa act ttc aaa Leu Ser Ala Glu Arg Glu Arg Trp Glu Lys Thr Ser Glu Thr Phe Lys 1005 1010 1015	3135
aac cag atg tcc acc att gct ggg gac tgt ctc ttg tca gct gcg ttc Asn Gln Met Ser Thr Ile Ala Gly Asp Cys Leu Leu Ser Ala Ala Phe 1020 1025 1030	3183
att gcc tac gcg ggt tac ttt gac cag cag atg cgt cag aac ttg ttc Ile Ala Tyr Ala Gly Tyr Phe Asp Gln Gln Met Arg Gln Asn Leu Phe 1035 1040 1045	3231
act acc tgg tcc cat cac cta cag caa gcc aac atc cag ttc cgt aca Thr Thr Trp Ser His His Leu Gln Gln Ala Asn Ile Gln Phe Arg Thr 1050 1055 1060 1065	3279
gat att gcc agg acg gaa tac ctt tcc aat gct gat gag cgt ctt cgc Asp Ile Ala Arg Thr Glu Tyr Leu Ser Asn Ala Asp Glu Arg Leu Arg 1070 1075 1080	3327
tgg cag gcc agc tcc ttg cct gct gat gac ctt tgc aca gaa aat gcc Trp Gln Ala Ser Ser Leu Pro Ala Asp Asn Leu Cys Thr Glu Asn Ala 1085 1090 1095	3375
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gat cca gtt ttg aac ccg gtg ctg aac cgt gaa gtg cgg cga aca ggg Asp Pro Val Leu Asn Pro Val Leu Asn Arg Glu Val Arg Arg Thr Gly 1165 1170 1175	3615
ggg aga gtg ctg atc act ctc ggg gac cag gac ata gac ctg tcg cca Gly Arg Val Leu Ile Thr Leu Gly Asp Gln Asp Ile Asp Leu Ser Pro 1180 1185 1190	3663
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cca gat ctc tgt tcc cgg gtt act ttt gta aac ttc aca gtt acc cgt Pro Asp Leu Cys Ser Arg Val Thr Phe Val Asn Phe Thr Val Thr Arg 1210 1215 1220 1225	3759
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cct gat gtg gac gag aaa cga tct gat ctt ctt aaa ctt caa ggg gaa Pro Asp Val Asp Glu Lys Arg Ser Asp Leu Leu Lys Leu Gln Gly Glu 1245 1250 1255	3855
ttt cag ctc cgt ttg cgt cag ctg gaa aaa tct cta cta caa gct ctg Phe Gln Leu Arg Leu Arg Gln Leu Glu Lys Ser Leu Leu Gln Ala Leu 1260 1265 1270	3903
aac gag gtg aaa ggg cgc att ttg gat gac gac acg atc ata acc act Asn Glu Val Lys Gly Arg Ile Leu Asp Asp Asp Thr Ile Ile Thr Thr 1275 1280 1285	3951
ctg gag aac ctg aag aga gag gct gca gag gtc acc agg aaa gtt gag Leu Glu Asn Leu Lys Arg Glu Ala Ala Glu Val Thr Arg Lys Val Glu 1290 1295 1300 1305	3999
gag acg gac att gtc atg cag gag gtg gag acc gtg tcc cag cag tac Glu Thr Asp Ile Val Met Gln Glu Val Glu Thr Val Ser Gln Gln Tyr 1310 1315 1320	4047
ctc ccg ctc tcc acc gcc tgc agc agc atc tac ttc acc atg gag tcc Leu Pro Leu Ser Thr Ala Cys Ser Ser Ile Tyr Phe Thr Met Glu Ser 1325 1330 1335	4095
ctc aag cag ata cac ttc ttg tac cag tac tcc ctc cag ttt ttc ctg Leu Lys Gln Ile His Phe Leu Tyr Gln Tyr Ser Leu Gln Phe Phe Leu 1340 1345 1350	4143
gac att tat cac aac gtc cta tac gag aac ccg aac ctg aag ggt gtc Asp Ile Tyr His Asn Val Leu Tyr Glu Asn Pro Asn Leu Lys Gly Val 1355 1360 1365	4191
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 Thr Phe Ala Met Leu Leu Ala Arg Ile Lys Leu Lys Gly Thr Val Gly
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 Glu Pro Thr Tyr Asp Ala Glu Phe Gln His Phe Leu Arg Gly Asn Glu
 1420 1425 1430

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 Ile Val Leu Ser Ala Gly Ser Thr Pro Arg Ile Gln Gly Leu Thr Val
 1435 1440 1445

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 Glu Gln Ala Glu Ala Val Arg Leu Ser Cys Leu Pro Ala Phe Lys
 1450 1455 1460 1465

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 Asp Leu Ile Ala Lys Val Gln Ala Asp Glu Gln Phe Gly Ile Trp Leu
 1470 1475 1480

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 Asp Ser Ser Ser Pro Glu Gln Thr Val Pro Tyr Leu Trp Ser Glu Glu
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 Thr Pro Ala Thr Pro Ile Gly Gln Ala Ile His Arg Leu Leu Leu Ile
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 Gln Ala Phe Arg Pro Asp Arg Leu Leu Ala Met Ala His Met Phe Val
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 Ser Thr Asn Leu Gly Glu Ser Phe Met Ser Ile Met Glu Gln Pro Leu
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 Leu Met Cys Ser Val Pro Gly Tyr Asp Ala Ser Gly His Val Glu Asp
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 Leu Ala Ala Glu Gln Asn Thr Gln Ile Thr Ser Ile Ala Ile Gly Ser
 1580 1585 1590

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 Ala Glu Gly Phe Asn Gln Ala Asp Lys Ala Ile Asn Thr Ala Val Lys
 1595 1600 1605

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cgg aca ctg cac acc acc gcg tcc aac tgg ctg cac ctc atc ccc cag Arg Thr Leu His Thr Thr Ala Ser Asn Trp Leu His Leu Ile Pro Gln 1900 1905 1910	5823

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ccc ctg acg cag ctg cgc tgg gtc aag cag aca aac acc gag aag aag Pro Leu Thr Gln Leu Arg Trp Val Lys Gln Thr Asn Thr Glu Lys Lys 2110 2115 2120	6447
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Met Gln Val Ser Ser Ala Glu Val	
1 5	
cgc atc ggg ccc atg aga ctg acg cag gac cct att cag gtt ttg ctg	281
Arg Ile Gly Pro Met Arg Leu Thr Gln Asp Pro Ile Gln Val Leu Leu	
10 15 20	
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Ile Phe Ala Lys Glu Asp Ser Gln Ser Asp Gly Phe Trp Trp Ala Cys	
25 30 35 40	
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Asp Arg Ala Gly Tyr Arg Cys Asn Ile Ala Arg Thr Pro Glu Ser Ala	
45 50 55	
ctt gaa tgc ttt ctt gat aag cat cat gaa att att gta att gat cat	425
Leu Glu Cys Phe Leu Asp Lys His His Glu Ile Ile Val Ile Asp His	
60 65 70	
aga caa act cag aac ttc gat gca gaa gca gtg tgc agg tcg atc cgg	473
Arg Gln Thr Gln Asn Phe Asp Ala Glu Ala Val Cys Arg Ser Ile Arg	
75 80 85	
gcc aca aat ccc tcc gag cac acg gtg atc ctc gca gtg gtt tcg cga	521
Ala Thr Asn Pro Ser Glu His Thr Val Ile Leu Ala Val Val Ser Arg	
90 95 100	
gta tcg gat gac cat gaa gag gcg tca gtc ctt cct ctt ctc cac gca	569
Val Ser Asp Asp His Glu Glu Ala Ser Val Leu Pro Leu Leu His Ala	
105 110 115 120	
ggc ttc aac agg aga ttt atg gag aat agc agc ata att gct tgc tat	617
Gly Phe Asn Arg Arg Phe Met Glu Asn Ser Ser Ile Ile Ala Cys Tyr	
125 130 135	

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Asn Glu Leu Ile Gln Ile Glu His Gly Glu Val Arg Ser Gln Phe Lys	
140 145 150	
tta cgg gcc tgt aat tca gtg ttt aca gca tta gat cac tgt cat gaa	713
Leu Arg Ala Cys Asn Ser Val Phe Thr Ala Leu Asp His Cys His Glu	
155 160 165	
gcc ata gaa ata aca agc gat gac cac gtg att cag tat gtc aac cca	761
Ala Ile Glu Ile Thr Ser Asp Asp His Val Ile Gln Tyr Val Asn Pro	
170 175 180	
gcc ttc gaa agg atg atg ggc tac cac aaa ggt gag ctc ctg gga aaa	809
Ala Phe Glu Arg Met Met Gly Tyr His Lys Gly Glu Leu Leu Gly Lys	
185 190 195 200	
gaa ctc gct gat ctg ccc aaa agc gat aag aac cgg gca gac ctt ctc	857
Glu Leu Ala Asp Leu Pro Lys Ser Asp Lys Asn Arg Ala Asp Leu Leu	
205 210 215	
gac acc atc aat aca tgc atc aag aag gga aag gag tgg cag ggg gtt	905
Asp Thr Ile Asn Thr Cys Ile Lys Lys Gly Lys Glu Trp Gln Gly Val	
220 225 230	
tac tat gcc aga cgg aaa tcc ggg gac agc atc caa cag cac gtg aag	953
Tyr Tyr Ala Arg Arg Lys Ser Gly Asp Ser Ile Gln Gln His Val Lys	
235 240 245	
atc acc cca gtg att ggc caa gga ggg aaa att agg cat ttt gtc tcg	1001
Ile Thr Pro Val Ile Gly Gln Gly Gly Lys Ile Arg His Phe Val Ser	
250 255 260	
ctc aag aaa ctg tgt tgt acc act gac aat aat aag cag att cac aag	1049
Leu Lys Lys Leu Cys Cys Thr Thr Asp Asn Asn Lys Gln Ile His Lys	
265 270 275 280	
att cat cgt gat tca gga gac aat tct cag aca gag cct cat tca ttc	1097
Ile His Arg Asp Ser Gly Asp Asn Ser Gln Thr Glu Pro His Ser Phe	
285 290 295	
aga tat aag aac agg agg aaa gag tcc att gac gtg aaa tcg ata tca	1145
Arg Tyr Lys Asn Arg Arg Lys Glu Ser Ile Asp Val Lys Ser Ile Ser	
300 305 310	
tct cga ggc agt gat gca cca agc ctg cag aat cgt cgc tat ccg tcc	1193
Ser Arg Gly Ser Asp Ala Pro Ser Leu Gln Asn Arg Arg Tyr Pro Ser	
315 320 325	
atg gcg agg atc cac tcc atg acc atc gag gct ccc atc aca aag gtt	1241
Met Ala Arg Ile His Ser Met Thr Ile Glu Ala Pro Ile Thr Lys Val	
330 335 340	
ata aat ata atc aat gca gcc caa gaa aac agc cca gtc aca gta gcg	1289
Ile Asn Ile Ile Asn Ala Ala Gln Glu Asn Ser Pro Val Thr Val Ala	
345 350 355 360	
gaa gcc ttg gac aga gtt cta gag att tta cgg acc aca gaa ctg tac	1337
Glu Ala Leu Asp Arg Val Leu Glu Ile Leu Arg Thr Thr Glu Leu Tyr	
365 370 375	
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Ser Pro Gln Leu Gly Thr Lys Asp Glu Asp Pro His Thr Ser Asp Leu	
380 385 390	

gtt gga ggc ctg atg act gac ggc ttg aga aga ctg tca gga aac gag	1433
Val Gly Gly Leu Met Thr Asp Gly Leu Arg Arg Leu Ser Gly Asn Glu	
395 400 405	
tat gtg ttt act aag aat gtg cac cag agt cac agt cac ctt gca atg	1481
Tyr Val Phe Thr Lys Asn Val His Gln Ser His Ser His Leu Ala Met	
410 415 420	
cca ata acc atc aat gat gtt ccc cct tgt atc tct caa tta ctt gat	1529
Pro Ile Thr Ile Asn Asp Val Pro Pro Cys Ile Ser Gln Leu Leu Asp	
425 430 435 440	
aat gag gag agt tgg gac ttc aac atc ttt gaa ttg gaa gcc att acg	1577
Asn Glu Glu Ser Trp Asp Phe Asn Ile Phe Glu Leu Glu Ala Ile Thr	
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His Lys Arg Pro Leu Val Tyr Leu Gly Leu Lys Val Phe Ser Arg Phe	
460 465 470	
gga gta tgt gag ttt tta aac tgt tct gaa acc act ctt cgg gcc tgg	1673
Gly Val Cys Glu Phe Leu Asn Cys Ser Glu Thr Thr Leu Arg Ala Trp	
475 480 485	
ttc caa gtg atc gaa gcc aac tac cac tct tcc aat gcc tac cac aac	1721
Phe Gln Val Ile Glu Ala Asn Tyr His Ser Ser Asn Ala Tyr His Asn	
490 495 500	
tcc acc cat gct gcc gac gtc ctg cac gcc acc gct ttc ttt ctt gga	1769
Ser Thr His Ala Ala Asp Val Leu His Ala Thr Ala Phe Phe Leu Gly	
505 510 515 520	
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Lys Glu Arg Val Lys Gly Ser Leu Asp Gln Leu Asp Glu Val Ala Ala	
525 530 535	
ctc att gct gcc aca gtc cat gac gtg gat cac ccg gga agg acc aac	1865
Leu Ile Ala Ala Thr Val His Asp Val Asp His Pro Gly Arg Thr Asn	
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Ser Phe Leu Cys Asn Ala Gly Ser Glu Leu Ala Val Leu Tyr Asn Asp	
555 560 565	
act gct gtt ctg gag agt cac cac acc gcc ctg gcc ttc cag ctc acg	1961
Thr Ala Val Leu Glu Ser His His Thr Ala Leu Ala Phe Gln Leu Thr	
570 575 580	
gtc aag gac acc aaa tgc aac att ttc aag aat att gac agg aac cat	2009
Val Lys Asp Thr Lys Cys Asn Ile Phe Lys Asn Ile Asp Arg Asn His	
585 590 595 600	
tat cga acg ctg cgc cag gct att att gac atg gtt ttg gca aca gag	2057
Tyr Arg Thr Leu Arg Gln Ala Ile Ile Asp Met Val Leu Ala Thr Glu	
605 610 615	
atg aca aaa cac ttt gaa cat gtg aat aag ttt gtg aac agc atc aac	2105
Met Thr Lys His Phe Glu His Val Asn Lys Phe Val Asn Ser Ile Asn	
620 625 630	
aag cca atg gca gct gag att gaa ggc agc gac tgt gaa tgc aac cct	2153
Lys Pro Met Ala Ala Glu Ile Glu Gly Ser Asp Cys Glu Cys Asn Pro	
635 640 645	

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gct ggg aag aac ttc cct gaa aac caa atc ctg atc aaa cgc atg atg      2201
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650                               655                               660

att aag tgt gct gac gtg gcc aac cca tgc cgc ccc ttg gac ctg tgc      2249
Ile Lys Cys Ala Asp Val Ala Asn Pro Cys Arg Pro Leu Asp Leu Cys
665                               670                               675                               680

att gaa tgg gct ggg agg atc tct gag gag tat ttt gca cag act gat      2297
Ile Glu Trp Ala Gly Arg Ile Ser Glu Glu Tyr Phe Ala Gln Thr Asp
685                               690                               695

gaa gag aag aga cag gga cta cct gtg gtg atg cca gtg ttt gac cgg      2345
Glu Glu Lys Arg Gln Gly Leu Pro Val Val Met Pro Val Phe Asp Arg
700                               705                               710

aat acc tgt agc atc ccc aag tct cag atc tct ttc att gac tac ttc      2393
Asn Thr Cys Ser Ile Pro Lys Ser Gln Ile Ser Phe Ile Asp Tyr Phe
715                               720                               725

ata aca gac atg ttt gat gct tgg gat gcc ttt gca cat ctg cca gcc      2441
Ile Thr Asp Met Phe Asp Ala Trp Asp Ala Phe Ala His Leu Pro Ala
730                               735                               740

ctg atg caa cat ttg gct gac aac tac aaa cac tgg aag aca cta gat      2489
Leu Met Gln His Leu Ala Asp Asn Tyr Lys His Trp Lys Thr Leu Asp
745                               750                               755                               760

gac cta aag tgc aaa agt ttg agg ctt cca tct gac agc taa agccaag      2538
Asp Leu Lys Cys Lys Ser Leu Arg Leu Pro Ser Asp Ser *
765                               770

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ggccttcctt tctaattgaca atgacaggta ttggtgaagg agctaattgtt taatatttga      2658

ccttgaatca ttcaagtccc caaatttcat tcttagaaag ttatgttcca tgaagaaaaa      2718

tatatgttct tttgaatact taatgacaga acaaatactt ggcaaactcc tttgctctgc      2778

tgtcatcctg tgtacccttg tcaatccatg gagctggttc actgtaacta gcaggccaca      2838

ggaagcaaag ccttggtgcc tgtgagctca tctcccagga tggtgactaa gtagcttagc      2898

tagtgatcag ctcatccttt accataaaag tcatcattgc tgttttagctt gactgttttc      2958

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<222> (1)...(1259)

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tgtttgata ttttgaagtc acatagacac caactaatat ctgtcaccca ctgtgtcatc      180
ggatggatcg ggtgacactc caaatcagtc gtgcaggtag ttctgagtgt gcagccatta      240
gccaatgttg agtcacctca tgttgcacgt gttggctgac tggctgcctt tccccctgcc      300
agggagaagc gcattggcat tgacctggtg cagcacacag tggagcatga gctgataaag      360
gaggctgaga tcatccaggg catt   atg gct ctg ctg acc cgt acc ttg gag      411
                               1       5
                               Met Ala Leu Leu Thr Arg Thr Leu Glu

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Glu Ala Ser Glu Gln Ile Arg Met Asn Arg Ser Ala Lys Tyr Asn Leu
  10                15                20                25

gag aag gat ttg aag gac aag ttt gtg gcc ctg acc ata gat gat atc      507
Glu Lys Asp Leu Lys Asp Lys Phe Val Ala Leu Thr Ile Asp Asp Ile
                30                35                40

tgc ttc tct ctc aac aac aac tca cca aac atc aga tat tct gag aac      555
Cys Phe Ser Leu Asn Asn Asn Ser Pro Asn Ile Arg Tyr Ser Glu Asn
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gcc gtg agg att gag cca aac tcc gtg agt ctg gaa gac tgg ttg gac      603
Ala Val Arg Ile Glu Pro Asn Ser Val Ser Leu Glu Asp Trp Leu Asp
                60                65                70

ttc tcc agc acc aat gtg gag aag gct gac aag cag cgg aac aac tcc      651
Phe Ser Ser Thr Asn Val Glu Lys Ala Asp Lys Gln Arg Asn Asn Ser
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ctg atg ctg aaa gcc ctg gtg gat cga atc ctg tcc atg aca gcc aat      699
Leu Met Leu Lys Ala Leu Val Asp Arg Ile Leu Ser Met Thr Ala Asn
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gat ctg cgc aag cag tgt gat gtg gtg cac acg gca ttc aag aat ggg      747
Asp Leu Arg Lys Gln Cys Asp Val Val His Thr Ala Phe Lys Asn Gly
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ctg aag gat aca aag gat gcc agg gac aag ctg gct gat cat ctg gcc      795
Leu Lys Asp Thr Lys Asp Ala Arg Asp Lys Leu Ala Asp His Leu Ala
                125                130                135

aag gtc atg gaa gag att gct tcc cag gag aaa aat att aca gct ctt      843
Lys Val Met Glu Glu Ile Ala Ser Gln Glu Lys Asn Ile Thr Ala Leu
                140                145                150

gaa aag gcc atc ctt gac caa gaa ggg cca gcc aag gtg gct cat acg      891
Glu Lys Ala Ile Leu Asp Gln Glu Gly Pro Ala Lys Val Ala His Thr
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cgc ttg gag acc agg aca cac cgg ccg aac gtg gag ctg tgt cgt gat      939
Arg Leu Glu Thr Arg Thr His Arg Pro Asn Val Glu Leu Cys Arg Asp
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 190 195 200
 gtc gca aga ttg aag gaa act tta gcc caa gct cag gca gag ctg aaa 1035
 Val Ala Arg Leu Lys Glu Thr Leu Ala Gln Ala Glu Leu Lys
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 ggg ctg cat cgc aga cag ctt gcc ctg cag gag gag atc cag gtc aaa 1083
 Gly Leu His Arg Arg Gln Leu Ala Leu Gln Glu Glu Ile Gln Val Lys
 220 225 230
 gag aac acc att tat atc gac gaa gtg ctg tgt atg cag atg agg aaa 1131
 Glu Asn Thr Ile Tyr Ile Asp Glu Val Leu Cys Met Gln Met Arg Lys
 235 240 245
 tcc atc cca ctt cgg gat ggg gaa gac cat ggg gtc tgg gct ggg ggc 1179
 Ser Ile Pro Leu Arg Asp Gly Glu Asp His Gly Val Trp Ala Gly Gly
 250 255 260 265
 ctc cgc cct gat gct gtc tgc taa tagtagggct agttccaatt ctcattaaac 1233
 Leu Arg Pro Asp Ala Val Cys *
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 cacattgtaa acagtaaaaa aaaaaa 1259

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 cgtgtacgag gagtattgca gcaaccatga gaaagccctg aggctgctgg tggagctgaa 480
 caagatccct accgtgcgcg ccttcctttt gagctgc atg ctt ctg gga ggc cgg 535
 Met Leu Leu Gly Gly Arg
 1 5
 aag acc acg gac atc cct ttg gaa ggc tac ctg ttg tct ccg atc cag 583
 Lys Thr Thr Asp Ile Pro Leu Glu Gly Tyr Leu Leu Ser Pro Ile Gln
 10 15 20
 agg atc tgc aag tac ccg ctc ctc ctt aag gag ctg gcc aag agg act 631

Arg Ile Cys Lys Tyr Pro Leu Leu Lys Glu Leu Ala Lys Arg Thr	
25 30 35	
ccc ggc aag cac cca gac cac ccc gcg gtc cag agt gcc ctg cag gcc	679
Pro Gly Lys His Pro Asp His Pro Ala Val Gln Ser Ala Leu Gln Ala	
40 45 50	
atg aag acc gtt tgc tcc aac atc aat gag acc aag cgg cag atg gag	727
Met Lys Thr Val Cys Ser Asn Ile Asn Glu Thr Lys Arg Gln Met Glu	
55 60 65 70	
aag ctg gaa gcc ctg gag cag ctg cag tcc cac atc gaa ggc tgg gag	775
Lys Leu Glu Ala Leu Glu Gln Leu Gln Ser His Ile Glu Gly Trp Glu	
75 80 85	
ggc tcc aac ctc aca gac atc tgc act cag ctc ctc ctg caa ggc act	823
Gly Ser Asn Leu Thr Asp Ile Cys Thr Gln Leu Leu Leu Gln Gly Thr	
90 95 100	
ttg tta aag atc tct gcg ggc aac atc cag gaa agg gcc ttc ttc ctc	871
Leu Leu Lys Ile Ser Ala Gly Asn Ile Gln Glu Arg Ala Phe Phe Leu	
105 110 115	
ttc gac aac ctt ctc gtc tac tgc aag cgg aaa tcc agg gtc acc ggc	919
Phe Asp Asn Leu Leu Val Tyr Cys Lys Arg Lys Ser Arg Val Thr Gly	
120 125 130	
agc aag aag tcc acc aag agg acc aaa tcc atc aac ggc tcc ctc tac	967
Ser Lys Lys Ser Thr Lys Arg Thr Lys Ser Ile Asn Gly Ser Leu Tyr	
135 140 145 150	
atc ttc agg ggt cga atc aac act gaa gtc atg gag gtg gag aat gtg	1015
Ile Phe Arg Gly Arg Ile Asn Thr Glu Val Met Glu Val Glu Asn Val	
155 160 165	
gaa gat ggc aca ggt agc ccc tcc ccc agc ctt gcc tga gccctgcctg	1064
Glu Asp Gly Thr Gly Ser Pro Ser Pro Ser Leu Ala *	
170 175	
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 accccagccc ggcccggaac actctggggc agacggcggg ggcaactctc cccttgccgc 180
 c atg cac gac gct ttc gag cca gtg ccg atc cta gaa aag ctg cct 226
 Met His Asp Ala Phe Glu Pro Val Pro Ile Leu Glu Lys Leu Pro
 1 5 10 15
 ctg caa atc gac tgt ctg gct gcc tgg gag gaa tgg ctt ctt gtg gga 274
 Leu Gln Ile Asp Cys Leu Ala Ala Trp Glu Glu Trp Leu Leu Val Gly
 20 25 30
 acc aaa caa gga cat ctt ctt ctc tat agg att cgg aag gac gtt ggt 322
 Thr Lys Gln Gly His Leu Leu Leu Tyr Arg Ile Arg Lys Asp Val Gly
 35 40 45
 tgc aac aga ttt gaa gtg aca cta gag aaa tcc aat aag aac ttc tcc 370
 Cys Asn Arg Phe Glu Val Thr Leu Glu Lys Ser Asn Lys Asn Phe Ser
 50 55 60
 aaa aag att cag cag atc cat gtg gtt tcc cag ttt aag att ctg gtc 418
 Lys Lys Ile Gln Gln Ile His Val Val Ser Gln Phe Lys Ile Leu Val
 65 70 75
 agc ttg tta gaa aat aac att tat gtc cat gac cta ttg aca ttt caa 466
 Ser Leu Leu Glu Asn Asn Ile Tyr Val His Asp Leu Leu Thr Phe Gln
 80 85 90 95
 caa atc act acg gtt tca aag gca aag gga gca tca ctg ttt act tgt 514
 Gln Ile Thr Thr Val Ser Lys Ala Lys Gly Ala Ser Leu Phe Thr Cys
 100 105 110
 gac ctc cag cac aca gag acc ggt gag gag gtg tta cgg atg tgt gtg 562
 Asp Leu Gln His Thr Glu Thr Gly Glu Glu Val Leu Arg Met Cys Val
 115 120 125
 gca gta aaa aag agg ctg cag ctc tat ttc tgg aag gac aga gaa ttt 610
 Ala Val Lys Lys Arg Leu Gln Leu Tyr Phe Trp Lys Asp Arg Glu Phe
 130 135 140
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 His Glu Leu Gln Gly Asp Phe Ser Val Pro Asp Val Pro Lys Ser Met
 145 150 155
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 Ala Trp Cys Glu Asn Ser Ile Cys Val Gly Phe Lys Arg Asp Tyr Tyr
 160 165 170 175
 cta ata agg gtg gat gga aag ggg tcc atc aaa gag ctc ttt cca aca 754
 Leu Ile Arg Val Asp Gly Lys Gly Ser Ile Lys Glu Leu Phe Pro Thr
 180 185 190
 gga aaa cag ctg gag ccc tta gtt gca cct ctg gca gat gga aaa gtg 802
 Gly Lys Gln Leu Glu Pro Leu Val Ala Pro Leu Ala Asp Gly Lys Val
 195 200 205
 gct gtg ggc cag gat gat ctc acc gtg gta ctc aat gag gaa ggg atc 850
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 210 215 220
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 Cys Thr Gln Lys Cys Ala Leu Asn Trp Thr Asp Ile Pro Val Ala Met

225	230	235	
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atc cga aca ttt gaa ccg agg ctt ctg gtc caa agc att gaa ttg caa Ile Arg Thr Phe Glu Pro Arg Leu Leu Val Gln Ser Ile Glu Leu Gln 260 265 270			994
agg ccc cgt ttc att acc tca gga gga tca aac att atc tat gtg gcc Arg Pro Arg Phe Ile Thr Ser Gly Gly Ser Asn Ile Ile Tyr Val Ala 275 280 285			1042
agc aat cat ttt gtt tgg aga ctc atc cct gtc ccc atg gca acc caa Ser Asn His Phe Val Trp Arg Leu Ile Pro Val Pro Met Ala Thr Gln 290 295 300			1090
atc caa caa ctt ctc cag gac aag cag ttt gaa ttg gct ctg cag ctc Ile Gln Gln Leu Leu Gln Asp Lys Gln Phe Glu Leu Ala Leu Gln Leu 305 310 315			1138
gca gaa atg aaa gat gat tct gac agt gaa aag cag caa caa att cat Ala Glu Met Lys Asp Asp Ser Asp Ser Glu Lys Gln Gln Gln Ile His 320 325 330 335			1186
cac atc aag aac ttg tat gcc ttc aac ctc ttc tgc cag aag cgt ttt His Ile Lys Asn Leu Tyr Ala Phe Asn Leu Phe Cys Gln Lys Arg Phe 340 345 350			1234
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gag agc gag cac gtg ctg aag aag gct cac aag tac agt gag ctt atc Glu Ser Glu His Val Leu Lys Lys Ala His Lys Tyr Ser Glu Leu Ile			1666

480	485	490	495	
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cga gtc ctc ggc ttc tta ata gag aat ttt aag ggt ctg gct att cct Arg Val Leu Gly Phe Leu Ile Glu Asn Phe Lys Gly Leu Ala Ile Pro 580 585 590				1954
tat ctg gaa cac atc atc cat gtt tgg gag gag aca ggc tct cgg ttc Tyr Leu Glu His Ile Ile His Val Trp Glu Glu Thr Gly Ser Arg Phe 595 600 605				2002
cac aac tgc ctg atc cag cta tac tgt gag aag gtg caa ggt ctg atg His Asn Cys Leu Ile Gln Leu Tyr Cys Glu Lys Val Gln Gly Leu Met 610 615 620				2050
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gat aca agg atg gct gag gag tac tgc cac aaa cac tat gac cga aac Asp Thr Arg Met Ala Glu Tyr Cys His Lys His Tyr Asp Arg Asn 705 710 715				2338
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tcg ccc ccc agc att cac tgc ctg ggg cca atc aag ctg gaa cta ctg Ser Pro Pro Ser Ile His Cys Leu Gly Pro Ile Lys Leu Glu Leu Leu 740 745 750 755				2434

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Thr Gln Ile Asn Asp Ile	Arg Ile Phe Leu Glu Lys	Val Leu Glu Glu	
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Lys Cys Ile Ile Thr	Glu Glu Lys Val Cys Met	Val Cys Lys Lys Lys	
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ctg gcc gcg gcc ctg gcc gcg ctg ctg tta ctg ccg ctg ccg ctg ccc 158
Leu Ala Ala Ala Leu Ala Ala Leu Leu Leu Leu Pro Leu Pro Leu Pro
15              20              25              30
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Pro	Ser	Arg	Pro	Ala	Ala	Pro	Ser	Leu	Arg	Pro	Asp	Asp	Val	Phe	Ile	
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Ala	Val	Lys	Thr	Thr	Arg	Lys	Asn	His	Gly	Pro	Arg	Leu	Arg	Leu	Leu	
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Leu	Arg	Thr	Trp	Ile	Ser	Arg	Ala	Arg	Gln	Gln	Thr	Phe	Ile	Phe	Thr	
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gac	ggg	gac	gac	cct	gag	ctc	gag	ctc	cag	ggc	ggc	gac	cgt	gtc	atc	398
Asp	Gly	Asp	Asp	Pro	Glu	Leu	Glu	Leu	Gln	Gly	Gly	Asp	Arg	Val	Ile	
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aac	acc	aac	tgc	tcg	gcg	gtg	cgc	act	cgt	cag	gcc	ctc	tgc	tgc	aag	446
Asn	Thr	Asn	Cys	Ser	Ala	Val	Arg	Thr	Arg	Gln	Ala	Leu	Cys	Cys	Lys	
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Cys	His	Val	Asp	Asp	Asp	Asn	Tyr	Val	Asn	Ala	Arg	Ser	Leu	Leu	His	
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Leu	Leu	Ser	Ser	Phe	Ser	Pro	Ser	Gln	Asp	Val	Tyr	Leu	Gly	Arg	Pro	
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Ser	Leu	Asp	His	Pro	Ile	Glu	Ala	Thr	Glu	Arg	Val	Gln	Gly	Gly	Arg	
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Thr	Val	Thr	Thr	Val	Lys	Phe	Trp	Phe	Ala	Thr	Gly	Gly	Ala	Gly	Phe	
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Asp	Thr	Leu	Leu	Gln	Gln	Val	Thr	Leu	Ser	His	Gly	Gly	Pro	Glu	Asn	
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Pro	Thr	Arg	Phe	Lys	Ser	Ile	His	Cys	Leu	Leu	Tyr	Pro	Asp	Thr	Asp	
		305					310				315					
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Trp	Cys	Pro	Arg	Gln	Lys	Gln	Gly	Ala	Pro	Thr	Ser	Arg	*			
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 Met Phe Leu Pro Gly Pro Gln Pro Ser Ala Val Leu Pro Gly Arg
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 Trp Leu Trp Ala Phe Arg Thr His Ser Gln Val Ser Ser Arg Arg Leu
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 80 85 90 95
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 Thr Pro His Cys Pro Pro Pro Ser Pro Leu Ala Val Pro Ser Ser Ser
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 115 120 125
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 Ser Leu Lys Gly Val Pro Thr Glu Val Lys Ile Gln Glu Met Thr Lys
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 aag ggc tgt gcc tgc gcc cag aag cag cta cac ttc atg gac cag ttg 1069
 Lys Gly Cys Ala Cys Ala Gln Lys Gln Leu His Phe Met Asp Gln Leu
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 210 215 220
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aag ctg gcg gag ctt gcc agg cag ctg cag gag agt gct gcc aag ttg			1357
Lys Leu Ala Glu Leu Ala Arg Gln Leu Gln Glu Ser Ala Ala Lys Leu			
	260	265	270
cac gcg ctt aga acg gag tac ttt gca cag cat gag caa ggg gct gct			1405
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Ala Gly Ala Ala Asp Ile Ser Thr Leu Asp Gln Lys Leu Arg Leu Val			
	290	295	300
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Thr Ser Asp Phe His Gln Leu Ile Leu Ala Phe Leu Gln Val Tyr Asp			
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Asp Glu Leu Gly Glu Cys Cys Gln Arg Pro Gly Pro Asp Leu His Pro			
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tgc ggc ccc atc atc cag gcc acg cac cag aat ctg act tcc tac agc			1597
Cys Gly Pro Ile Ile Gln Ala Thr His Gln Asn Leu Thr Ser Tyr Ser			
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Val Glu Thr Val Lys Lys Gln Gln Gly Glu Gln Ile Cys Trp Gly Gly			
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Ser Ser Ser Val Met Ser Leu Ala Thr Lys Met Asn Glu Leu Met Glu			
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Lys *			
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Met Leu Leu Lys Val Gln
1 5
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Tyr Ile Ser Cys Trp Ala Val Met Ser Phe Ser Ser Phe Val Leu Asn
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Pro Leu Arg Leu Ser Tyr Asn Leu Val Cys Lys Ala Phe Ser Gly Met
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Val Phe Pro Pro Pro Val Phe Val Val Thr Glu Pro Ala Asp Thr Asp
40 45 50
ggc cag ctg tac ttg tgt ttc tca ttt gat cct tat att gca gta tcg 367
Gly Gln Leu Tyr Leu Cys Phe Ser Phe Asp Pro Tyr Ile Ala Val Ser
55 60 65 70
gag tta cag aag ctt att cgg caa ctc ttg ctt ttg cag tta ttt cca 415
Glu Leu Gln Lys Leu Ile Arg Gln Leu Leu Leu Leu Gln Leu Phe Pro
75 80 85
aaa tat ctg ata tat att gac att aac aag gct ctt ctt gcc aag aga 463
Lys Tyr Leu Ile Tyr Ile Asp Ile Asn Lys Ala Leu Leu Ala Lys Arg
90 95 100
aag aga cta gaa atg tat acc aag gct tct ctc aaa act agt aac cag 511
Lys Arg Leu Glu Met Tyr Thr Lys Ala Ser Leu Lys Thr Ser Asn Gln
105 110 115
aaa att gaa cat gtt tgg aaa aca caa caa gat caa agg cag aag ctt 559
Lys Ile Glu His Val Trp Lys Thr Gln Gln Asp Gln Arg Gln Lys Leu
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Asn Gln Glu Tyr Ser Gln Gln Phe Leu Thr Leu Phe Gln Gln Trp Asp
135 140 145 150
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Leu Asp Met Gln Lys Ala Glu Glu Gln Glu Glu Lys Ile Leu Asn Met
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170 175 180
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Gln Arg Leu Lys Thr Ile Lys Gln Leu Tyr Glu Gln Phe Ile Lys Ser
185 190 195
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Met Glu Glu Leu Glu Lys Asn His Asp Asn Leu Leu Thr Gly Ala Gln
200 205 210
aat gaa ttt aaa aaa gaa atg gct atg ttg caa aaa aaa att atg atg 847
Asn Glu Phe Lys Lys Glu Met Ala Met Leu Gln Lys Lys Ile Met Met
215 220 225 230

gaa act cag cag caa gag ata gca agt gtt cgg aag tct ctt caa tcc 895
 Glu Thr Gln Gln Gln Glu Ile Ala Ser Val Arg Lys Ser Leu Gln Ser
 235 240 245

atg tta ttc tga tga ctctttgaag aaagaacttg aacctaagta atatgatata 950
 Met Leu Phe *
 250

attataacgt tagctaagaa gcatattgta agtcctttaga atagtttaaat tgtaacatct 1010

ttaatcataa acctgtttca ttgtaagacc tccctttctg ttaagtcaaa tctaaatagt 1070

tatgagttag ttagcaacta ttcctaaaga atatgtatta agctttcagc tcttttagtaa 1130

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 ccgcggggcca cccctgaag tcgcctgccg ccgcgcgcgc cgcacctagc ggacgggcgg 180
 gcggggcgcg gtgtgcccag gagtgcgcgc ctgtcgcggg ggtgggtgca ggactggacc 240
 cacggggcca ttgtgcgccc gccgcgggca gccaggacc atg tgg gtg aac ccg 294
 Met Trp Val Asn Pro
 1 5

gag gag gtg ttg ctg gcc aac gcg ctg tgg atc acc gag agg gcc aac 342
 Glu Glu Val Leu Leu Ala Asn Ala Leu Trp Ile Thr Glu Arg Ala Asn
 10 15 20

cca tac ttc atc ctg cag cgg agg aag ggc cac gcc ggc gat gga ggc 390
 Pro Tyr Phe Ile Leu Gln Arg Arg Lys Gly His Ala Gly Asp Gly Gly
 25 30 35

ggc ggc ggc gga ctg gcg ggc ctg ctg gtg ggt acc ctt gat gtt gtg 438
 Gly Gly Gly Gly Leu Ala Gly Leu Leu Val Gly Thr Leu Asp Val Val
 40 45 50

ttg gac tcc agc gcc cgg gtc gct cct tac cga atc ttg tac cag act 486
 Leu Asp Ser Ser Ala Arg Val Ala Pro Tyr Arg Ile Leu Tyr Gln Thr
 55 60 65

cca gac tcc ctg ggt cta ctg gac cat cgc ctg tgg gtg gtt cca gga 534
 Pro Asp Ser Leu Gly Leu Leu Asp His Arg Leu Trp Val Val Pro Gly
 70 75 80 85

aag aaa tca ctg aac act ggg aat ggc ttg agc aaa atc tct tgc aga 582
 Lys Lys Ser Leu Asn Thr Gly Asn Gly Leu Ser Lys Ile Ser Cys Arg

90

95

100

cac ttt cca tct ttg aaa atg aga atg ata tca cca cat ttg tga gag 630
 His Phe Pro Ser Leu Lys Met Arg Met Ile Ser Pro His Leu *
 105 110 115

gaaaaataca gggcatcatt gcagaataca aaaaaatcaa tgatgtaaag gaagatgatg 690
 acacggagaa gtttaaagaa gccattgtga aatttcataag gctgtttggg atgccagagg 750
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 agacttttat gaatacatgg tttcaatcaa gtccccagag aacacatttg tcttctgagc 180
 tgctggcagt tttgagaatc tgatgacctc cgagggggacc ctgcactcag ccatcaaagt 240
 gttcctgccc ctctggacac tcataattca atg gta gat gca ggt gga gtt 291
 Met Val Asp Ala Gly Gly Val
 1 5
 gag aac atc acc cag ctt ccc cag gag ctt cct cag atg atg gct gca 339
 Glu Asn Ile Thr Gln Leu Pro Gln Glu Leu Pro Gln Met Met Ala Ala
 10 15 20
 gca gcc gat ggt ttg ggg agt ata gcg ata gac acg acc cag ctc aac 387
 Ala Ala Asp Gly Leu Gly Ser Ile Ala Ile Asp Thr Thr Gln Leu Asn
 25 30 35
 atg tcc gtg aca gat ccc aca gcc tgg gct aca gcc atg aat aac ctg 435
 Met Ser Val Thr Asp Pro Thr Ala Trp Ala Thr Ala Met Asn Asn Leu
 40 45 50 55
 ggc atg gtt ccc gta ggg ttg cct gga cag cag ctc gtg tct gac tca 483
 Gly Met Val Pro Val Gly Leu Pro Gly Gln Gln Leu Val Ser Asp Ser
 60 65 70
 atc tgt gtc cca ggc ttt gat cca agc ctc aac atg atg act gga atc 531
 Ile Cys Val Pro Gly Phe Asp Pro Ser Leu Asn Met Met Thr Gly Ile
 75 80 85
 acc ccc att aac cca atg ata cca ggc ctt gga ctg gta cct ccc cca 579
 Thr Pro Ile Asn Pro Met Ile Pro Gly Leu Gly Leu Val Pro Pro Pro
 90 95 100
 cca cca aca gaa gtg gct gtt gtc aaa gaa ata atc cac tgc aaa agc 627
 Pro Pro Thr Glu Val Ala Val Val Lys Glu Ile Ile His Cys Lys Ser
 105 110 115

tgt act ctt ttt cct caa aat cca aat ctt cca cct cct tcc aca aga	675
Cys Thr Leu Phe Pro Gln Asn Pro Asn Leu Pro Pro Pro Ser Thr Arg	
120 125 130 135	
 gaa cga cct cct ggg tgt aag acc gtg ttt gtc gga gga tta cca gaa	723
Glu Arg Pro Pro Gly Cys Lys Thr Val Phe Val Gly Gly Leu Pro Glu	
140 145 150	
 aat gct act gag gaa att att caa gaa gtc ttt gaa cag tgc ggt gat	771
Asn Ala Thr Glu Glu Ile Ile Gln Glu Val Phe Glu Gln Cys Gly Asp	
155 160 165	
 att aca gca att cgg aaa agc aag aag aat ttt tgt cac att cgc ttt	819
Ile Thr Ala Ile Arg Lys Ser Lys Lys Asn Phe Cys His Ile Arg Phe	
170 175 180	
 gca gag gaa ttc atg gtt gat aaa gcc att tac ctt tct ggt tat agg	867
Ala Glu Glu Phe Met Val Asp Lys Ala Ile Tyr Leu Ser Gly Tyr Arg	
185 190 195	
 atg cga tta ggg tct agc acc gac aaa aag gat tca ggc cgc ctt cat	915
Met Arg Leu Gly Ser Ser Thr Asp Lys Lys Asp Ser Gly Arg Leu His	
200 205 210 215	
 gtg gac ttt gcc cag gcc agg gat gac ttc tat gag tgg gaa tgc aag	963
Val Asp Phe Ala Gln Ala Arg Asp Asp Phe Tyr Glu Trp Glu Cys Lys	
220 225 230	
 cag agg atg cgt gcc cgg gag gag cgg cac cgg cgc aag ctg gag gag	1011
Gln Arg Met Arg Ala Arg Glu Glu Arg His Arg Arg Lys Leu Glu Glu	
235 240 245	
 gac cgg ctc agg ccc cca tcc ccg cct gcc ata atg cac tac tcg gag	1059
Asp Arg Leu Arg Pro Pro Ser Pro Pro Ala Ile Met His Tyr Ser Glu	
250 255 260	
 cac gaa gcc gct ctg ctg gct gaa aag ctg aaa gat gat agc aag ttt	1107
His Glu Ala Ala Leu Leu Ala Glu Lys Leu Lys Asp Asp Ser Lys Phe	
265 270 275	
 tca gag gct atc aca gtg ctg ctt tcc tgg att gaa cga ggg gaa gtg	1155
Ser Glu Ala Ile Thr Val Leu Leu Ser Trp Ile Glu Arg Gly Glu Val	
280 285 290 295	
 aat cgg cgc tct gca aac cag ttc tat tcc atg gtg cag tcg gcc aac	1203
Asn Arg Arg Ser Ala Asn Gln Phe Tyr Ser Met Val Gln Ser Ala Asn	
300 305 310	
 agc cac gtc cgc cgg cta atg aat gaa aaa gcc acc cat gag caa gag	1251
Ser His Val Arg Arg Leu Met Asn Glu Lys Ala Thr His Glu Gln Glu	
315 320 325	
 atg gag gaa gcc aag gag aat ttt aaa aat gcc tta act ggg att ctc	1299
Met Glu Glu Ala Lys Glu Asn Phe Lys Asn Ala Leu Thr Gly Ile Leu	
330 335 340	
 act caa ttt gag cag att gtg gcc gtt ttc aac gct tct acc aga caa	1347
Thr Gln Phe Glu Gln Ile Val Ala Val Phe Asn Ala Ser Thr Arg Gln	
345 350 355	
 aaa gct tgg gac cat ttc tcg aaa gcc cag cgc aag aac ata gac att	1395
Lys Ala Trp Asp His Ser Ser Lys Ala Gln Arg Lys Asn Ile Asp Ile	
360 365 370 375	

tgg cga aag cat tct gag gag ctc cgg aat gct caa agt gag cag ctc	1443
Trp Arg Lys His Ser Glu Glu Leu Arg Asn Ala Gln Ser Glu Gln Leu	
380 385 390	
atg ggc atc cgc cgc gaa gaa gaa atg gaa atg tct gat gat gag aac	1491
Met Gly Ile Arg Arg Glu Glu Glu Met Glu Met Ser Asp Asp Glu Asn	
395 400 405	
tgt gac agc cct aca aag aaa atg aga gtc gat gaa tca gcc ctg gct	1539
Cys Asp Ser Pro Thr Lys Lys Met Arg Val Asp Glu Ser Ala Leu Ala	
410 415 420	
gcc cag gcc tac gct ctg aaa gag gag aat gac agt ctc cgc tgg cag	1587
Ala Gln Ala Tyr Ala Leu Lys Glu Glu Asn Asp Ser Leu Arg Trp Gln	
425 430 435	
ctg gat gcc tac agg aat gag gtg gag ctg ctg aaa caa gaa aaa gaa	1635
Leu Asp Ala Tyr Arg Asn Glu Val Glu Leu Leu Lys Gln Glu Lys Glu	
440 445 450 455	
cag ctt ttc cga aca gaa gaa aac ctc acc aag gac cag caa ctg cag	1683
Gln Leu Phe Arg Thr Glu Glu Asn Leu Thr Lys Asp Gln Gln Leu Gln	
460 465 470	
ttt ctg cag caa acc atg caa ggc atg cag cag caa ttg cta acc atc	1731
Phe Leu Gln Gln Thr Met Gln Gly Met Gln Gln Gln Leu Leu Thr Ile	
475 480 485	
cag gag gag tta aac aac aaa aag tca gaa ttg gaa caa gca aag gaa	1779
Gln Glu Glu Leu Asn Asn Lys Lys Ser Glu Leu Glu Gln Ala Lys Glu	
490 495 500	
gag cag tcc cat aca caa gcg tta cta aaa gtc ctg cag gaa caa tta	1827
Glu Gln Ser His Thr Gln Ala Leu Leu Lys Val Leu Gln Glu Gln Leu	
505 510 515	
aaa ggt acc aag gaa ttg gtc gag acc aat ggc cac agc cat gag gat	1875
Lys Gly Thr Lys Glu Leu Val Glu Thr Asn Gly His Ser His Glu Asp	
520 525 530 535	
tca aat gaa atc aat gtg ttg aca gtt gca tta gtc aac caa gac cga	1923
Ser Asn Glu Ile Asn Val Leu Thr Val Ala Leu Val Asn Gln Asp Arg	
540 545 550	
gag aac aat att gag aaa aga agc caa ggc tta aaa tca gag aaa gaa	1971
Glu Asn Asn Ile Glu Lys Arg Ser Gln Gly Leu Lys Ser Glu Lys Glu	
555 560 565	
gct ctg cta ata ggt atc ata tca acg ttt ctt cac gtc cat cct ttt	2019
Ala Leu Leu Ile Gly Ile Ile Ser Thr Phe Leu His Val His Pro Phe	
570 575 580	
gga gcc aac ata gaa tat ctt tgg tca tac atg cag cag ctg gac tcc	2067
Gly Ala Asn Ile Glu Tyr Leu Trp Ser Tyr Met Gln Gln Leu Asp Ser	
585 590 595	
aag ata tct gca aat gaa ata gaa atg ctt ttg atg agg ctg cca cgc	2115
Lys Ile Ser Ala Asn Glu Ile Glu Met Leu Leu Met Arg Leu Pro Arg	
600 605 610 615	
atg ttc aaa cag gaa ttc acg ggt gtg gga gcc acg ctg gaa aaa aga	2163
Met Phe Lys Gln Glu Phe Thr Gly Val Gly Ala Thr Leu Glu Lys Arg	
620 625 630	

tgg aag ttg tgt gcc ttt gaa gga att aaa acc acc taa ctgcgaagag 2212
 Trp Lys Leu Cys Ala Phe Glu Gly Ile Lys Thr Thr *
 635 640

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 tttaaagtta atgatggtgt agcaatgatt gttgctaggc tacagagttg tatatgtaat 2572
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 ggc gtg agc cac cgc gca ggc agc cgg gat tgc tta cca cct gca gcg 96
 Gly Val Ser His Arg Ala Gly Ser Arg Asp Cys Leu Pro Pro Ala Ala
 20 25 30
 tgc ttt cgg agg cgg cgg ctg gca cgg agg ccg ggc tac atg aga agc 144
 Cys Phe Arg Arg Arg Arg Leu Ala Arg Arg Pro Gly Tyr Met Arg Ser
 35 40 45
 tcg aca ggg cct ggg atc ggg ttc ctt tcc cca gca gtg ggc aca ctg 192
 Ser Thr Gly Pro Gly Ile Gly Phe Leu Ser Pro Ala Val Gly Thr Leu
 50 55 60
 ttc cgg ttc cca gga ggg gtg tct ggc gag gag tcc cac cac tcg gag 240
 Phe Arg Phe Pro Gly Gly Val Ser Gly Glu Ser His His Ser Glu
 65 70 75 80
 tcc agg gcc aga cag tgt ggc ctt gac tcg aga ggc ctc ttg gtc cgg 288
 Ser Arg Ala Arg Gln Cys Gly Leu Asp Ser Arg Gly Leu Leu Val Arg
 85 90 95
 agc cct gtt tcc aag agt gca gca gcc cct act gtg acc tct gtg aga 336
 Ser Pro Val Ser Lys Ser Ala Ala Pro Thr Val Thr Ser Val Arg
 100 105 110
 gga acc tcg gcg cac ttt ggg att cag ctc aga ggt ggc acc aga ttg 384
 Gly Thr Ser Ala His Phe Gly Ile Gln Leu Arg Gly Gly Thr Arg Leu
 115 120 125

cct gac agg ctt agc tgg ccg tgt ggc cct ggg agt gct ggg tgg cag	432
Pro Asp Arg Leu Ser Trp Pro Cys Gly Pro Gly Ser Ala Gly Trp Gln	
130 135 140	
caa gag ttt gca gcc atg gat agt tct gag acc ctg gac gcc agc tgg	480
Gln Glu Phe Ala Ala Met Asp Ser Ser Glu Thr Leu Asp Ala Ser Trp	
145 150 155 160	
gag gca gcc tgc agc gat gga gca agg cgt gtc cgg gca gca gcc tct	528
Glu Ala Ala Cys Ser Asp Gly Ala Arg Arg Val Arg Ala Ala Gly Ser	
165 170 175	
ctg cca tca gca gag ttg agt agc aac agc tgc agc cct ggc tgt ggc	576
Leu Pro Ser Ala Glu Leu Ser Ser Asn Ser Cys Ser Pro Gly Cys Gly	
180 185 190	
cct gag gtc ccc cca acc cct cct ggc tct cac agt gcc ttt acc tca	624
Pro Glu Val Pro Pro Thr Pro Pro Gly Ser His Ser Ala Phe Thr Ser	
195 200 205	
agc ttt agc ttt att cgg ctc tcg ctt ggc tct gcc ggg gaa cgt gga	672
Ser Phe Ser Phe Ile Arg Leu Ser Leu Gly Ser Ala Gly Glu Arg Gly	
210 215 220	
gaa gca gaa ggc tgc cca cca tcc aga gag gct gag tcc cat tgc cag	720
Glu Ala Glu Gly Cys Pro Pro Ser Arg Glu Ala Glu Ser His Cys Gln	
225 230 235 240	
agc ccc cag gag atg gga gcc aaa gct gcc agc ttg gac ggg cct cac	768
Ser Pro Gln Glu Met Gly Ala Lys Ala Ala Ser Leu Asp Gly Pro His	
245 250 255	
gag gac ccg cga tgt ctc tct cag ccc ttc agt ctc ttg gct aca cgg	816
Glu Asp Pro Arg Cys Leu Ser Gln Pro Phe Ser Leu Leu Ala Thr Arg	
260 265 270	
gtc tct gca gac ttg gcc cag gcc gca agg aac agc tcc agg cca gag	864
Val Ser Ala Asp Leu Ala Gln Ala Ala Arg Asn Ser Ser Arg Pro Glu	
275 280 285	
cgt gac atg cat tct tta cca gac atg gac cct ggc tcc tcc agt tct	912
Arg Asp Met His Ser Leu Pro Asp Met Asp Pro Gly Ser Ser Ser Ser	
290 295 300	
ctg gat ccc tca ctg gct ggc tgt ggt ggt gat ggg agc agc ggc tca	960
Leu Asp Pro Ser Leu Ala Gly Cys Gly Gly Asp Gly Ser Ser Gly Ser	
305 310 315 320	
ggg gat gcc cac tct tgg gac acc ctg ctc agg aaa tgg gag cca gtg	1008
Gly Asp Ala His Ser Trp Asp Thr Leu Leu Arg Lys Trp Glu Pro Val	
325 330 335	
ctg cgg gac tgc ctg ctg aga aac cgg agg cag atg gag gta ata tcc	1056
Leu Arg Asp Cys Leu Leu Arg Asn Arg Arg Gln Met Glu Val Ile Ser	
340 345 350	
tta aga tta aaa ctt cag aaa ctt cag gaa gat gca gtt gag aat gat	1104
Leu Arg Leu Lys Leu Gln Lys Leu Gln Glu Asp Ala Val Glu Asn Asp	
355 360 365	
gat tat gat aaa gct gag acg tta caa caa aga tta gaa gac ctg gaa	1152
Asp Tyr Asp Lys Ala Glu Thr Leu Gln Gln Arg Leu Glu Asp Leu Glu	
370 375 380	

caa gag aaa atc agc ctg cac ttt caa ctt cct tca agg cag cca gct Gln Glu Lys Ile Ser Leu His Phe Gln Leu Pro Ser Arg Gln Pro Ala 385 390 395 400	1200
ctt agc agt ttc ctg ggt cac ctg gca gca caa gtc cag gct gcc ttg Leu Ser Ser Phe Leu Gly His Leu Ala Ala Gln Val Gln Ala Ala Leu 405 410 415	1248
cgc cgt ggg gcc act cag cag gcc agc gga gat gac acc cac acc cca Arg Arg Gly Ala Thr Gln Gln Ala Ser Gly Asp Asp Thr His Thr Pro 420 425 430	1296
ctg aga atg gag ccg agg ctg ttg gaa ccc act gct cag gac agc ttg Leu Arg Met Glu Pro Arg Leu Leu Glu Pro Thr Ala Gln Asp Ser Leu 435 440 445	1344
cac gtg tcc atc acg aga cga gac tgg ctt ctt cag gaa aag cag cag His Val Ser Ile Thr Arg Arg Asp Trp Leu Leu Gln Glu Lys Gln Gln 450 455 460	1392
cta cag aaa gaa atc gaa gct ctc caa gca agg atg ttt gtg ctg gaa Leu Gln Lys Glu Ile Glu Ala Leu Gln Ala Arg Met Phe Val Leu Glu 465 470 475 480	1440
gcc aaa gat caa cag ctg aga agg gaa ata gag gag caa gag cag caa Ala Lys Asp Gln Gln Leu Arg Arg Glu Ile Glu Glu Gln Glu Gln Gln 485 490 495	1488
ctc cag tgg cag ggc tgc gac ctg acc cca ctg gtg ggc cag ctg tcc Leu Gln Trp Gln Gly Cys Asp Leu Thr Pro Leu Val Gly Gln Leu Ser 500 505 510	1536
ctg ggt cag ctg cag gag gtc agc aag gcc ttg cag gac acc ctg gcc Leu Gly Gln Leu Gln Glu Val Ser Lys Ala Leu Gln Asp Thr Leu Ala 515 520 525	1584
tca gcc ggt cag att ccc ttc cat gca gag cca ccg gaa acc ata agg Ser Ala Gly Gln Ile Pro Phe His Ala Glu Pro Pro Glu Thr Ile Arg 530 535 540	1632
agc ctc cag gaa aga ata aaa tcc ctc aac ttg tca ctt aaa gaa atc Ser Leu Gln Glu Arg Ile Lys Ser Leu Asn Leu Ser Leu Lys Glu Ile 545 550 555 560	1680
act act aag gtg tgt atg agt gag aaa ttc tgc agc acc ctg agg aag Thr Thr Lys Val Cys Met Ser Glu Lys Phe Cys Ser Thr Leu Arg Lys 565 570 575	1728
aaa gtt aac gat att gaa acc caa cta cca gcc ttg ctt gaa gcc aaa Lys Val Asn Asp Ile Glu Thr Gln Leu Pro Ala Leu Leu Glu Ala Lys 580 585 590	1776
atg cat gcc ata tca gga aac cat ttc tgg acg gct aaa gac ctc acc Met His Ala Ile Ser Gly Asn His Phe Trp Thr Ala Lys Asp Leu Thr 595 600 605	1824
gag gag att aga tca tta aca tca gag aga gaa ggg ctg gag gga ctc Glu Glu Ile Arg Ser Leu Thr Ser Glu Arg Glu Gly Leu Glu Gly Leu 610 615 620	1872
ctc agc aag ctg ttg gtg ttg agt tcc agg aat gtc aaa aag ctg gga Leu Ser Lys Leu Leu Val Leu Ser Ser Arg Asn Val Lys Lys Leu Gly 625 630 635 640	1920

agt gtt aaa gaa gat tac aac aga ctg aga aga gaa gtg gag cac cag	1968
Ser Val Lys Glu Asp Tyr Asn Arg Leu Arg Arg Glu Val Glu His Gln	
645 650 655	
gag act gcc tat gaa aca agt gtg aag gaa aat act atg aag tac atg	2016
Glu Thr Ala Tyr Glu Thr Ser Val Lys Glu Asn Thr Met Lys Tyr Met	
660 665 670	
gaa aca ctt aag aat aaa ctg tgc agc tgc aag tgt cca ctg ctt ggg	2064
Glu Thr Leu Lys Asn Lys Leu Cys Ser Cys Lys Cys Pro Leu Leu Gly	
675 680 685	
aaa gtg tgg gaa gct gac ttg gaa gct tgt cga ttg ctt atc cag tgc	2112
Lys Val Trp Glu Ala Asp Leu Glu Ala Cys Arg Leu Leu Ile Gln Cys	
690 695 700	
cta cag ctc cag gaa gcc agg gga agc ctg tct gta gaa gat gag agg	2160
Leu Gln Leu Gln Glu Ala Arg Gly Ser Leu Ser Val Glu Asp Glu Arg	
705 710 715 720	
cag atg gat gac tta gag gga gct gct cct cct att ccc ccc agg ctc	2208
Gln Met Asp Asp Leu Glu Gly Ala Ala Pro Pro Ile Pro Pro Arg Leu	
725 730 735	
cac tcc gag gat aaa agg aag acc cct ttg aag gta ttg gaa gaa tgg	2256
His Ser Glu Asp Lys Arg Lys Thr Pro Leu Lys Val Leu Glu Glu Trp	
740 745 750	
aag act cac ctc atc ccc tct ctg cac tgt gct gga ggt gaa cag aaa	2304
Lys Thr His Leu Ile Pro Ser Leu His Cys Ala Gly Gly Glu Gln Lys	
755 760 765	
gag gaa tct tac atc ctt tct gca gaa ctt gga gaa aag tgt gaa gac	2352
Glu Glu Ser Tyr Ile Leu Ser Ala Glu Leu Gly Glu Lys Cys Glu Asp	
770 775 780	
ata ggc aag aag cta ttg tac ttg gaa gat caa ctt cac aca gca atc	2400
Ile Gly Lys Lys Leu Leu Tyr Leu Glu Asp Gln Leu His Thr Ala Ile	
785 790 795 800	
cac agt cat gat gaa gat ctc att cag tct ctc agg agg gag ctc cag	2448
His Ser His Asp Glu Asp Leu Ile Gln Ser Leu Arg Arg Glu Leu Gln	
805 810 815	
atg gtg aag gaa act ctg cag gcc atg atc ctg cag ctc cag cca gca	2496
Met Val Lys Glu Thr Leu Gln Ala Met Ile Leu Gln Leu Gln Pro Ala	
820 825 830	
aag gag gcg gga gaa aga gaa gct gca gct tcc tgc atg aca gct ggt	2544
Lys Glu Ala Gly Glu Arg Glu Ala Ala Ser Cys Met Thr Ala Gly	
835 840 845	
gtc cac gaa gca caa gcc tga	2565
Val His Glu Ala Gln Ala *	
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Met Met Glu Thr Glu Leu Lys Pro Pro Gly Pro Gln Gln Thr Ser Gly
      5                      10                      15

ggc ggc ggc ggc aac tcc acc gcg gcg gcg gcc ggc ggc aac cag aaa      150
Gly Gly Gly Gly Asn Ser Thr Ala Ala Ala Gly Gly Asn Gln Lys
      20                      25                      30                      35

aac agc ccg gac cgc gtc aag cgg ccc atg aat gcc ttc atg gtg tgg      198
Asn Ser Pro Asp Arg Val Lys Arg Pro Met Asn Ala Phe Met Val Trp
                      40                      45                      50

tcc cgc ggg cag cgg cgc aag atg gcc cag gag aac ccc aag atg cac      246
Ser Arg Gly Gln Arg Arg Lys Met Ala Gln Glu Asn Pro Lys Met His
                      55                      60                      65

aac tcg gag atc agc aag cgc ctg ggc gcc gag tgg aaa ctt ttg tcg      294
Asn Ser Glu Ile Ser Lys Arg Leu Gly Ala Glu Trp Lys Leu Leu Ser
                      70                      75                      80

gag acg gag aag cgg ccg ttc atc gac gag gct aag cgg ctg cga gcg      342
Glu Thr Glu Lys Arg Pro Phe Ile Asp Glu Ala Lys Arg Leu Arg Ala
      85                      90                      95

ctg cac atg aag gag cac ccg gat tat aaa tac cgg ccc cgg cgg aaa      390
Leu His Met Lys Glu His Pro Asp Tyr Lys Tyr Arg Pro Arg Arg Lys
      100                      105                      110                      115

acc aag acg ctc atg aag aag gat aag tac acg ctg ccc ggc ggg ctg      438
Thr Lys Thr Leu Met Lys Lys Asp Lys Tyr Thr Leu Pro Gly Gly Leu
                      120                      125                      130

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Leu Ala Pro Gly Gly Asn Ser Met Ala Ser Gly Val Gly Val Gly Ala
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Gly Leu Gly Ala Gly Val Asn Gln Arg Met Asp Ser Tyr Ala His Met
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Asn Gly Trp Ser Asn Gly Ser Tyr Ser Met Met Gln Asp Gln Leu Gly
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tac ccg cag cac ccg ggc ctc aat gcg cac ggc gca gcg cag atg cag      630
Tyr Pro Gln His Pro Gly Leu Asn Ala His Gly Ala Ala Gln Met Gln
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ccc atg cac cgc tac gac gtg agc gcc ctg cag tac aac tcc atg acc      678
Pro Met His Arg Tyr Asp Val Ser Ala Leu Gln Tyr Asn Ser Met Thr
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Ser Ser Gln Thr Tyr Met Asn Gly Ser Pro Thr Tyr Ser Met Ser Tyr

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Ser Gln Gln Gly Thr Pro Gly Met Ala Leu Gly Ser Met Gly Ser Val			
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Val Lys Ser Glu Ala Ser Ser Ser Pro Pro Val Val Thr Ser Ser Ser			
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His Ser Arg Ala Pro Cys Gln Ala Gly Asp Leu Arg Asp Met Ile Ser			
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atg tat ctc ccc ggc gcc gag gtg ccg gaa ccc gcc gcc ccc agc aga			918
Met Tyr Leu Pro Gly Ala Glu Val Pro Glu Pro Ala Ala Pro Ser Arg			
280	285	290	
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Leu His Met Ser Gln His Tyr Gln Ser Gly Pro Val Pro Gly Thr Ala			
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Glu Pro Leu Phe Pro Gly Ser Arg Arg Ser Arg Ser Val Trp Asp Ala	
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Val Arg Leu Glu Val Gly Val Pro Asp Ser Cys Pro Val Val Leu His	
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Ser Phe Thr Gln Leu Asp Pro Asp Leu Pro Arg Pro Glu Ser Ser Thr	
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cag gag atc ggt gag gag ctg atc aac gga gtc atc tac tcc atc tcc	240
Gln Glu Ile Gly Glu Glu Leu Ile Asn Gly Val Ile Tyr Ser Ile Ser	
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Leu Gly Tyr Glu Asn Glu Ser Ala Leu Asn Leu Tyr Glu Thr Cys Lys	
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gtg cgg acc gtg aag gct ggc acg ctg gag aag ctg gtg gag cac ctg	384
Val Arg Thr Val Lys Ala Gly Thr Leu Glu Lys Leu Val Glu His Leu	
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Val Pro Ala Phe Gln Gly Ser Asp Leu Ser Tyr Val Thr Ile Phe Leu	
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tgt acc tat aga gcc ttc acc acc acc caa cag gtc ctg gac ctg ctg	480
Cys Thr Tyr Arg Ala Phe Thr Thr Thr Gln Gln Val Leu Asp Leu Leu	
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Phe Lys Arg Tyr Gly Arg Cys Asp Ala Leu Thr Ala Ser Ser Arg Tyr	
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Leu Lys Asn Ala Ile Ser Ser Ile Leu Gly Thr Trp Leu Asp Gln Tyr	
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Ser Glu Asp Phe Cys Gln Pro Pro Asp Phe Pro Cys Leu Lys Gln Leu	
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Val Ala Tyr Val Gln Leu Asn Met Pro Gly Ser Asp Leu Glu Arg Arg	
225 230 235 240	
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Ala His Leu Leu Ala Gln Leu Glu His Ser Glu Pro Ile Glu Ala	
245 250 255	
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Glu Pro Glu Gly Glu Glu Asp Trp Ala Leu Ser Pro Val Pro Ala Leu	
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Lys Pro Thr Pro Glu Leu Glu Leu Ala Leu Thr Pro Ala Arg Ala Pro	
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Ser Pro Val Pro Ala Pro Ala Pro Glu Pro Glu Pro Ala Pro Thr Pro	
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Ala Pro Gly Ser Glu Leu Glu Val Ala Pro Ala Pro Ala Pro Glu Leu	
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Gln Gln Ala Pro Glu Pro Ala Val Gly Leu Glu Ser Ala Pro Ala Pro	
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Ala Leu Glu Leu Glu Pro Ala Pro Glu Gln Asp Pro Ala Pro Ser Gln	
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Thr Leu Glu Leu Glu Pro Ala Pro Ala Pro Val Pro Ser Leu Gln Pro	
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Ser Trp Pro Ser Pro Val Val Ala Glu Asn Gly Leu Ser Glu Glu Lys	
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Pro His Leu Leu Val Phe Pro Pro Asp Leu Val Ala Glu Gln Phe Thr	
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Leu Met Asp Ala Glu Leu Phe Lys Lys Val Val Pro Tyr His Cys Leu	
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Gly Ser Ile Trp Ser Gln Arg Asp Lys Lys Gly Lys Glu His Leu Ala	
420 425 430	
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Pro Thr Ile Arg Ala Thr Val Thr Gln Phe Asn Ser Val Ala Asn Cys	
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Val Ile Thr Thr Cys Leu Gly Asn Arg Ser Thr Lys Ala Pro Asp Arg	
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Ala Arg Val Val Glu His Trp Ile Glu Val Ala Arg Glu Cys Arg Ile	
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Leu Lys Asn Phe Ser Ser Leu Tyr Ala Ile Leu Ser Ala Leu Gln Ser	
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Asn Ser Ile His Arg Leu Lys Lys Thr Trp Glu Asp Val Ser Arg Asp	
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Ser Phe Arg Ile Phe Gln Lys Leu Ser Glu Ile Phe Ser Asp Glu Asn	
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Asn Tyr Ser Leu Ser Arg Glu Leu Leu Ile Lys Glu Gly Thr Ser Lys	
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Glu Thr Gly Ile Ile Gln Gly Thr Val Pro Tyr Leu Gly Thr Phe Leu	
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Thr Asp Leu Val Met Leu Asp Thr Ala Met Lys Asp Tyr Leu Tyr Gly	
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Gln	Ile	Lys	Leu	Leu	Gln	Ser	Ala	Cys	Asn	Asn	Tyr	Ser	Ile	Ala	Pro		
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Asp	Glu	Gln	Phe	Gly	Ala	Trp	Phe	Arg	Ala	Val	Glu	Arg	Leu	Ser	Glu		
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Trp	Ser	Asp	Arg	Gln	Ala	Pro	Ser	Thr	Glu	Leu	Ser	Thr	Ser	Gly	Ser		
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Ser	His	Ser	Lys	Ser	Cys	Asp	Gln	Leu	Arg	Cys	Gly	Pro	Tyr	Leu	Ser		
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Glu	Thr	Ser	Gly	Ile	Ser	Ser	Ala	Ser	Ser	Ser	Thr	Ser	Ser	Ser	Ser		
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Val	Gly	Asp	Cys	Cys	Ile	Ile	Arg	Val	Ser	Leu	Asp	Val	Asp	Asn	Gly		
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Asn	Met	Tyr	Lys	Ser	Ile	Leu	Val	Thr	Ser	Gln	Asp	Lys	Ala	Pro	Ala		
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gta	atc	cgc	aag	gcc	atg	gac	aaa	cac	aac	ctg	gag	gag	gag	gag	ccg	2544	
Val	Ile	Arg	Lys	Ala	Met	Asp	Lys	His	Asn	Leu	Glu	Glu	Glu	Glu	Pro		
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Ile Pro Glu Asn Ala Asn Val Phe Tyr Ala Met Asn Ser Thr Ala Asn	
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Tyr Asp Phe Val Leu Lys Lys Arg Thr Phe Thr Lys Gly Val Lys Val	
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Lys His Gly Ala Ser Ser Thr Leu Pro Arg Met Lys Gln Lys Gly Leu	
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Lys Ile Ala Lys Gly Ile Phe *	
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Gly Gln Leu Ala Ala Ile Lys Val Met Asp Val Thr Glu Asp Glu Glu	
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Glu Glu Ile Lys Gln Glu Ile Asn Met Leu Lys Lys Tyr Ser His His	
65 70 75	
cgc aac atc gcc acc tac tac gga gcc ttc atc aag aag agc ccc ccg	469
Arg Asn Ile Ala Thr Tyr Tyr Gly Ala Phe Ile Lys Lys Ser Pro Pro	
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Ser Val Thr Asp Leu Val Lys Asn Thr Lys Gly Asn Ala Leu Lys Glu	
115 120 125	
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Asp Cys Ile Ala Tyr Ile Cys Arg Glu Ile Leu Arg Gly Leu Ala His	
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Pro Tyr Trp Met Ala Pro Glu Val Ile Ala Cys Asp Glu Asn Pro Asp	
195 200 205	
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Ala Thr Tyr Asp Tyr Arg Ser Asp Ile Trp Ser Leu Gly Ile Thr Ala	
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Ile Glu Met Ala Glu Gly Ala Pro Pro Leu Cys Asp Met His Pro Met	
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Lys Lys Trp Ser Lys Lys Phe Ile Asp Phe Ile Asp Thr Cys Leu Ile	
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acc tca tct atc gcc act gcc ctt aac acc agt ggg gcc gga ggg tcc Thr Ser Ser Ile Ala Thr Ala Leu Asn Thr Ser Gly Ala Gly Gly Ser 675 680 685	2245
cgg cca gcc cag gca gtc cgt gcc agt aac ccc gac ctc agg agg agc Arg Pro Ala Gln Ala Val Arg Ala Ser Asn Pro Asp Leu Arg Arg Ser 690 695 700	2293
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cac ctc ccc cag gct ggc tca ctg gag cgg aac cgc gtg gga gtc tcc His Leu Pro Gln Ala Gly Ser Leu Glu Arg Asn Arg Val Gly Val Ser 720 725 730 735	2389
tcc aaa ccg gac agc tcc cct gtg ctc tcc cct ggg aat aaa gcc aag Ser Lys Pro Asp Ser Ser Pro Val Leu Ser Pro Gly Asn Lys Ala Lys 740 745 750	2437
ccc gac gac cac cgc tca cgg cca ggc cgg ccc gca agc tat aag cga Pro Asp Asp His Arg Ser Arg Pro Gly Arg Pro Ala Ser Tyr Lys Arg 755 760 765	2485
gca att ggt gag gac ttt gtg ttg ctg aaa gag cgg act ctg gac gag Ala Ile Gly Glu Asp Phe Val Leu Leu Lys Glu Arg Thr Leu Asp Glu 770 775 780	2533
gcc cct cgg cct ccc aag aag gcc atg gac tac tcg tcg tcc agc gag Ala Pro Arg Pro Pro Lys Lys Ala Met Asp Tyr Ser Ser Ser Ser Glu 785 790 795	2581

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Glu Val Glu Ser Ser Glu Asp Asp Glu Glu Glu Gly Glu Gly Gly Pro	
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gca gag ggg agc aga gat acc cct ggg ggc cgc agc gat ggg gat aca	2677
Ala Glu Gly Ser Arg Asp Thr Pro Gly Gly Arg Ser Asp Gly Asp Thr	
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gac agc gtc agc acc atg gtg gtc cac gac gtc gag gag atc acc ggg	2725
Asp Ser Val Ser Thr Met Val Val His Asp Val Glu Glu Ile Thr Gly	
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Thr Gln Pro Pro Tyr Gly Gly Gly Thr Met Val Val Gln Arg Thr Pro	
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gaa gag gag cgg aac ctg ctg cat gct gac agc aat ggg tac aca aac	2821
Glu Glu Glu Arg Asn Leu Leu His Ala Asp Ser Asn Gly Tyr Thr Asn	
865 870 875	
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Leu Pro Asp Val Val Gln Pro Ser His Ser Pro Thr Glu Asn Ser Lys	
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Gly Gln Ser Pro Pro Ser Lys Asp Gly Ser Gly Asp Tyr Gln Ser Arg	
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Gly Leu Val Lys Ala Pro Gly Lys Ser Ser Phe Thr Met Phe Val Asp	
915 920 925	
cta ggg atc tac cag cct gga ggc agt ggg gac agc atc ccc atc aca	3013
Leu Gly Ile Tyr Gln Pro Gly Gly Ser Gly Asp Ser Ile Pro Ile Thr	
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Ala Leu Val Gly Gly Glu Gly Thr Arg Leu Asp Gln Leu Gln Tyr Asp	
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gtg agg aag ggt tct gtg gtc aac gtg aat ccc acc aac acc cgg gcc	3109
Val Arg Lys Gly Ser Val Val Asn Val Asn Pro Thr Asn Thr Arg Ala	
960 965 970 975	
cac agt gag acc cct gag atc cgg aag tac aag aag cga ttc aac tcc	3157
His Ser Glu Thr Pro Glu Ile Arg Lys Tyr Lys Lys Arg Phe Asn Ser	
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Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu Val Gly Thr	
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Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln Gly Lys Val Tyr	
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Gly Leu Ile Gly Arg Arg Arg Phe Gln Gln Met Asp Val Leu Glu Gly	
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Leu Asn Leu Leu Ile Thr Ile Ser Gly Lys Arg Asn Lys Leu Arg Val	
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gcc ctc aag agc tcc gtg gag gtg tat gcc tgg gcc ccc aaa ccc tac Ala Leu Lys Ser Ser Val Glu Val Tyr Ala Trp Ala Pro Lys Pro Tyr 1105 1110 1115	3541
cac aaa ttc atg gcc ttc aag tcc ttt gcc gac ctc ccc cac cgc cct His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu Pro His Arg Pro 1120 1125 1130 1135	3589
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cgc tct gtg gag acg ggc cac ctc gac ggg gtc ttc atg cac aaa cga Arg Ser Val Glu Thr Gly His Leu Asp Gly Val Phe Met His Lys Arg 1250 1255 1260	3973
gct cag agg ctc aag ttc ctg tgt gag cgg aat gac aag gtg ttt ttt Ala Gln Arg Leu Lys Phe Leu Cys Glu Arg Asn Asp Lys Val Phe Phe 1265 1270 1275	4021
gcc tca gtc cgc tct ggg ggc agc agc caa gtt tac ttc atg act ctg Ala Ser Val Arg Ser Gly Gly Ser Ser Gln Val Tyr Phe Met Thr Leu 1280 1285 1290 1295	4069
aac cgt aac tgc atc atg aac tgg tga cgggg ccctgggctg gggctgtccc Asn Arg Asn Cys Ile Met Asn Trp *	4121
1300	

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 Met Asn Gly Ile Arg Leu Gly
 1 5
 acc tat ggg ctg gct gag gct ggg ggc tac ctg cac aca gcc gaa ggc 161
 Thr Tyr Gly Leu Ala Glu Ala Gly Gly Tyr Leu His Thr Ala Glu Gly
 10 15 20
 acc cac agt cct gcc cgc agc gca gca gct ggg gcc atg gct ggg gtc 209
 Thr His Ser Pro Ala Arg Ser Ala Ala Ala Gly Ala Met Ala Gly Val
 25 30 35
 atg gga gcc tac ttg ggg agc ccc atc tac atg gtg aag aca cac ctg 257
 Met Gly Ala Tyr Leu Gly Ser Pro Ile Tyr Met Val Lys Thr His Leu
 40 45 50 55
 cag gca cag gca gcc tca gaa att gct gta ggg cac cag tat aag cat 305
 Gln Ala Gln Ala Ala Ser Glu Ile Ala Val Gly His Gln Tyr Lys His
 60 65 70
 cag ggc atg ttt cag gcg cta acc gag att ggc cag aaa cat ggt ctg 353
 Gln Gly Met Phe Gln Ala Leu Thr Glu Ile Gly Gln Lys His Gly Leu
 75 80 85

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Val Gly Leu Trp Arg Gly Ala Leu Gly Gly Leu Pro Arg Val Ile Val
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ggt tcc tcc acc cag ctg tgc acc ttc tca tcc acc aag gac ctc ctg      449
Gly Ser Ser Thr Gln Leu Cys Thr Phe Ser Ser Thr Lys Asp Leu Leu
      105                      110                      115

agc cag tgg gag atc ttt cct ccc cag agc tgg aag ttg gcg ctg gtg      497
Ser Gln Trp Glu Ile Phe Pro Pro Gln Ser Trp Lys Leu Ala Leu Val
      120                      125                      130                      135

gct gcc atg atg agt ggc att gca gtt gtc ttg gcc atg gca ccc ttt      545
Ala Ala Met Met Ser Gly Ile Ala Val Val Leu Ala Met Ala Pro Phe
      140                      145                      150

gat gtg gcc tgc aca agg ctc tac aac cag ccc aca gat gca cag ggc      593
Asp Val Ala Cys Thr Arg Leu Tyr Asn Gln Pro Thr Asp Ala Gln Gly
      155                      160                      165

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Lys Gly Leu Met Tyr Arg Gly Ile Leu Asp Ala Leu Leu Gln Thr Ala
      170                      175                      180

cgg acc gag ggc att ttt ggc atg tac aag ggt ata ggt gcc tcc tac      689
Arg Thr Glu Gly Ile Phe Gly Met Tyr Lys Gly Ile Gly Ala Ser Tyr
      185                      190                      195

ttc cgc ctc ggc ccc cac acc atc ctc tcc ctc ttc ttc tgg gac cag      737
Phe Arg Leu Gly Pro His Thr Ile Leu Ser Leu Phe Phe Trp Asp Gln
      200                      205                      210                      215

ctg cgc tcc ctc tac tca aca gac act aaa taa cagccgct ttcccgctct      788
Leu Arg Ser Leu Tyr Tyr Thr Asp Thr Lys *
      220                      225

ccaccaaatg agcactcctt ggccacttgt gcctccacca ctatgtcctg gtgactactg      848

attaggtgac ctttcatcca tccatggggg acagccaacc ccaactcccca tctgtttctca      908

gggttgaatc actacaagag atgagtttcc cttctttcct tgggtgttgc tttaaacctt      968

ccctacccat tccctgggta actcacaccc ctctctcagg gctgaacgag tcatcccaaa      1028

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 gggggaag atg ctc gcc tac tgc gtg cag gat gcc acc gtg gtg gac gtg 350
 Met Leu Ala Tyr Cys Val Gln Asp Ala Thr Val Val Asp Val
 1 5 10
 gag aag cgg agg aac ccc tcc aag cac tac gta tac ata atc aat gtg 398
 Glu Lys Arg Arg Asn Pro Ser Lys His Tyr Val Tyr Ile Ile Asn Val
 15 20 25 30
 acc tgg tct gac tcc acc tcc cag act atc tac cgg agg tac agc aag 446
 Thr Trp Ser Asp Ser Thr Ser Gln Thr Ile Tyr Arg Arg Tyr Ser Lys
 35 40 45
 ttc ttt gac ctg cag atg cag ctt ttg gat aag ttt ccc att gaa ggc 494
 Phe Phe Asp Leu Gln Met Gln Leu Leu Asp Lys Phe Pro Ile Glu Gly
 50 55 60
 ggc cag aag gac ccc aag caa agg atc atc ccc ttc ctc cca ggc aag 542
 Gly Gln Lys Asp Pro Lys Gln Arg Ile Ile Pro Phe Leu Pro Gly Lys
 65 70 75
 atc ctc ttc cgc aga agc cac atc cgg gac gta gct gtg aag aga ctg 590
 Ile Leu Phe Arg Arg Ser His Ile Arg Asp Val Ala Val Lys Arg Leu
 80 85 90
 aag ccc atc gat gaa tac tgc cgg gca ctt gtc cgg ctg ccc ccc cac 638
 Lys Pro Ile Asp Glu Tyr Cys Arg Ala Leu Val Arg Leu Pro Pro His
 95 100 105 110
 atc tca cag tgt gac gaa gtc ttc cgg ttc ttc gag gct cga ccc gag 686
 Ile Ser Gln Cys Asp Glu Val Phe Arg Phe Phe Glu Ala Arg Pro Glu
 115 120 125
 gat gtc aac cct cca aaa gag caa ggc ccc tca ccc cca gat gca gtc 734
 Asp Val Asn Pro Pro Lys Glu Gln Gly Pro Ser Pro Pro Asp Ala Val
 130 135 140
 ctc cca tat ggt gtc aac aag ggc aaa cag gag cta aag gca ggc cca 782
 Leu Pro Tyr Gly Val Asn Lys Gly Lys Gln Glu Leu Lys Ala Gly Pro
 145 150 155
 aac tgg ccc ggc agg act cac cac gtg gtc aac tgc gtg acc cag aaa 830
 Asn Trp Pro Gly Arg Thr His His Val Val Asn Cys Val Thr Gln Lys
 160 165 170
 tgc ctc ttt gtg ttc cat ttt aaa ttc tca tcc agt gga aat aag gaa 878
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 175 180 185 190
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Pro Lys Pro Ala Arg Ala Ala Pro Lys Ile Ala Asn Gly Lys Ala Ala	
200 205 210 215	
agt agc agc agt agc agc agc agc agt agc agt gat gac tca gag	785
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Asp Ser Glu	
220 225 230	
gag gag aag gca gca gcc acc ccc aag aag act gta cct aaa aag caa	833
Glu Glu Lys Ala Ala Ala Thr Pro Lys Lys Thr Val Pro Lys Lys Gln	
235 240 245	
gtt gtg gcc aag gcc cca gtg aaa gca gct acc acc cct acc cgg aag	881
Val Val Ala Lys Ala Pro Val Lys Ala Ala Thr Thr Pro Thr Arg Lys	
250 255 260	
agt tct agc agt gag gat tcc tcc agt gac gag gaa gag gag caa aaa	929
Ser Ser Ser Ser Glu Asp Ser Ser Ser Asp Glu Glu Glu Glu Gln Lys	
265 270 275	
aaa ccc atg aaa aat aaa cca ggt ccc tac agt tca gtc ccc ccg cct	977
Lys Pro Met Lys Asn Lys Pro Gly Pro Tyr Ser Ser Val Pro Pro Pro	
280 285 290 295	
tct gct ccc cca cca aag aag tct ctg gga acc cag cct ccc aag aag	1025
Ser Ala Pro Pro Pro Lys Lys Ser Leu Gly Thr Gln Pro Pro Lys Lys	
300 305 310	
gct gtg gag aag cag cag cct gtg gaa agc agt gaa gac agc agt gat	1073
Ala Val Glu Lys Gln Gln Pro Val Glu Ser Ser Glu Asp Ser Ser Asp	
315 320 325	
gag tct gat tca agt tct gaa gaa gag aag aaa ccc cca act aag gca	1121
Glu Ser Asp Ser Ser Ser Glu Glu Glu Lys Lys Pro Pro Thr Lys Ala	
330 335 340	
gta gtc tct aaa gca acc act aaa cca cct cca gca aag aaa gca gca	1169
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Glu Ser Ser Ser Asp Ser Ser Asp Ser Asp Ser Ser Glu Asp Asp Glu	
360 365 370 375	
gct cct tct aag cca gct ggt acc acc aag aat tct tca aat aag cca	1265
Ala Pro Ser Lys Pro Ala Gly Thr Thr Lys Asn Ser Ser Asn Lys Pro	
380 385 390	
gct gtc acc acc aag tca cct gca gtg aag cca gct gca gcc ccc aag	1313
Ala Val Thr Thr Lys Ser Pro Ala Val Lys Pro Ala Ala Ala Pro Lys	
395 400 405	
caa cct gtg ggc ggt ggc cag aag ctt ctg acg aga aag gct gac agc	1361
Gln Pro Val Gly Gly Gly Gln Lys Leu Leu Thr Arg Lys Ala Asp Ser	
410 415 420	
agc tcc agc gag gaa gag agc agc tcc agt gag gag gag aag aca aag	1409
Ser Ser Ser Glu Glu Glu Ser Ser Ser Ser Glu Glu Glu Lys Thr Lys	
425 430 435	

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Lys Met Val Ala Thr Thr Lys Pro Lys Ala Thr Ala Lys Ala Ala Leu	
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Ser Leu Pro Ala Lys Gln Ala Pro Gln Gly Ser Arg Asp Ser Ser Ser	
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Asp Ser Asp Ser Ser Ser Ser Glu Glu Glu Glu Glu Lys Thr Ser Lys	
475 480 485	
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Ser Ala Val Lys Lys Lys Pro Gln Lys Val Ala Gly Gly Ala Ala Pro	
490 495 500	
tcc aag cca gcc tct gca aag aaa gga aag gct gag agc agc aac agt	1649
Ser Lys Pro Ala Ser Ala Lys Lys Gly Lys Ala Glu Ser Ser Asn Ser	
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Ser Ser Ser Asp Asp Ser Ser Glu Glu Glu Glu Glu Lys Leu Lys Gly	
520 525 530 535	
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Leu Thr Ala Gln Asn Gly Lys Ala Ala Lys Asn Ser Glu Glu Glu Glu	
555 560 565	
gaa gaa aag aaa aag gcg gca gtg gta gtt tcc aaa tca ggt tca tta	1841
Glu Glu Lys Lys Lys Ala Ala Val Val Val Ser Lys Ser Gly Ser Leu	
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aag aag cgg aag cag aat gag gct gcc aag gag gca gag act cct cag	1889
Lys Lys Arg Lys Gln Asn Glu Ala Ala Lys Glu Ala Glu Thr Pro Gln	
585 590 595	
gcc aag aag ata aag ctt cag acc cct aac aca ttt cca aaa agg aag	1937
Ala Lys Lys Ile Lys Leu Gln Thr Pro Asn Thr Phe Pro Lys Arg Lys	
600 605 610 615	
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Lys Gly Glu Lys Arg Ala Ser Ser Pro Phe Arg Arg Val Arg Glu Glu	
620 625 630	
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Glu Ile Glu Val Asp Ser Arg Val Ala Asp Asn Ser Phe Asp Ala Lys	
635 640 645	
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Phe Thr Lys Gly Lys Ser Phe Arg His Glu Lys Thr Lys Lys Lys Arg	
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Gly Ser Tyr Arg Gly Gly Ser Ile Ser Val Gln Val Asn Ser Ile Lys	
680 685 690 695	

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 Phe Asp Ser Glu *
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 Met Thr Ser Arg Lys Leu Ala Ser Ala Thr Ala Asn Asp Ser Ala
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 Asn Pro Leu His Leu Ser Ala Ala Pro Glu Asn Ser Arg Gly Pro Ala
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 Leu Ser Ala Glu His Thr Ser Ser Leu Val Pro Ser Leu His Ile Thr
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 Thr Leu Gly Gln Glu Gln Ala Ile Leu Ser Gly Ala Val Pro Ala Ser
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 Pro Ser Thr Gly Thr Ala Asp Phe Pro Ser Ile Leu Thr Phe Leu Gln
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 Pro Thr Glu Asn His Ala Ser Pro Ser Pro Val Pro Glu Met Pro Thr
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 Leu Leu Ser Ser Lys Val Pro Asn Leu Leu Ser Thr Ser Trp Thr Phe
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 Pro Arg Trp Lys Lys Asp Ser Val Thr Ala Ile Leu Gly Lys Asn Glu
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 Ser Gly Pro Pro Leu Pro Ser Ile Leu Ser Ile Gln Ala Thr Gln Thr
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His Ser Val Thr Ala Glu Gly Phe Ser Ile Gln Asp Leu Val Leu Gly	
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Tyr His Ser Ala Ala Glu Ser Ser Ile Ser Thr Ser Val Phe Pro Arg	
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Lys Asn Val Thr Asn Lys Ala Ala Ser Gly Pro Lys Arg Thr Pro Gly	
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Leu Lys Phe Ser Ile Ala Lys Gly Leu Thr Gln Ala Leu Arg Lys Ala	
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Phe His Gln Asn Asp Val Ser Ala His Val Asp Ile Leu Glu Tyr Ser	
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His Asn Val Thr Val Gly Tyr Tyr Ala Thr Lys Gly Lys Leu Val Tyr	
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Leu Pro Ala Val Val Ile Glu Met Leu Gly Val Tyr Gly Val Ser Asn	
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Lys Thr Val Leu Gln Phe Val Ser Gln Ala Asp Asn Ile Gln Ser Cys	
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Arg Leu Ala Gln Leu Phe Met Met Ser Gln Gln Gln Gly Arg Arg Phe	
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Lys Arg Ala Thr Thr Leu Gly Ser Tyr Thr Val Gln Met Val Lys Met	
980 985 990	
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Gln Arg Val	Pro Gly Pro	Lys Asp Pro	Ala Glu Leu	Thr Tyr Tyr	Thr	
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Leu Tyr Asn	Gly Lys Pro	Leu Leu Gly	Thr Val Ala	Ala Lys Ile	Leu	
	1010	1015		1020		
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Ser Thr Ile	Asp Ser Gln	Arg Met Ala	Leu Thr Leu	His His Val	Val	
	1025	1030		1035		
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Leu Leu Gln	Ala Asp Pro	Val Val Lys	Asn Pro Pro	Asn Asn Leu	Trp	
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Ile Ile Ala	Ala Val Leu	Ala Pro Ile	Ala Val Val	Thr Val Ile	Ile	
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Ile Ile Ile	Thr Ala Val	Leu Cys Arg	Lys Asn Lys	Asn Asp Phe	Lys	
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Pro Asp Thr	Met Ile Asn	Leu Pro Gln	Arg Ala Lys	Pro Val Gln	Gly	
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Phe Asp Tyr	Ala Lys Gln	His Leu Gly	Gln Gln Gly	Ala Asp Glu	Glu	
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Val Ile Pro	Val Thr Gln	Glu Thr Val	Val Val Leu	Pro Leu Pro	Ile Arg	
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Asp Ala Pro	Gln Glu Arg	Asp Val Ala	Gln Asp Gly	Ser Thr Ile	Lys	
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Thr Ala Lys	Ser Thr Glu	Thr Arg Lys	Ser Arg Ser	Pro Ser Glu	Asn	
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Gly Ser Val	Ile Ser Asn	Glu Ser Gly	Lys Pro Ser	Ser Ser Gly	Arg Arg	
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Ser Pro Gln	Asn Val Met	Ala Gln Gln	Lys Val Thr	Lys Glu Glu	Ala	
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Arg Lys Arg	Asn Val Pro	Ala Ser Asp	Glu Glu Glu	Gly Ala Val	Leu	
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Phe Asp Asn	Ser Ser Lys	Val Ala Ala	Glu Pro Phe	Asp Thr Ser	Ser	
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Gly Ser Val	Gln Leu Ile	Ala Ile Lys	Pro Thr Ala	Leu Pro Met	Val	
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Asn Lys Leu Arg Leu Lys Ala Lys Arg Lys Gly Tyr Tyr Asp Phe Pro	
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Lys Ala Pro Lys Glu Met Glu His Val Leu Asp Pro Asp Ser Glu Leu	
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Cys Ala Pro Phe Thr Glu Ser Lys Asn Arg Gln Gln Met Lys Asn Ser	
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Pro Leu Gly Lys Ile Met Asp Tyr Ile Gln Glu Asp Val Asp Ala Met	
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tat att tac agg aaa ccc tca cat acg tct cgt aaa aaa gca aca ggc Tyr Ile Tyr Arg Lys Pro Ser His Thr Ser Arg Lys Lys Ala Thr Gly 1680 1685 1690	5149
ttt gct gct gtt cat cag cta ttt aca gaa cgc tgg cca aca aca cca Phe Ala Ala Val His Gln Leu Phe Thr Glu Arg Trp Pro Thr Thr Pro 1695 1700 1705 1710	5197
gtc aat aga agt ctt agt ggc aca gct aca gag aga aat att gac ttt Val Asn Arg Ser Leu Ser Gly Thr Ala Thr Glu Arg Asn Ile Asp Phe 1715 1720 1725	5245
gaa ctt gat ata cgg gtt gaa att gat agt gga aaa tgt gta ctc cac Glu Leu Asp Ile Arg Val Glu Ile Asp Ser Gly Lys Cys Val Leu His 1730 1735 1740	5293
cca acc acc ctt cta caa gaa cat gat gat ata agt ttg aga agg agt Pro Thr Thr Leu Leu Gln Glu His Asp Asp Ile Ser Leu Arg Arg Ser 1745 1750 1755	5341
tat gat cga agt tcc agg agc tta gat caa gat tca cct tca aaa aag Tyr Asp Arg Ser Ser Arg Ser Leu Asp Gln Asp Ser Pro Ser Lys Lys 1760 1765 1770	5389
aag aag ttt caa act aat tat gct tct acc acc cat tta atg acc ggc Lys Lys Phe Gln Thr Asn Tyr Ala Ser Thr Thr His Leu Met Thr Gly 1775 1780 1785 1790	5437
aag aaa gtg cca tca tct cta cag aca aag cct agt gac tta gaa aca Lys Lys Val Pro Ser Ser Leu Gln Thr Lys Pro Ser Asp Leu Glu Thr 1795 1800 1805	5485
aca gta ttt tac att ccc gga gtt gat gta aag ttg cat tac aat tcc Thr Val Phe Tyr Ile Pro Gly Val Asp Val Lys Leu His Tyr Asn Ser 1810 1815 1820	5533

aag acg cta aag act gaa tca cct aat gcc tcc agg gga tct tcc ttg Lys Thr Leu Lys Thr Glu Ser Pro Asn Ala Ser Arg Gly Ser Ser Leu 1825 1830 1835	5581
cca aga aca ctg tcc aaa gag tcc aag ctg tat ggt atg aaa gat agt Pro Arg Thr Leu Ser Lys Glu Ser Lys Leu Tyr Gly Met Lys Asp Ser 1840 1845 1850	5629
gca aca tct cct cct tct cct cct tta cct tcc act gtc cag agc aag Ala Thr Ser Pro Pro Ser Pro Pro Leu Pro Ser Thr Val Gln Ser Lys 1855 1860 1865 1870	5677
act aac acc tta ctt cct ccc cag ccc cca cct att cct gca gcc aaa Thr Asn Thr Leu Leu Pro Pro Gln Pro Pro Pro Ile Pro Ala Ala Lys 1875 1880 1885	5725
gga aaa gga agt gga gga gta aaa aca gcc aag tta tat gcc tgg gta Gly Lys Gly Ser Gly Gly Val Lys Thr Ala Lys Leu Tyr Ala Trp Val 1890 1895 1900	5773
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tta tcc cct gga ggt aat gct act cag agt gga aca aag act tct gct Leu Ser Pro Gly Asn Ala Thr Gln Ser Gly Thr Lys Thr Ser Ala 2035 2040 2045	6205
agc aaa act gga ata cca ggt tca tcg gga tta ggc agc cct ctt ggc Ser Lys Thr Gly Ile Pro Gly Ser Ser Gly Leu Gly Ser Pro Leu Gly 2050 2055 2060	6253
cga agt cga cat agt agt agt cag tca gac ctg acc agt tcc agc agt Arg Ser Arg His Ser Ser Ser Gln Ser Asp Leu Thr Ser Ser Ser Ser 2065 2070 2075	6301

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agc caa cac ctt tcc cct gaa tca tca aga aaa gct tac tgc aag acc Ser Gln His Leu Ser Pro Glu Ser Ser Arg Lys Ala Tyr Cys Lys Thr 2240 2245 2250	6829
tgg gag cag cca agt cag tca gcc tcc ttc acc cac atg cct cag tca Trp Glu Gln Pro Ser Gln Ser Ala Ser Phe Thr His Met Pro Gln Ser 2255 2260 2265 2270	6877
cct aat gtg ttc aat gag cat atg aca aac agc acc atg tca cca ggg Pro Asn Val Phe Asn Glu His Met Thr Asn Ser Thr Met Ser Pro Gly 2275 2280 2285	6925
aca gta gga cag agc cta aaa tcc cca gct tcc ata aga tca agg agt Thr Val Gly Gln Ser Leu Lys Ser Pro Ala Ser Ile Arg Ser Arg Ser 2290 2295 2300	6973
gta tct gat tct tca gtt cct cga aga gat tca ctt tca aaa aca tca Val Ser Asp Ser Ser Val Pro Arg Arg Asp Ser Leu Ser Lys Thr Ser 2305 2310 2315	7021
act cct ttt aac aaa tca aac aaa gca gca agc caa caa ggg acc cca Thr Pro Phe Asn Lys Ser Asn Lys Ala Ala Ser Gln Gln Gly Thr Pro 2320 2325 2330	7069

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caa atg aat atg agt aat gta atg gga aat aca act tgg aca act agt Gln Met Asn Met Ser Asn Val Met Gly Asn Thr Thr Trp Thr Thr Ser 2355 2360 2365	7165
ggt ttg aag agc cag ggc cgt ctg tca gta gga agt aat cgt gat cga Gly Leu Lys Ser Gln Gly Arg Leu Ser Val Gly Ser Asn Arg Asp Arg 2370 2375 2380	7213
gag atc agc atg tct gtt ggt ctg gga aga tca caa tta gat tct aaa Glu Ile Ser Met Ser Val Gly Leu Gly Arg Ser Gln Leu Asp Ser Lys 2385 2390 2395	7261
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tgg aaa gta aac ttg tat aat aca ttg gat tca agc ata act gat aaa Trp Lys Val Asn Leu Tyr Asn Thr Leu Asp Ser Ser Ile Thr Asp Lys 2465 2470 2475	7501
agt gag att ttc gtc cat gga gat ttg aag tgg gat att ttc caa gta Ser Glu Ile Phe Val His Gly Asp Leu Lys Trp Asp Ile Phe Gln Val 2480 2485 2490	7549
atg ata tca agg tca acc aca cca gat ctg ata aaa ata gga atg aag Met Ile Ser Arg Ser Thr Thr Pro Asp Leu Ile Lys Ile Gly Met Lys 2495 2500 2505 2510	7597
ctc cag gaa ttt ttc aca caa caa ttt gat acc agc aaa cga gct ctg Leu Gln Glu Phe Phe Thr Gln Gln Phe Asp Thr Ser Lys Arg Ala Leu 2515 2520 2525	7645
tct acc tgg gga cca gtt cct tac ctt ccg cca aag aca atg act agc Ser Thr Trp Gly Pro Val Pro Tyr Leu Pro Pro Lys Thr Met Thr Ser 2530 2535 2540	7693
aac cta gaa aaa agt tca caa gaa caa tta ctt gat gca gca cat cat Asn Leu Glu Lys Ser Ser Gln Glu Gln Leu Leu Asp Ala Ala His His 2545 2550 2555	7741
cga cac tgg cct gga gta ttg aag gtg gta tca gga tgc cac ata tcc Arg His Trp Pro Gly Val Leu Lys Val Val Ser Gly Cys His Ile Ser 2560 2565 2570	7789
tta ttt cag att cca tta cca gaa gat gga atg caa ttt gga gga tca Leu Phe Gln Ile Pro Leu Pro Glu Asp Gly Met Gln Phe Gly Gly Ser 2575 2580 2585 2590	7837

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gta gca agt gtg aaa gaa tgg ttc aat tat gtt aca gct aca agg aat Val Ala Ser Val Lys Glu Trp Phe Asn Tyr Val Thr Ala Thr Arg Asn 2690 2695 2700	8173
gaa gag cta aat ctg ctt cgt aat gtt gat gct aac aac act gag aat Glu Glu Leu Asn Leu Leu Arg Asn Val Asp Ala Asn Asn Thr Glu Asn 2705 2710 2715	8221
agc act act gtg aag aat tct agt ttg ttg agt gga ttc aga gga ggt Ser Thr Thr Val Lys Asn Ser Ser Leu Leu Ser Gly Phe Arg Gly Gly 2720 2725 2730	8269
tct agc tac aac cat gaa aca gag act atc ttt gca tta cca agg atg Ser Ser Tyr Asn His Glu Thr Glu Thr Ile Phe Ala Leu Pro Arg Met 2735 2740 2745 2750	8317
cag ctt gac ttt aaa tcc att cat gtt caa gaa cca cag gag cct tca Gln Leu Asp Phe Lys Ser Ile His Val Gln Glu Pro Gln Glu Pro Ser 2755 2760 2765	8365
tta cag gat gcc agc ctg aag cca aaa gta gaa tgt agt gtg gtg aca Leu Gln Asp Ala Ser Leu Lys Pro Lys Val Glu Cys Ser Val Val Thr 2770 2775 2780	8413
gag ttc act gac cac att tgt gtg act atg gat gct gag ctc atc atg Glu Phe Thr Asp His Ile Cys Val Thr Met Asp Ala Glu Leu Ile Met 2785 2790 2795	8461
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atc ttt cca cct cgg att tta tct act cga cca gga caa aaa agt cca Ile Phe Pro Pro Arg Ile Leu Ser Thr Arg Pro Gly Gln Lys Ser Pro 2815 2820 2825 2830	8557
att att ata cat gac gac aat tcc tct gat aaa gat aga gaa gat agc Ile Ile Ile His Asp Asp Asn Ser Ser Asp Lys Asp Arg Glu Asp Ser 2835 2840 2845	8605

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atc act tat act act gtg gac tgg aga gat ttt atg tgc aat aca tgg      8653
Ile Thr Tyr Thr Thr Val Asp Trp Arg Asp Phe Met Cys Asn Thr Trp
      2850                      2855                      2860

cat cta gaa cct act ctt aga tta att tct tgg act gga aga aag att      8701
His Leu Glu Pro Thr Leu Arg Leu Ile Ser Trp Thr Gly Arg Lys Ile
      2865                      2870                      2875

gat cca gta ggt gtt gat tat att ctt caa aaa ttg ggc ttt cat cat      8749
Asp Pro Val Gly Val Asp Tyr Ile Leu Gln Lys Leu Gly Phe His His
      2880                      2885                      2890

gct agg act act att cct aaa tgg ctt caa aga gga gtc atg gat cca      8797
Ala Arg Thr Thr Ile Pro Lys Trp Leu Gln Arg Gly Val Met Asp Pro
2895                      2900                      2905                      2910

ctg gac aag gtt ctg tca gtt ctt atc aaa aag ctc ggt act gca cta      8845
Leu Asp Lys Val Leu Ser Val Leu Ile Lys Lys Leu Gly Thr Ala Leu
      2915                      2920                      2925

cag gat gaa aag gaa aag aaa ggc aaa gac aaa gaa gaa cac taa aaa      8893
Gln Asp Glu Lys Glu Lys Lys Gly Lys Asp Lys Glu Glu His *
      2930                      2935                      2940

agtaatttga tctgtgaaca aattatgatt gtgtctgttt tattacactg gagtggtttt      8953

ttagtataat aatttgaaat ataacttta aataattcta aatttgtggc tataattaaa      9013

agtttgtaag ttaacctgtt ctagtccat cattctgtgt acagtgaagt attgcatgat      9073

aatgtaaatt ttgtgaaaaa ctagattaaa atatataact gcttgttatg gtttataatt      9133

atataatgtg caatacaatt cctgcatctt taaaatgtct gcagaataac tgtgaatttt      9193

tttgttattg gattggccgt aactttttaga aaaaaatctt gttgatgata atgtgatttt      9253

ggggagggtca ttaattgctt tttctttttt aaatgtagac ttatataaat acctgtttgt      9313

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taaagtcaca gtaatggttt aaaaaaaaaa aaaaaaaaaa                        9412

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<210> 840
 <211> 621
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (40)..(621)

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              Met Glu Gly Cys Val
              1                      5

tct aac cta atg gtc tgc aac ctg gcc tac agc ggg aag ctg gaa gag      102
Ser Asn Leu Met Val Cys Asn Leu Ala Tyr Ser Gly Lys Leu Glu Glu
      10                      15                      20

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ttg aag gag agt att ctg gcc gat aaa tcc ctg gct act aga act gac      150
Leu Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu Ala Thr Arg Thr Asp
                25                      30                      35

cag gca ggt tgg tct cct ctt cat att gcg gct tct gct ggc cgg gat      198
Gln Ala Gly Trp Ser Pro Leu His Ile Ala Ala Ser Ala Gly Arg Asp
                40                      45                      50

gag att gta aaa gcc ctt ctg gga aaa ggt gct caa gtg aat gct gtc      246
Glu Ile Val Lys Ala Leu Leu Gly Lys Gly Ala Gln Val Asn Ala Val
                55                      60                      65

aat caa aat ggc tgt act ccc tta cat tat gca gct tcg aaa aac agg      294
Asn Gln Asn Gly Cys Thr Pro Leu His Tyr Ala Ala Ser Lys Asn Arg
                70                      75                      80                      85

cat gag atc gct gtc atg tta ctg gaa ggc ggg gct aat cca gat gct      342
His Glu Ile Ala Val Met Leu Leu Glu Gly Gly Ala Asn Pro Asp Ala
                90                      95                      100

aag gac cat tat gag gct aca gca atg cac cgg gca gca gcc aag ggt      390
Lys Asp His Tyr Glu Ala Thr Ala Met His Arg Ala Ala Ala Lys Gly
                105                      110                      115

aac ttg aag atg att cat atc ctt ctg tac tac aaa gca tcc aca aac      438
Asn Leu Lys Met Ile His Ile Leu Leu Tyr Tyr Lys Ala Ser Thr Asn
                120                      125                      130

atc caa gac act gag ggt aac act cct cta cac tta gcc tgt gat gag      486
Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu His Leu Ala Cys Asp Glu
                135                      140                      145

gag aga gtg gaa gaa gca aaa ctg ctg gtg tcc caa gga gca agt att      534
Glu Arg Val Glu Glu Ala Lys Leu Leu Val Ser Gln Gly Ala Ser Ile
                150                      155                      160                      165

tac att gag aat aaa gaa gaa aag aca ccc ctg caa gtg gcc aaa ggt      582
Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro Leu Gln Val Ala Lys Gly
                170                      175                      180

ggc ctg ggt tta ata ctc aag aga atg gtg gaa ggt taa      621
Gly Leu Gly Leu Ile Leu Lys Arg Met Val Glu Gly *
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 <211> 1128
 <212> DNA
 <213> Homo sapiens

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gacaactttg tactcccacc accccaatc aagaagctgg tcccacggaa agtggtatct      180

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cggggaatcag	ctcctattaa	ggaacaaaaa	aagttgatgc	ccaaaacatc	cctccccaca		240
gtcaagaagc	tagcaacagc	caccactggg	cccagcaaag	ccaagacatc	tcggacaccc		300
agcaggggaca	gtcagaagct	cacctcccga	gactcaggag	gaagagcaca	gcagcccggt		360
aaaggccccc	tctgtgaaga	gaaccccc	atg ccg gac aag act gcc acc cca				412
			Met Pro Asp Lys Thr Ala Thr Pro				
			1	5			
gag agg ccc cca gct cca gag aac gcc ccc agc tcc aag aag atc ccg							460
Glu Arg Pro Pro Ala Pro Glu Asn Ala Pro Ser Ser Lys Lys Ile Pro							
10	15	20					
gct cct gac aaa gtc ccc tcc cca gag aag acc ctc act cta ggg gac							508
Ala Pro Asp Lys Val Pro Ser Pro Glu Lys Thr Leu Thr Leu Gly Asp							
25	30	35	40				
aag gcc tct gtc cca ggg aac tcc acc tcg ggg aag atc cca gct cct							556
Lys Ala Ser Val Pro Gly Asn Ser Thr Ser Gly Lys Ile Pro Ala Pro							
45	50	55					
gac aaa gtc ccc acc cca gag aag atg gtg act ccg gag gac aag gct							604
Asp Lys Val Pro Thr Pro Glu Lys Met Val Thr Pro Glu Asp Lys Ala							
60	65	70					
tct atc cca gag aac tcc atc atc cca gag gag acc ctg act gtg gac							652
Ser Ile Pro Glu Asn Ser Ile Ile Pro Glu Glu Thr Leu Thr Val Asp							
75	80	85					
aaa ccc tcc act cca gag agg gtc ttt tca gtg gaa gag tcc cct gcc							700
Lys Pro Ser Thr Pro Glu Arg Val Phe Ser Val Glu Glu Ser Pro Ala							
90	95	100					
cta gaa gcc cca cct atg gat aaa gtc cct aat cca aag atg gcc cct							748
Leu Glu Ala Pro Pro Met Asp Lys Val Pro Asn Pro Lys Met Ala Pro							
105	110	115	120				
ctg ggg gat gag gcc ccc act cta gaa aag gtc ttg acc cca gag ctt							796
Leu Gly Asp Glu Ala Pro Thr Leu Glu Lys Val Leu Thr Pro Glu Leu							
125	130	135					
tct gaa gaa gag gtg tcc acc aga gat gac att caa ttc cat cac ttc							844
Ser Glu Glu Glu Val Ser Thr Arg Asp Asp Ile Gln Phe His His Phe							
140	145	150					
tct tcg gag gaa gcc ctg cag aag gtc aag tac ttt gta gcc aaa gag							892
Ser Ser Glu Glu Ala Leu Gln Lys Val Lys Tyr Phe Val Ala Lys Glu							
155	160	165					
gat cca tca tcc cag gag gag gcc cac acg cca gag gca ccc cca ccc							940
Asp Pro Ser Ser Gln Glu Glu Ala His Thr Pro Glu Ala Pro Pro Pro							
170	175	180					
cag gcc act aac agc aac aac aga gag gct gga gct ctg cct gcg tgc							988
Gln Ala Thr Asn Ser Asn Asn Arg Glu Ala Gly Ala Leu Pro Ala Cys							
185	190	195	200				
ggg cca agg gct aaa cct tgg aca ggt tct ttc act tac tcc gcc tga							1036
Gly Pro Arg Ala Lys Pro Trp Thr Gly Ser Phe Thr Tyr Ser Ala *							
205	210	215					
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gagattgagg tgaatttggc taacctgtaa aa

1128

<210> 842
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 Met Gly Ala Tyr Lys Tyr Ile Gln
 1 5
 gag cta tgg aga aag aag cag tct gat gtc atg cgc ttt ctt ctg agg 161
 Glu Leu Trp Arg Lys Lys Gln Ser Asp Val Met Arg Phe Leu Leu Arg
 10 15 20
 gtc cgc tgc tgg cag tac cgc cag ctc tct gct ctc cac agg gct ccc 209
 Val Arg Cys Trp Gln Tyr Arg Gln Leu Ser Ala Leu His Arg Ala Pro
 25 30 35 40
 cgc ccc acc cgg cct gat aaa gcg cgc cga ctg ggc tac aag gcc aag 257
 Arg Pro Thr Arg Pro Asp Lys Ala Arg Leu Gly Tyr Lys Ala Lys
 45 50 55
 caa ggt tac gtt ata tat agg att cgt gtt cgc cgt ggt ggc cga aaa 305
 Gln Gly Tyr Val Ile Tyr Arg Ile Arg Val Arg Arg Gly Gly Arg Lys
 60 65 70
 cgc cca gtt cct aag ggt gca act tac ggc aag cct gtc cat cat ggt 353
 Arg Pro Val Pro Lys Gly Ala Thr Tyr Gly Lys Pro Val His His Gly
 75 80 85
 gtt aac cag cta aag ttt gct cga agc ctt cag tcc gtt gca gag gag 401
 Val Asn Gln Leu Lys Phe Ala Arg Ser Leu Gln Ser Val Ala Glu Glu
 90 95 100
 cga gct gga cgc cac tgt ggg gct ctg aga gtc ctg aat tct tac tgg 449
 Arg Ala Gly Arg His Cys Gly Ala Leu Arg Val Leu Asn Ser Tyr Trp
 105 110 115 120
 gtt ggt gaa gat tcc aca tac aaa ttt ttt gag gtt atc ctc att gat 497
 Val Gly Glu Asp Ser Thr Tyr Lys Phe Phe Glu Val Ile Leu Ile Asp
 125 130 135
 cca ttc cat aaa gct atc aga aga aat cct gac acc cag tgg atc acc 545
 Pro Phe His Lys Ala Ile Arg Arg Asn Pro Asp Thr Gln Trp Ile Thr
 140 145 150
 aaa cca gtc cac aag cac agg gag atg cgt ggg ctg aca tct gca ggc 593
 Lys Pro Val His Lys His Arg Glu Met Arg Gly Leu Thr Ser Ala Gly

155	160	165	
cga aag agc cat ggg ctt gga aag gac cgt atg ttc cac cat gct att			641
Arg Lys Ser His Gly Leu Gly Lys Asp Arg Met Phe His His Ala Ile			
170	175	180	
ggg ggt tct tgc cgg gca gct tag agaaggcgca aaactctcca gttccctgt			695
Gly Gly Ser Cys Arg Ala *			
185	190		
taccactaat ataagtaaag tttgtaaaat tcatgcctca taatttaggg cagtcaaaaa			755
aataaataaa taagctatatt taatattttt attctccttc aagggaccag aggccacaaa			815
agtcttgtag actatgtgtc cccagtaaag gacacataga atgnccggac gcggggtcgc			875
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ctaagggtggg atg gat agc agg gtc tca ggc aca acc agt aat gga gag			169
Met Asp Ser Arg Val Ser Gly Thr Thr Ser Asn Gly Glu			
1 5 10			
aca aaa cca gtg tat cca gtc atg gaa aag aag gag gaa gat ggc acc			217
Thr Lys Pro Val Tyr Pro Val Met Glu Lys Lys Glu Glu Asp Gly Thr			
15 20 25			
ctg gag cgg ggg cac tgg aac aac aag atg gag ttt gtg ctg tca gtg			265
Leu Glu Arg Gly His Trp Asn Asn Lys Met Glu Phe Val Leu Ser Val			
30 35 40 45			
gct ggg gag atc att ggc tta ggc aac gtc tgg agg ttt ccc tat ctc			313
Ala Gly Glu Ile Ile Gly Leu Gly Asn Val Trp Arg Phe Pro Tyr Leu			
50 55 60			
tgc tac aaa aat ggg gga ggt gcc ttc ttc atc ccc tac ctc gtc ttc			361
Cys Tyr Lys Asn Gly Gly Gly Ala Phe Phe Ile Pro Tyr Leu Val Phe			
65 70 75			
ctc ttt acc tgt ggc att cct gtc ttc ctt ctg gag aca gca cta ggc			409
Leu Phe Thr Cys Gly Ile Pro Val Phe Leu Leu Glu Thr Ala Leu Gly			
80 85 90			
cag tac act agc cag gga ggc gtc aca gcc tgg agg aag atc tgc ccc			457
Gln Tyr Thr Ser Gln Gly Gly Val Thr Ala Trp Arg Lys Ile Cys Pro			
95 100 105			
atc ttt gag ggc att ggc tat gcc tcc cag atg atc gtc atc ctc ctc			505

Ile Phe Glu Gly Ile Gly Tyr Ala Ser Gln Met Ile Val Ile Leu Leu	
110 115 120 125	
aac gtc tac tac atc att gtg ttg gcc tgg gcc ctg ttc tac ctc ttc	553
Asn Val Tyr Tyr Ile Ile Val Leu Ala Trp Ala Leu Phe Tyr Leu Phe	
130 135 140	
agc agc ttc acc atc gac ctg ccc tgg ggc ggc tgc tac cat gag tgg	601
Ser Ser Phe Thr Ile Asp Leu Pro Trp Gly Gly Cys Tyr His Glu Trp	
145 150 155	
aac aca gaa cac tgt atg gag ttc cag aag acc aac ggc tcc ctg aat	649
Asn Thr Glu His Cys Met Glu Phe Gln Lys Thr Asn Gly Ser Leu Asn	
160 165 170	
ggt acc tct gag aat gcc acc tct cct gtc atc gag ttc tgg gag cgg	697
Gly Thr Ser Glu Asn Ala Thr Ser Pro Val Ile Glu Phe Trp Glu Arg	
175 180 185	
cgg gtc ttg aag atc tct gat ggg atc cag cac ctg ggg gcc ctg cgc	745
Arg Val Leu Lys Ile Ser Asp Gly Ile Gln His Leu Gly Ala Leu Arg	
190 195 200 205	
tgg gag ctg gct ctg tgc ctc ctg ctg gcc tgg gtc atc tgc tac ttc	793
Trp Glu Leu Ala Leu Cys Leu Leu Leu Ala Trp Val Ile Cys Tyr Phe	
210 215 220	
tgc atc tgg aag ggg gtg aag tcc aca ggc aag gtg gtg tac ttc acg	841
Cys Ile Trp Lys Gly Val Lys Ser Thr Gly Lys Val Val Tyr Phe Thr	
225 230 235	
gcc aca ttt cct tac ctc atg ctg gtg gtc ctg tta att cga ggg gtg	889
Ala Thr Phe Pro Tyr Leu Met Leu Val Val Leu Leu Ile Arg Gly Val	
240 245 250	
acg ttg cct ggg gca gcc caa gga att cag ttt tac ctg tac cca aac	937
Thr Leu Pro Gly Ala Ala Gln Gly Ile Gln Phe Tyr Leu Tyr Pro Asn	
255 260 265	
ctc acg cgt ctg tgg gat ccc cag gtg tgg atg gat gca ggc acc cag	985
Leu Thr Arg Leu Trp Asp Pro Gln Val Trp Met Asp Ala Gly Thr Gln	
270 275 280 285	
ata ttc ttc tcc ttc gcc atc tgt ctt ggg tgc ctg aca gcc ctg ggc	1033
Ile Phe Phe Ser Phe Ala Ile Cys Leu Gly Cys Leu Thr Ala Leu Gly	
290 295 300	
agc tac aac aag tac cac aac aac tgc tac agc ggc acc agc ttt gtg	1081
Ser Tyr Asn Lys Tyr His Asn Asn Cys Tyr Ser Gly Thr Ser Phe Val	
305 310 315	
gcc ggc ttt gcc atc ttc tcc atc ctg ggc ttc atg tct cag gag cag	1129
Ala Gly Phe Ala Ile Phe Ser Ile Leu Gly Phe Met Ser Gln Glu Gln	
320 325 330	
ggg gtg ccc att tct gag gtg gcc gag tca ggc cct ggc ctg gct ttc	1177
Gly Val Pro Ile Ser Glu Val Ala Glu Ser Gly Pro Gly Leu Ala Phe	
335 340 345	
atc gct tac ccg cgg gct gtg gtg atg ctg ccc ttc tct cct ctc tgg	1225
Ile Ala Tyr Pro Arg Ala Val Val Met Leu Pro Phe Ser Pro Leu Trp	
350 355 360 365	
gcc tgc tgt ttc ttc ttc atg gtc gtt ctc ctg gga ctg gat agc cag	1273

Ala Cys Cys Phe Phe Phe Met Val Val Leu Leu Gly Leu Asp Ser Gln	
370 375 380	
ttt gtg tgt gta gaa agc ctg gtg aca gcg ctg gtg gac atg tac cct	1321
Phe Val Cys Val Glu Ser Leu Val Thr Ala Leu Val Asp Met Tyr Pro	
385 390 395	
cac gtg ttc cgc aag aag aac cgg agg gaa gtc ctc atc ctt gga gta	1369
His Val Phe Arg Lys Lys Asn Arg Arg Glu Val Leu Ile Leu Gly Val	
400 405 410	
tct gtc gtc tcc ttc cct gtg ggg ctg atc atg ctc aca gag ggc gga	1417
Ser Val Val Ser Phe Pro Val Gly Leu Ile Met Leu Thr Glu Gly Gly	
415 420 425	
atg tac gtg ttc cag ctc ttt gac tac tat gcg gcc agt ggc atg tgc	1465
Met Tyr Val Phe Gln Leu Phe Asp Tyr Tyr Ala Ala Ser Gly Met Cys	
430 435 440 445	
ctc ctg ttc gtg gcc atc ttc gag tcc ctc tgt gtg gct tgg gtt tac	1513
Leu Leu Phe Val Ala Ile Phe Glu Ser Leu Cys Val Ala Trp Val Tyr	
450 455 460	
gga gcc aag cgc ttc tac gac aac atc gaa gac atg att ggg tac agg	1561
Gly Ala Lys Arg Phe Tyr Asp Asn Ile Glu Asp Met Ile Gly Tyr Arg	
465 470 475	
cca tgg cct ctt atc aaa tac tgt tgg ctc ttc ctc aca cca gct gtg	1609
Pro Trp Pro Leu Ile Lys Tyr Cys Trp Leu Phe Leu Thr Pro Ala Val	
480 485 490	
tgc aca gcc acc ttt ctc ttc tcc ctg ata aag tac act ccg ctg acc	1657
Cys Thr Ala Thr Phe Leu Phe Ser Leu Ile Lys Tyr Thr Pro Leu Thr	
495 500 505	
tac aac aag aag tac acg tac ccg tgg tgg gcc gat gcc ctg ggc tgg	1705
Tyr Asn Lys Lys Tyr Thr Tyr Pro Trp Trp Gly Asp Ala Leu Gly Trp	
510 515 520 525	
ctc ctg gct ctg tcc tcc tgg tct gca ttc ctg cct gga gcc tct aca	1753
Leu Leu Ala Leu Ser Ser Trp Ser Ala Phe Leu Pro Gly Ala Ser Thr	
530 535 540	
gac tcg gaa ccc tca agg gcc cct tca gag aga gaa tcc gtc agc tca	1801
Asp Ser Glu Pro Ser Arg Ala Pro Ser Glu Arg Glu Ser Val Ser Ser	
545 550 555	
tgt gcc cag ccg agg acc tgc ccc agc gga acc cag cag gac cct cgg	1849
Cys Ala Gln Pro Arg Thr Cys Pro Ser Gly Thr Gln Gln Asp Pro Arg	
560 565 570	
ctc ccg cca ccc cca gga cct cac tgc tca gac tca cag agc tag agt	1897
Leu Pro Pro Pro Gly Pro His Cys Ser Asp Ser Gln Ser *	
575 580 585	
ctcactgcta gggggcaggc ccttgatgg tgctgtgtg cctggccttg gggatggctg	1957
tgagggaac gtggcagaag cagcccatg tggtccctgc ccccgacctg gaggataa	2017
gacaagaggg gtattttgga gtccacctgc tgagctggag gcctccact gcaacttttc	2077
agctcagggg ttgttgaaca gatgtgaaaa ggccagtgcc aagagtgtcc ctccgagacc	2137
cttgaaggc	2146

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 <211> 930
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (39)..(593)

<400> 844
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 Met Ala Pro Leu Leu
 1 5

ccc atc cgg acc ttg ccc ttg atc ctg att ctg ctg gct ctg ctg tcc 101
 Pro Ile Arg Thr Leu Pro Leu Ile Leu Ile Leu Leu Ala Leu Leu Ser
 10 15 20

cca ggg gct gca gac ttc aac atc tca agc ctc tct ggt ctg ctg tcc 149
 Pro Gly Ala Ala Asp Phe Asn Ile Ser Ser Leu Ser Gly Leu Leu Ser
 25 30 35

ccg gcg cta acg gag agc ctg ctg gtt gcc ttg ccc ccc tgt cac ctc 197
 Pro Ala Leu Thr Glu Ser Leu Leu Val Ala Leu Pro Pro Cys His Leu
 40 45 50

aca gga ggc aat gcc aca ctg atg gtc cgg aga gcc aat gac agc aaa 245
 Thr Gly Gly Asn Ala Thr Leu Met Val Arg Arg Ala Asn Asp Ser Lys
 55 60 65

gtg gtg acg tcc agc ttt gtg gtg cct ccg tgc cgt ggg cgc agg gaa 293
 Val Val Thr Ser Ser Phe Val Val Pro Pro Cys Arg Gly Arg Arg Glu
 70 75 80 85

ctg gtg agt gtg gtg gac agt ggt gct ggc ttc aca gtc act cgg ctc 341
 Leu Val Ser Val Val Asp Ser Gly Ala Gly Phe Thr Val Thr Arg Leu
 90 95 100

agt gca tac cag gtg aca aac ctc gtg cca gga acc aaa ttc tac att 389
 Ser Ala Tyr Gln Val Thr Asn Leu Val Pro Gly Thr Lys Phe Tyr Ile
 105 110 115

tcc tac cta gtg aag aag ggg aca gcc act gag tcc agc aga gag atc 437
 Ser Tyr Leu Val Lys Lys Gly Thr Ala Thr Glu Ser Ser Arg Glu Ile
 120 125 130

cca atg tcc aca ctc cct cga agg aac atg gaa tcc att ggg ctg ggt 485
 Pro Met Ser Thr Leu Pro Arg Arg Asn Met Glu Ser Ile Gly Leu Gly
 135 140 145

atg gcc cgc aca ggg ggc atg gtg gtc atc acg gtg ctg ctc tct gtc 533
 Met Ala Arg Thr Gly Gly Met Val Val Ile Thr Val Leu Leu Ser Val
 150 155 160 165

gcc atg ttc ctg ctg gtg ctg ggc ttc atc att gcc ctg gca ctg ggc 581
 Ala Met Phe Leu Leu Val Leu Gly Phe Ile Ile Ala Leu Ala Leu Gly
 170 175 180

tcc cgc aag taa gga ggtctgcccc gagcagcagc ttctccagga agcccagggc 636
 Ser Arg Lys *

185

accatccagc tccccagccc acctgctccc agggcccagg cctgtggctc ccttggtgcc 696
 ctgcctcct cctcctgccc tctctcccc tagagccctc tctccctctc gtccctctcc 756
 ttgccccag tgcctcacct tccaacactc cattattcct ctcaccccccac tcctgtcaga 816
 gttgactttc ctcccatttt accactttta acacccccat aacaattccc ccaccttca 876
 gtgaactaag tccctataat aaaggctgag gctgcatctg ccaaaaaaaaaaaaaa 930

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 <211> 2153
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (68)..(1645)

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 gcgtccg atg gcg gct gtg gtg ctg gcg gcg acg cgg ttg ctg cgg ggc 109
 Met Ala Ala Val Val Leu Ala Ala Thr Arg Leu Leu Arg Gly
 1 5 10
 tcg ggt tct tgg ggc tgt tcg cgg ctg agg ttt gga cct cct gcg tat 157
 Ser Gly Ser Trp Gly Cys Ser Arg Leu Arg Phe Gly Pro Pro Ala Tyr
 15 20 25 30
 aga cgg ttt agt agt ggt ggt gcc tat ccc aac atc ccc ctc tct tct 205
 Arg Arg Phe Ser Ser Gly Gly Ala Tyr Pro Asn Ile Pro Leu Ser Ser
 35 40 45
 ccc tta cct gga gta ccc aag cct gtt ttt gct aca gtt gat gga cag 253
 Pro Leu Pro Gly Val Pro Lys Pro Val Phe Ala Thr Val Asp Gly Gln
 50 55 60
 gaa aag ttt gaa acc aaa gta acc aca ttg gat aat ggg ctt cgc gtg 301
 Glu Lys Phe Glu Thr Lys Val Thr Thr Leu Asp Asn Gly Leu Arg Val
 65 70 75
 gca tct cag aat aag ttt gga cag ttt tgt aca gta gga att ctt atc 349
 Ala Ser Gln Asn Lys Phe Gly Gln Phe Cys Thr Val Gly Ile Leu Ile
 80 85 90
 aat tca gga tcg aga tat gaa gcg aaa tac ctt agt gga att gct cac 397
 Asn Ser Gly Ser Arg Tyr Glu Ala Lys Tyr Leu Ser Gly Ile Ala His
 95 100 105 110
 ttt ttg gaa aaa ttg gca ttt tcg tct act gct cga ttt gac agc aaa 445
 Phe Leu Glu Lys Leu Ala Phe Ser Ser Thr Ala Arg Phe Asp Ser Lys
 115 120 125
 gat gaa att ctg ctt acg ttg gaa aag cat ggg ggt atc tgt gac tgc 493
 Asp Glu Ile Leu Leu Thr Leu Glu Lys His Gly Gly Ile Cys Asp Cys
 130 135 140
 cag aca tca aga gac acc acc atg tat gct gtg tct gct gat agc aaa 541

Gln Thr Ser Arg Asp Thr Thr Met Tyr Ala Val Ser Ala Asp Ser Lys	
145 150 155	
ggc ttg gac acg gtg gtt gcc tta ctg gct gat gtg gtt ctg cag ccc	589
Gly Leu Asp Thr Val Val Ala Leu Leu Ala Asp Val Val Leu Gln Pro	
160 165 170	
cgg cta aca gat gaa gaa gtc gag atg acg cgg atg gcg gtc cag ttt	637
Arg Leu Thr Asp Glu Glu Val Glu Met Thr Arg Met Ala Val Gln Phe	
175 180 185 190	
gag ctg gag gac ctg aac ctg cgg cct gac cca gag cca ctt ctc acc	685
Glu Leu Glu Asp Leu Asn Leu Arg Pro Asp Pro Glu Pro Leu Leu Thr	
195 200 205	
gag atg att cat gaa gcg gct tac agg gag aac aca gtt ggc ctc cac	733
Glu Met Ile His Glu Ala Ala Tyr Arg Glu Asn Thr Val Gly Leu His	
210 215 220	
cgt ttc tgc ccc aca gaa aac gta gca aag atc aat cga gag gtg ctg	781
Arg Phe Cys Pro Thr Glu Asn Val Ala Lys Ile Asn Arg Glu Val Leu	
225 230 235	
cat tcc tac ctg agg aac tac tac act ccc gac cgc atg gtg ctg gcc	829
His Ser Tyr Leu Arg Asn Tyr Tyr Thr Pro Asp Arg Met Val Leu Ala	
240 245 250	
ggc gtg ggc gtg gag cac gag cat ctg gtg gac tgt gcc cgg aag tac	877
Gly Val Gly Val Glu His Glu His Leu Val Asp Cys Ala Arg Lys Tyr	
255 260 265 270	
ctc ctg ggg gtc cag ccg gcc tgg ggg agc gca gag gcc gtg gat att	925
Leu Leu Gly Val Gln Pro Ala Trp Gly Ser Ala Glu Ala Val Asp Ile	
275 280 285	
gac aga tct gtg gcc cag tac act ggg ggg att gcc aag cta gaa aga	973
Asp Arg Ser Val Ala Gln Tyr Thr Gly Gly Ile Ala Lys Leu Glu Arg	
290 295 300	
gac atg tcc aat gtc agc ctg ggc ccg acc ccc atc ccc gag ctc acg	1021
Asp Met Ser Asn Val Ser Leu Gly Pro Thr Pro Ile Pro Glu Leu Thr	
305 310 315	
cac atc atg gtt gga ctg gag agc tgc tcc ttc ctg gag gag gac ttc	1069
His Ile Met Val Gly Leu Glu Ser Cys Ser Phe Leu Glu Glu Asp Phe	
320 325 330	
atc ccc ttt gca gtg ttg aac atg atg atg ggc gga ggt ggc tcc ttc	1117
Ile Pro Phe Ala Val Leu Asn Met Met Met Gly Gly Gly Ser Phe	
335 340 345 350	
tcg gct ggt ggg ccc ggc aag ggc atg ttc tcc agg ctc tac ctc aac	1165
Ser Ala Gly Gly Pro Gly Lys Gly Met Phe Ser Arg Leu Tyr Leu Asn	
355 360 365	
gtg ctc aac agg cac cac tgg atg tat aac gcg acc tcc tac cac cac	1213
Val Leu Asn Arg His His Trp Met Tyr Asn Ala Thr Ser Tyr His His	
370 375 380	
agc tac gag gac act ggc ctc ctt tgc atc cat gcc agc gcc gac cca	1261
Ser Tyr Glu Asp Thr Gly Leu Leu Cys Ile His Ala Ser Ala Asp Pro	
385 390 395	
aga cag gtt cga gaa atg gta gaa atc atc aca aag gag ttt att tta	1309

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Arg  Gln Val Arg  Glu Met Val  Glu Ile Ile Thr Lys Glu Phe Ile Leu
400                               405                               410

atg ggc gga acc gtg gac acg gtg gag ctg gaa cga gcc aag acg cag      1357
Met Gly Gly Thr Val Asp Thr Val Glu Leu Glu Arg Ala Lys Thr Gln
415                               420                               425                               430

ctg aca tca atg ctc atg atg aac ctg gaa tcc agg cct gtg atc ttc      1405
Leu Thr Ser Met Leu Met Met Asn Leu Glu Ser Arg Pro Val Ile Phe
435                               440                               445

gag gat gtg ggg agg cag gtg ctg gcc act cgc tcc aga aag ctg ccg      1453
Glu Asp Val Gly Arg Gln Val Leu Ala Thr Arg Ser Arg Lys Leu Pro
450                               455                               460

cac gag ctg tgc acg ctc atc cgc aac gtg aag ccg gaa gat gtg aag      1501
His Glu Leu Cys Thr Leu Ile Arg Asn Val Lys Pro Glu Asp Val Lys
465                               470                               475

aga gtc gct tct aag atg ctc cga ggg aag ccg gca gtg gcc gcc ctg      1549
Arg Val Ala Ser Lys Met Leu Arg Gly Lys Pro Ala Val Ala Ala Leu
480                               485                               490

ggt gac ctg act gac ctg ccc acg tat gag cac atc cag acc gcc ctg      1597
Gly Asp Leu Thr Asp Leu Pro Thr Tyr Glu His Ile Gln Thr Ala Leu
495                               500                               505                               510

tcg agt aag gac ggg cgc ctg ccc agg acg tac cgg ctc ttc cgg tag      1645
Ser Ser Lys Asp Gly Arg Leu Pro Arg Thr Tyr Arg Leu Phe Arg *
515                               520                               525

aaccgctccc cggcctgaca gacccaggga gctgcagctg gagcccgttc ccgtgcgtgt      1705

tagtttgac acgaatttag tctaaaaagc tgtctggttg tataaacggt gcaaacaatg      1765

tcgccacagc acccacgcgg tttgcattct tttggaactc aatgtgccga tcagtggagt      1825

cagtatcgag cctgaccacc gcaagccagg aagcaggtga agtgcccagc gctggagtgc      1885

agcgtgccac gaggagggcg gtcggtgctt cctcctcctcg gctgtgggca catggggccc      1945

cgcaggttcc ttggaggagc cctgagctgg gaggcagcaa aggctgacct atcaaagcct      2005

cccgagggcc accgtgctgg gtaccaggac tcacctctga caagcaggag aaggtaaggg      2065

cccggtcagc tccaaggagc gcgctccacg cgcgtgcaca cagcttcctt ggtaataaag      2125

agctggcatc tttcttaaaa aaaaaaaa      2153

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<210> 846
 <211> 4455
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(4080)

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<400> 846
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Met Ala Glu Ala Gly Leu Arg Gly Trp Leu Leu Trp Ala Leu Leu Leu

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1	5	10	15	
cgc ttg gcc cag agt gag cct tac aca acc atc cac cag cct ggc tac				96
Arg Leu Ala Gln Ser Glu Pro Tyr Thr Thr Ile His Gln Pro Gly Tyr				
20	25	30		
tgc gcc ttc tat gac gaa tgt ggg aag aac cca gag ctg tct gga agc				144
Cys Ala Phe Tyr Asp Glu Cys Gly Lys Asn Pro Glu Leu Ser Gly Ser				
35	40	45		
ctc atg aca ctc tcc aac gtg tcc tgc ctg tcc aac acg ccg gcc cgc				192
Leu Met Thr Leu Ser Asn Val Ser Cys Leu Ser Asn Thr Pro Ala Arg				
50	55	60		
aag atc aca ggt gat cac ctg atc cta tta cag aag atc tgc ccc cgc				240
Lys Ile Thr Gly Asp His Leu Ile Leu Leu Gln Lys Ile Cys Pro Arg				
65	70	75	80	
ctc tac acc ggc ccc aac acc caa gcc tgc tgc tcc gcc aag cag ctg				288
Leu Tyr Thr Gly Pro Asn Thr Gln Ala Cys Ser Ala Lys Gln Leu				
85	90	95		
gta tca ctg gaa gcg agt ctg tcg atc acc aag gcc ctc ctc acc cgc				336
Val Ser Leu Glu Ala Ser Leu Ser Ile Thr Lys Ala Leu Leu Thr Arg				
100	105	110		
tgc cca gcc tgc tct gac aat ttt gtg aac ctg cac tgc cac aac acg				384
Cys Pro Ala Cys Ser Asp Asn Phe Val Asn Leu His Cys His Asn Thr				
115	120	125		
tgc agc ccc aat cag agc ctc ttc atc aat gtg acc cgc gtg gcc cag				432
Cys Ser Pro Asn Gln Ser Leu Phe Ile Asn Val Thr Arg Val Ala Gln				
130	135	140		
cta ggg gct gga caa ctc cca gct gtg gtg gcc tat gag gcc ttc tac				480
Leu Gly Ala Gly Gln Leu Pro Ala Val Val Ala Tyr Glu Ala Phe Tyr				
145	150	155	160	
cag cat agc ttt gcc gag cag agc tat gac tcc tgc agc cgt gtg cgc				528
Gln His Ser Phe Ala Glu Gln Ser Tyr Asp Ser Cys Ser Arg Val Arg				
165	170	175		
gtc cct gca gct gcc acg ctg gct gtg ggc acc atg tgt ggc gtg tat				576
Val Pro Ala Ala Ala Thr Leu Ala Val Gly Thr Met Cys Gly Val Tyr				
180	185	190		
ggc tct gcc ctt tgc aat gcc cag cgc tgg ctc aac ttc cag gga gac				624
Gly Ser Ala Leu Cys Asn Ala Gln Arg Trp Leu Asn Phe Gln Gly Asp				
195	200	205		
aca ggc aat ggt ctg gcc cca ctg gac atc acc ttc cac ctc ttg gag				672
Thr Gly Asn Gly Leu Ala Pro Leu Asp Ile Thr Phe His Leu Leu Glu				
210	215	220		
cct ggc cag gcc gtg ggg agt ggg att cag cct ctg aat gag ggg gtt				720
Pro Gly Gln Ala Val Gly Ser Gly Ile Gln Pro Leu Asn Glu Gly Val				
225	230	235	240	
gca cgt tgc aat gag tcc caa ggt gac gac gtg gcg acc tgc tcc tgc				768
Ala Arg Cys Asn Glu Ser Gln Gly Asp Asp Val Ala Thr Cys Ser Cys				
245	250	255		
caa gac tgt gct gca tcc tgt cct gcc ata gcc cgc ccc cag gcc ctc				816
Gln Asp Cys Ala Ala Ser Cys Pro Ala Ile Ala Arg Pro Gln Ala Leu				

260	265	270	
gac tcc acc ttc tac ctg ggc cag atg ccg ggc agt ctg gtc ctc atc Asp Ser Thr Phe Tyr Leu Gly Gln Met Pro Gly Ser Leu Val Leu Ile 275 280 285			864
atc atc ctc tgc tct gtc ttc gct gtg gtc acc atc ctg ctt gtg gga Ile Ile Leu Cys Ser Val Phe Ala Val Val Thr Ile Leu Leu Val Gly 290 295 300			912
ttc cgt gtg gcc ccc gcc agg gac aaa agc aag atg gtg gac ccc aag Phe Arg Val Ala Pro Ala Arg Asp Lys Ser Lys Met Val Asp Pro Lys 305 310 315 320			960
aag ggc acc agc ctc tct gac aag ctc agc ttc tcc acc cac acc ctc Lys Gly Thr Ser Leu Ser Asp Lys Leu Ser Phe Ser Thr His Thr Leu 325 330 335			1008
ctt ggc cag ttc ttc cag ggc tgg ggc acg tgg gtg gct tcg tgg cct Leu Gly Gln Phe Phe Gln Gly Trp Gly Thr Trp Val Ala Ser Trp Pro 340 345 350			1056
ctg acc atc ttg gtg cta tct gtc atc ccg gtg gtg gcc ttg gca gcg Leu Thr Ile Leu Val Leu Ser Val Ile Pro Val Val Ala Leu Ala Ala 355 360 365			1104
ggc ctg gtc ttt aca gaa ctc act acg gac ccc gtg gag ctg tgg tcg Gly Leu Val Phe Thr Glu Leu Thr Thr Asp Pro Val Glu Leu Trp Ser 370 375 380			1152
gcc ccc aac agc caa gcc cgg agt gag aaa gct ttc cat gac cag cat Ala Pro Asn Ser Gln Ala Arg Ser Glu Lys Ala Phe His Asp Gln His 385 390 395 400			1200
ttc ggc ccc ttc ttc cga acc aac cag gtg atc ctg acg gct cct aac Phe Gly Pro Phe Phe Arg Thr Asn Gln Val Ile Leu Thr Ala Pro Asn 405 410 415			1248
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Pro Tyr Thr Ile Thr Asn Val Phe Tyr Glu Gln Tyr Leu Thr Ile Leu				
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Cys Ala Phe Tyr Asp Glu Cys Gly Lys Asn Pro Glu Leu Ser Gly Ser	
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Lys Ile Thr Gly Asp His Leu Ile Leu Leu Gln Lys Ile Cys Pro Arg	
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Cys Ser Pro Asn Gln Ser Leu Phe Ile Asn Val Thr Arg Val Ala Gln	
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cat aag tat ctt ccc tgg ttc ctg aac gac cgg ccc aac atc aaa tgt His Lys Tyr Leu Pro Trp Phe Leu Asn Asp Arg Pro Asn Ile Lys Cys 1010 1015 1020	3072
ccc aaa ggc ggc ctg gca gca tac agc acc tct gtg aac ttg act tca Pro Lys Gly Gly Leu Ala Ala Tyr Ser Thr Ser Val Asn Leu Thr Ser 1025 1030 1035 1040	3120
gat ggc cag gtt tta gcc tcc agg ttc atg gcc tat cac aag ccc ctg Asp Gly Gln Val Leu Ala Ser Arg Phe Met Ala Tyr His Lys Pro Leu 1045 1050 1055	3168
aaa aac tca cag gat tac aca gaa gct ctg cgg gca gct cga gag ctg Lys Asn Ser Gln Asp Tyr Thr Glu Ala Leu Arg Ala Ala Arg Glu Leu 1060 1065 1070	3216
gca gcc aac atc act gct gac ctg cgg aaa gtg cct gga aca gac ccg Ala Ala Asn Ile Thr Ala Asp Leu Arg Lys Val Pro Gly Thr Asp Pro 1075 1080 1085	3264
gct ttt gag gtc ttc ccc tac acg atc acc aat gtg ttt tat gag cag Ala Phe Glu Val Phe Pro Tyr Thr Ile Thr Asn Val Phe Tyr Glu Gln 1090 1095 1100	3312

tac ctg acc atc ctc cct gag ggg ctc ttc atg ctc agc ctc tgc ctt Tyr Leu Thr Ile Leu Pro Glu Gly Leu Phe Met Leu Ser Leu Cys Leu 1105 1110 1115 1120	3360
gtg ccc acc ttc gct gtc tcc tgc ctc ctg ctg ggc ctg gac ctg cgc Val Pro Thr Phe Ala Val Ser Cys Leu Leu Leu Gly Leu Asp Leu Arg 1125 1130 1135	3408
tcc ggc ctc ctc aac ctg ctc tcc att gtc atg atc ctc gtg gac act Ser Gly Leu Leu Asn Leu Leu Ser Ile Val Met Ile Leu Val Asp Thr 1140 1145 1150	3456
gtc ggc ttc atg gcc ctg tgg ggc atc agt tac aat gct gtg tcc ctc Val Gly Phe Met Ala Leu Trp Gly Ile Ser Tyr Asn Ala Val Ser Leu 1155 1160 1165	3504
atc aac ctg gtc tcg gcg gtg ggc atg tct gtg gag ttt gtg tcc cac Ile Asn Leu Val Ser Ala Val Gly Met Ser Val Glu Phe Val Ser His 1170 1175 1180	3552
att acc cgc tcc ttt gcc atc agc acc aag ccc acc tgg ctg gag agg Ile Thr Arg Ser Phe Ala Ile Ser Thr Lys Pro Thr Trp Leu Glu Arg 1185 1190 1195 1200	3600
gcc aaa gag gcc acc atc tct atg gga agt gcg gtg ttt gca ggt gtg Ala Lys Glu Ala Thr Ile Ser Met Gly Ser Ala Val Phe Ala Gly Val 1205 1210 1215	3648
gcc atg acc aac ctg cct ggc atc ctt gtc ctg ggc ctc gcc aag gcc Ala Met Thr Asn Leu Pro Gly Ile Leu Val Leu Gly Leu Ala Lys Ala 1220 1225 1230	3696
cag ctc att cag atc ttc ttc ttc cgc ctc aac ctc ctg atc act ctg Gln Leu Ile Gln Ile Phe Phe Phe Arg Leu Asn Leu Leu Ile Thr Leu 1235 1240 1245	3744
ctg ggc ctg ctg cat ggc ttg gtc ttc ctg ccc gtc atc ctc agc tac Leu Gly Leu Leu His Gly Leu Val Phe Leu Pro Val Ile Leu Ser Tyr 1250 1255 1260	3792
gtg ggg cct gac gtt aac ccg gct ctg gca ctg gag cag aag cgg gct Val Gly Pro Asp Val Asn Pro Ala Leu Ala Leu Glu Gln Lys Arg Ala 1265 1270 1275 1280	3840
gag gag gcg gtg gca gca gtc atg gtg gcc tct tgc cca aat cac ccc Glu Glu Ala Val Ala Val Met Val Ala Ser Cys Pro Asn His Pro 1285 1290 1295	3888
tcc cga gtc tcc aca gct gac aac atc tat gtc aac cac agc ttt gaa Ser Arg Val Ser Thr Ala Asp Asn Ile Tyr Val Asn His Ser Phe Glu 1300 1305 1310	3936
ggc tct atc aaa ggt gct ggt gcc atc agc aac ttc ttg ccc aac aat Gly Ser Ile Lys Gly Ala Gly Ala Ile Ser Asn Phe Leu Pro Asn Asn 1315 1320 1325	3984
ggg cgg cag ttc tga tacagccaga ggccctgtct aggcctctatg gccctgaacc Gly Arg Gln Phe * 1330	4039
aaaggggttat ggggatcttc cttgtgactg ccccttgaca cacgccctcc tcaaataccta	4099
ggggaggcca ttcccatgag actgcctgtc actggaggat ggccctgtct tgaggatatcc	4159

aggcagcacc actgatggct cttggggctg ggctggctcct cccatcttca cctcgggcct 4219
 ggatcccagg cctcaaacca gcccaacccg aacctttgga acagttttcc aaaaccttga 4279
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 tttattaatt tacttccaaa cgcaacgaaa ggtccatgga caatttggtg gccatttaat 180
 tcagggcccc caattcgtac gtggagaagt gggaaatgcaa aagtactttg acctttaacc 240
 ttccggtccg cgcggtggag ggaaacgcct ccgtctctat ataaggaatt ttccggtctc 300
 ttccgggtcct ttttcctctc ttcagcgtgg ggcgccca atttgccgcg tctctttctg 360
 ctgctcccca gctctcggat acagccgaca cc atg ggt ttc gga gac ctg aaa 413
 Met Gly Phe Gly Asp Leu Lys
 1 5
 agc cct gcc ggc ctc cag gtg ctc aac gat tac ctg gcg gac aag agc 461
 Ser Pro Ala Gly Leu Gln Val Leu Asn Asp Tyr Leu Ala Asp Lys Ser
 10 15 20
 tac atc gag ggg tat gtg cca tca caa gca gat gtg gca gta ttt gaa 509
 Tyr Ile Glu Gly Tyr Val Pro Ser Gln Ala Asp Val Ala Val Phe Glu
 25 30 35
 gcc gtg tcc agc cca ccg cct gcc gac ttg tgt cat gcc cta cgt tgg 557
 Ala Val Ser Ser Pro Pro Pro Ala Asp Leu Cys His Ala Leu Arg Trp
 40 45 50 55
 tat aat cac atc aag tct tac gaa aag gaa aag gcc agc ctg cca gga 605
 Tyr Asn His Ile Lys Ser Tyr Glu Lys Glu Lys Ala Ser Leu Pro Gly
 60 65 70
 gtg aag aaa gct ttg ggc aaa tat ggt cct gcc gat gtg gaa gac act 653
 Val Lys Lys Ala Leu Gly Lys Tyr Gly Pro Ala Asp Val Glu Asp Thr
 75 80 85
 aca gga agt gga gct aca gat agt aaa gat gat gat gac att gac ctc 701

Thr Gly Ser Gly Ala Thr Asp Ser Lys Asp Asp Asp Asp Ile Asp Leu	
90 95 100	
ttt gga tct gat gat gag gag gaa agt gaa gaa gca aag agg cta agg	749
Phe Gly Ser Asp Asp Glu Glu Glu Ser Glu Glu Ala Lys Arg Leu Arg	
105 110 115	
gaa gaa cgt ctt gca caa tat gaa tca aag aaa gcc aaa aaa cct gca	797
Glu Glu Arg Leu Ala Gln Tyr Glu Ser Lys Lys Ala Lys Lys Pro Ala	
120 125 130 135	
ctt gtt gcc aag tct tcc atc tta cta gat gtg aaa cct tgg gat gat	845
Leu Val Ala Lys Ser Ser Ile Leu Leu Asp Val Lys Pro Trp Asp Asp	
140 145 150	
gag aca gat atg gcg aaa tta gag gag tgc gtc aga agc att caa gca	893
Glu Thr Asp Met Ala Lys Leu Glu Glu Cys Val Arg Ser Ile Gln Ala	
155 160 165	
gac ggc tta gtc tgg ggc tca tct aaa cta gtt cca gtg gga tac gga	941
Asp Gly Leu Val Trp Gly Ser Ser Lys Leu Val Pro Val Gly Tyr Gly	
170 175 180	
att aag aaa ctt caa ata cag tgt gta gtt gaa gat gat aaa gtt gga	989
Ile Lys Lys Leu Gln Ile Gln Cys Val Val Glu Asp Asp Lys Val Gly	
185 190 195	
aca gat atg ctg gag gag cag atc act gct ttt gag gac tat gtg cag	1037
Thr Asp Met Leu Glu Glu Gln Ile Thr Ala Phe Glu Asp Tyr Val Gln	
200 205 210 215	
tcc atg gat gtg gct gct ttc aac aag atc taa aatccatc ctggatcatg	1088
Ser Met Asp Val Ala Ala Phe Asn Lys Ile *	
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Met Ile Asn Met Cys Phe Gln Glu Leu	
1 5	
gta aca ttc agg gat gtg gcc ata gaa ttc tcc cct gaa gag tgg aaa	160
Val Thr Phe Arg Asp Val Ala Ile Glu Phe Ser Pro Glu Glu Trp Lys	
10 15 20 25	
tgt ctg gac cct gcc cag cag aat ttg tat aga gat gtg atg ttg gag	208
Cys Leu Asp Pro Ala Gln Gln Asn Leu Tyr Arg Asp Val Met Leu Glu	
30 35 40	

aac tac agg aac ctg gtc tcc ctg ggt ttt gtg atc tct aac cca gac	256
Asn Tyr Arg Asn Leu Val Ser Leu Gly Phe Val Ile Ser Asn Pro Asp	
45 50 55	
ctg gtc acc tgt ctg gag caa ata aaa gag ccc tgc aat ttg aag ata	304
Leu Val Thr Cys Leu Glu Gln Ile Lys Glu Pro Cys Asn Leu Lys Ile	
60 65 70	
cat gag aca gca gcc aaa ccc cca gct ata tgt tct cct ttc agc caa	352
His Glu Thr Ala Ala Lys Pro Pro Ala Ile Cys Ser Pro Phe Ser Gln	
75 80 85	
gac ctt tca cca gtg cag ggg ata gaa gat tca ttc cac aaa ctt ata	400
Asp Leu Ser Pro Val Gln Gly Ile Glu Asp Ser Phe His Lys Leu Ile	
90 95 100 105	
ctg aaa aga tac gag aaa tgt gga cat gag aat tta caa tta aga aaa	448
Leu Lys Arg Tyr Glu Lys Cys Gly His Glu Asn Leu Gln Leu Arg Lys	
110 115 120	
ggc tgt aaa cgt gtg aat gag tgt aag gtg cag aaa gga gtt aat aat	496
Gly Cys Lys Arg Val Asn Glu Cys Lys Val Gln Lys Gly Val Asn Asn	
125 130 135	
gga gtt tac cag tgc ttg tca act acc cag agc aaa ata ttt caa tgt	544
Gly Val Tyr Gln Cys Leu Ser Thr Thr Gln Ser Lys Ile Phe Gln Cys	
140 145 150	
aat aca tgt gtt aaa gtt ttt agt aaa ttt tca aat tca aac aaa cat	592
Asn Thr Cys Val Lys Val Phe Ser Lys Phe Ser Asn Ser Asn Lys His	
155 160 165	
aag ata aga cat act gga gag aaa ccc ttt aaa tgt aca gaa tgt ggc	640
Lys Ile Arg His Thr Gly Glu Lys Pro Phe Lys Cys Thr Glu Cys Gly	
170 175 180 185	
aga tcg ttt tac atg tca cac cta act caa cat aca gga att cat gct	688
Arg Ser Phe Tyr Met Ser His Leu Thr Gln His Thr Gly Ile His Ala	
190 195 200	
gga gag aaa ccc tac aat gtg aaa aat gtg gca aag ctt tac agg gtc	736
Gly Glu Lys Pro Tyr Asn Val Lys Asn Val Ala Lys Leu Tyr Arg Val	
205 210 215	
cac aat cca ctg aat gaa cat aag aga att cat act gga gag aaa ccc	784
His Asn Pro Leu Asn Glu His Lys Arg Ile His Thr Gly Glu Lys Pro	
220 225 230	
tac aca tgt gaa gaa tgt ggc aaa gct tta gac gtt ctg aac gaa cat	832
Tyr Thr Cys Glu Glu Cys Gly Lys Ala Leu Asp Val Leu Asn Glu His	
235 240 245	
aag aaa att cat act gga gag aaa ccc tac aaa tgt gaa gaa tgt ggc	880
Lys Lys Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Glu Glu Cys Gly	
250 255 260 265	
aaa gcc ttt aca agg tcc aca aca ctg aat gaa cac aag aaa att cat	928
Lys Ala Phe Thr Arg Ser Thr Thr Leu Asn Glu His Lys Lys Ile His	
270 275 280	
act gga gag aaa ccc tac aaa tgt aaa gaa tgt ggc aaa gcc ttt aga	976
Thr Gly Glu Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala Phe Arg	
285 290 295	

tggtccacaagcctgaataagaacatattcatactggaagagaaa	1024
Trp Ser Thr Ser Leu Asn Glu His Lys Asn Ile His Thr Gly Glu Lys	
300 305 310	
ccctactaaatgtaaaagaatgtggcgaagcctttagaagctccaggagc	1072
Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala Phe Arg Gln Ser Arg Ser	
315 320 325	
ctgaatgaacataaaatattcatactggcgaaaaaacctactacacatgt	1120
Leu Asn Glu His Lys Asn Ile His Thr Gly Glu Lys Pro Tyr Thr Cys	
330 335 340 345	
gaagaaatgtggcgaagcttttaaccaaaccctcaagctcttattatacac	1168
Glu Lys Cys Gly Lys Ala Phe Asn Gln Ser Ser Ser Leu Ile Ile His	
350 355 360	
aggagcattcatctgaacaaaaactttactaaatgtgaagaaatgtggc	1216
Arg Ser Ile His Ser Glu Gln Lys Leu Tyr Lys Cys Glu Glu Cys Gly	
365 370 375	
aaagcctttacttggtccctcatcttcaataaaatagaagagattcat	1264
Lys Ala Phe Thr Trp Ser Ser Ser Leu Asn Lys His Lys Arg Ile His	
380 385 390	
actggaagagaaaacctactacacatgtgaagaaatgtggcgaagcttttat	1312
Thr Gly Glu Lys Pro Tyr Thr Cys Glu Glu Cys Gly Lys Ala Phe Tyr	
395 400 405	
aggctctcacactctgctaaaatagaagagaattcatactggaagagaaa	1360
Arg Ser Ser His Leu Ala Lys His Lys Arg Ile His Thr Gly Glu Lys	
410 415 420 425	
ccctactacgtgcgaagaaatgtggcgaagcttttaaccaaaccctcaact	1408
Pro Tyr Thr Cys Glu Glu Cys Gly Lys Ala Phe Asn Gln Ser Ser Thr	
430 435 440	
cttatattaacaaagagaatccatcttggacaaaaacctactaaaatgt	1456
Leu Ile Leu His Lys Arg Ile His Ser Gly Gln Lys Pro Tyr Lys Cys	
445 450 455	
gaagaaatgtggcgaagctttacaaggctccacacactgaacgaacat	1504
Glu Glu Cys Gly Lys Ala Phe Thr Arg Ser Thr Thr Leu Asn Glu His	
460 465 470	
aagaaatcatactggcgagaaacccctacaaaatgtgaagaaatgtggc	1552
Lys Lys Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Glu Glu Cys Gly	
475 480 485	
aaagctttcataatgggtccgcaagcctgaataagaacatattcat	1600
Lys Ala Phe Ile Trp Ser Ala Ser Leu Asn Glu His Lys Asn Ile His	
490 495 500 505	
actggaagagaaaacctactaaaatgtaaaagaatgtggcgaagcttttaac	1648
Thr Gly Glu Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala Phe Asn	
510 515 520	
caaaccctacggccttattatacacaggagcattcatcttgaaacaaa	1696
Gln Ser Ser Gly Leu Ile Ile His Arg Ser Ile His Ser Glu Gln Lys	
525 530 535	
cttactaaaatgtgaagaaatgtggcgaagctttactcggctccacagcc	1744
Leu Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Thr Arg Ser Thr Ala	
540 545 550	

ctg aat gaa cat aag aaa att cat tct gga gag aaa ccc tac aaa tgc 1792
 Leu Asn Glu His Lys Lys Ile His Ser Gly Glu Lys Pro Tyr Lys Cys
 555 560 565

 aaa gaa tgt ggc aaa gcc tat aac tta tcc tca acc ctt act aaa cat 1840
 Lys Glu Cys Gly Lys Ala Tyr Asn Leu Ser Ser Thr Leu Thr Lys His
 570 575 580 585

 aag aga att cat act gga gag aaa ccc ttc aca tgt gaa gaa tgt ggc 1888
 Lys Arg Ile His Thr Gly Glu Lys Pro Phe Thr Cys Glu Glu Cys Gly
 590 595 600

 aaa gcc ttc aat tgg tcc tca tcc ctt act aaa cat aag ata att cat 1936
 Lys Ala Phe Asn Trp Ser Ser Ser Leu Thr Lys His Lys Ile Ile His
 605 610 615

 act gga gag aaa tcc tac aaa tgt gaa gaa tgt ggc aaa ggt ttt aat 1984
 Thr Gly Glu Lys Ser Tyr Lys Cys Glu Glu Cys Gly Lys Gly Phe Asn
 620 625 630

 cgg ccc tca acc ctt act gta cac aag cga ttc ata ctg gca agg aac 2032
 Arg Pro Ser Thr Leu Thr Val His Lys Arg Phe Ile Leu Ala Arg Asn
 635 640 645

 ata gtt gaa tga 2044
 Ile Val Glu *
 650

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 Met Asp Leu Thr Lys Gly Cys Val Thr
 1 5

 ttt gag gac atc gcc att tac ttc tca cag gac gag tgg gga ctt ctt 99
 Phe Glu Asp Ile Ala Ile Tyr Phe Ser Gln Asp Glu Trp Gly Leu Leu
 10 15 20 25

 gat gag gct cag aga ctc ctg tac ctt gaa gtg atg ctg gag aac ttt 147
 Asp Glu Ala Gln Arg Leu Leu Tyr Leu Glu Val Met Leu Glu Asn Phe
 30 35 40

 gcc ctt gta gcc tca ctg ggt tgt ggc cat gga aca gag gat gaa gag 195
 Ala Leu Val Ala Ser Leu Gly Cys Gly His Gly Thr Glu Asp Glu Glu
 45 50 55

 aca cct tct gac cag aat gtt tot gta gga gtg tca cag tca aag gca 243
 Thr Pro Ser Asp Gln Asn Val Ser Val Gly Val Ser Gln Ser Lys Ala
 60 65 70

 ggt tca tcc aca cag aag act caa tcc tgt gag atg tgt gtc cca gtc 291
 Gly Ser Ser Thr Gln Lys Thr Gln Ser Cys Glu Met Cys Val Pro Val

75	80	85	
ctg aaa gat att ttg cat cta gct gat ctc cct ggg cag aaa cca tac Leu Lys Asp Ile Leu His Leu Ala Asp Leu Pro Gly Gln Lys Pro Tyr 90 95 100 105			339
ttg gtt gga gaa tgt aca aac cat cac cag cac cag aag cat cac agt Leu Val Gly Glu Cys Thr Asn His His Gln His Gln Lys His His Ser 110 115 120			387
gca aag aaa tcc ttg aag agg gac atg gac aga gcc tca tat gtg aag Ala Lys Lys Ser Leu Lys Arg Asp Met Asp Arg Ala Ser Tyr Val Lys 125 130 135			435
tgc tgc cta ttc tgt atg tca ttg aag ccc ttt cgc aaa tgg gag gtt Cys Cys Leu Phe Cys Met Ser Leu Lys Pro Phe Arg Lys Trp Glu Val 140 145 150			483
gga aag gac ctt cca gcc atg ttg cgg ctt ctg agg tcc ctg gtc ttt Gly Lys Asp Leu Pro Ala Met Leu Arg Leu Leu Arg Ser Leu Val Phe 155 160 165			531
cct gga ggc aag aaa ccc ggc aca att act gaa tgt ggg gag gac att Pro Gly Gly Lys Lys Pro Gly Thr Ile Thr Glu Cys Gly Glu Asp Ile 170 175 180 185			579
cgc agt caa aaa agt cat tac aag tca ggt gaa tgt ggg aag gct tcc Arg Ser Gln Lys Ser His Tyr Lys Ser Gly Glu Cys Gly Lys Ala Ser 190 195 200			627
agg cac aaa cac act cct gtt tac cat cca aga gtc tac act gga aaa Arg His Lys His Thr Pro Val Tyr His Pro Arg Val Tyr Thr Gly Lys 205 210 215			675
aag ctt tat gag tgt agc aaa tgt ggg aaa gcc ttc cgt ggc aag tac Lys Leu Tyr Glu Cys Ser Lys Cys Gly Lys Ala Phe Arg Gly Lys Tyr 220 225 230			723
tca ctt gtt cag cac cag aga gtc cat act gga gaa agg cct tgg gag Ser Leu Val Gln His Gln Arg Val His Thr Gly Glu Arg Pro Trp Glu 235 240 245			771
tgc aat gaa tgt gga aaa ttc ttt agc caa acc tcc cac ctg aat gat Cys Asn Glu Cys Gly Lys Phe Phe Ser Gln Thr Ser His Leu Asn Asp 250 255 260 265			819
cat cgg aga atc cac acc gga gaa agg cct tat gag tgc agc gaa tgt His Arg Arg Ile His Thr Gly Glu Arg Pro Tyr Glu Cys Ser Glu Cys 270 275 280			867
gga aaa tta ttt aga caa aac tcc agc ctt gtt gac cac cag aaa ata Gly Lys Leu Phe Arg Gln Asn Ser Ser Leu Val Asp His Gln Lys Ile 285 290 295			915
cac act gga gca agg cct tat gag tgt agc cag tgt ggg aaa tcc ttt His Thr Gly Ala Arg Pro Tyr Glu Cys Ser Gln Cys Gly Lys Ser Phe 300 305 310			963
agc caa aaa gcc acc ctt gtt aaa cac caa aga gtt cac act gga gaa Ser Gln Lys Ala Thr Leu Val Lys His Gln Arg Val His Thr Gly Glu 315 320 325			1011
agg cct tat aag tgt ggt gaa tgt ggg aat tcc ttt agt caa agt gcc Arg Pro Tyr Lys Cys Gly Glu Cys Gly Asn Ser Phe Ser Gln Ser Ala			1059

330	335	340	345	
att ctt aat caa cac cga aga att cac act gga gca aag cct tat gag				1107
Ile Leu Asn Gln His Arg Arg Ile His Thr Gly Ala Lys Pro Tyr Glu				
	350	355	360	
tgt ggc cag tgt ggg aaa tcc ttt agt caa aaa gct acc ctc att aaa				1155
Cys Gly Gln Cys Gly Lys Ser Phe Ser Gln Lys Ala Thr Leu Ile Lys				
	365	370	375	
cac cag aga gtt cac act gga gaa agg cct tat aag tgt ggt gac tgt				1203
His Gln Arg Val His Thr Gly Glu Arg Pro Tyr Lys Cys Gly Asp Cys				
	380	385	390	
ggg aaa tcc ttt agt caa agc tcc atc ctt att caa cac cgg aga att				1251
Gly Lys Ser Phe Ser Gln Ser Ser Ile Leu Ile Gln His Arg Arg Ile				
	395	400	405	
cat act gga gca agg cct tat gag tgt ggc cag tgt gga aag tcc ttt				1299
His Thr Gly Ala Arg Pro Tyr Glu Cys Gly Gln Cys Gly Lys Ser Phe				
	410	415	420	425
agc caa aag tct ggt ctc att caa cac caa gtg gtt cac act gga gaa				1347
Ser Gln Lys Ser Gly Leu Ile Gln His Gln Val Val His Thr Gly Glu				
	430	435	440	
agg cct tat gag tgc aac aaa tgt ggg aat tcc ttt agc caa tgc tcc				1395
Arg Pro Tyr Glu Cys Asn Lys Cys Gly Asn Ser Phe Ser Gln Cys Ser				
	445	450	455	
agc ctc ata cat cac caa aaa tgt cat aac aca tag				1431
Ser Leu Ile His His Gln Lys Cys His Asn Thr *				
	460	465		

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atatctacag ttctctaaac aatttttagat ttttcttttc aaggacagct agagaagata	180
atgacataat aactatttcc ttttttagga tctgaatcta aaaatggtga agcagacagt	240
tcagataaag aa atg aaa cat ggg caa aaa tct ccc act gga aaa caa	288
Met Lys His Gly Gln Lys Ser Pro Thr Gly Lys Gln	
1 5 10	
aca agt cag cac tta aaa cga tta aaa aag tct ggt tta ggg cac ttg	336
Thr Ser Gln His Leu Lys Arg Leu Lys Lys Ser Gly Leu Gly His Leu	
15 20 25	

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aaa tgg acc aaa gct gag gac att gac ata gaa acc cca gga tct att    384
Lys Trp Thr Lys Ala Glu Asp Ile Asp Ile Glu Thr Pro Gly Ser Ile
      30              35              40

ctt gtc aac act aac ttg agg gca tta ata aat aaa cat acg ttt gct    432
Leu Val Asn Thr Asn Leu Arg Ala Leu Ile Asn Lys His Thr Phe Ala
      45              50              55              60

tcc tta cct cag cat ttt caa caa tac ctc ctg ctt ttg ctc cca gaa    480
Ser Leu Pro Gln His Phe Gln Gln Tyr Leu Leu Leu Leu Leu Pro Glu
              65              70              75

gtg gat agg cag atg gga agt gat gga att tta cgc ctc agt act tca    528
Val Asp Arg Gln Met Gly Ser Asp Gly Ile Leu Arg Leu Ser Thr Ser
              80              85              90

gct cta aat aat gaa ttc ttt gca tat gca gca caa ggg tgg aaa cag    576
Ala Leu Asn Asn Glu Phe Phe Ala Tyr Ala Ala Gln Gly Trp Lys Gln
              95              100              105

cga ctg gca gaa ggt aaa ttt gta ttt tct att att atg tga catattg    625
Arg Leu Ala Glu Gly Lys Phe Val Phe Ser Ile Ile Met *
      110              115              120

gagtacacat accgtactga gcttgtagct ttctctgatt tttcagtctt ttccccgaca    685

cagtacactt taatttagta aaaactcata tccctttcca aatgagttca ctgattcttt    745

tggtatactt gacattattg atgtcagata tttttgaaga aagcataatt ttatcttgga    805

catcataaaaa tttttgatgc agcaacattt tcttgccgat ggtaatttta atgacattgt    865

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<220>
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 <222> (99)..(1976)

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<400> 852
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aagaggcagg aggaacagtg tatccacagc gtgggacc      atg cca ggc aca aaa    113
              Met Pro Gly Thr Lys
              1              5

cgg ttt caa cat gtc att gag acc ccg gag cct ggc aag tgg gag ttg    161
Arg Phe Gln His Val Ile Glu Thr Pro Glu Pro Gly Lys Trp Glu Leu
              10              15              20

tct ggg tac gag gca gct gtg cca atc acg gag aag tca aac cca ctg    209
Ser Gly Tyr Glu Ala Ala Val Pro Ile Thr Glu Lys Ser Asn Pro Leu
              25              30              35

acc cag gat cta gac aaa gca gat gct gag aac att gtt cga ctg cta    257
Thr Gln Asp Leu Asp Lys Ala Asp Ala Glu Asn Ile Val Arg Leu Leu
              40              45              50

ggg caa tgt gat gct gag atc ttc cag gag gag ggg caa gcc ctg tcc    305

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Gly	Gln	Cys	Asp	Ala	Glu	Ile	Phe	Gln	Glu	Glu	Gly	Gln	Ala	Leu	Ser		
55						60					65						
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Thr	Tyr	Gln	Arg	Leu	Tyr	Ser	Glu	Ser	Ile	Leu	Thr	Thr	Met	Val	Gln		
70					75					80					85		
gtg	gct	ggg	aaa	gtt	cag	gaa	gtg	ctg	aag	gag	cca	gat	ggg	ggg	ctg	401	
Val	Ala	Gly	Lys	Val	Gln	Glu	Val	Leu	Lys	Glu	Pro	Asp	Gly	Gly	Leu		
				90					95					100			
gtt	gtg	ctg	agt	gga	ggg	ggc	acc	tct	ggc	cgg	atg	gca	ttc	ctc	atg	449	
Val	Val	Leu	Ser	Gly	Gly	Gly	Thr	Ser	Gly	Arg	Met	Ala	Phe	Leu	Met		
			105					110					115				
tcg	gtg	tcc	ttt	aat	cag	ctg	atg	aaa	ggg	ctg	gga	cag	aaa	cct	ctt	497	
Ser	Val	Ser	Phe	Asn	Gln	Leu	Met	Lys	Gly	Leu	Gly	Gln	Lys	Pro	Leu		
			120				125					130					
tac	acc	tac	ctc	att	gca	ggg	ggg	gac	agg	tct	gtg	gtg	gcc	tct	agg	545	
Tyr	Thr	Tyr	Leu	Ile	Ala	Gly	Gly	Asp	Arg	Ser	Val	Val	Ala	Ser	Arg		
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gag	ggg	aca	gaa	gat	agt	gcc	ttg	cac	ggg	att	gag	gaa	ctg	aag	aag	593	
Glu	Gly	Thr	Glu	Asp	Ser	Ala	Leu	His	Gly	Ile	Glu	Glu	Leu	Lys	Lys		
150					155				160					165			
gtg	gct	gcc	ggg	aag	aag	aga	gtg	att	gtc	att	ggc	att	tct	gtg	gga	641	
Val	Ala	Ala	Gly	Lys	Lys	Arg	Val	Ile	Val	Ile	Gly	Ile	Ser	Val	Gly		
				170				175						180			
ctc	tct	gct	ccc	ttt	gtg	gca	ggc	cag	atg	gac	tgc	tgc	atg	aac	aac	689	
Leu	Ser	Ala	Pro	Phe	Val	Ala	Gly	Gln	Met	Asp	Cys	Cys	Met	Asn	Asn		
			185					190					195				
aca	gct	gtc	ttc	ttg	cca	gtc	ctg	gtt	ggc	ttc	aat	cca	gtg	agc	atg	737	
Thr	Ala	Val	Phe	Leu	Pro	Val	Leu	Val	Gly	Phe	Asn	Pro	Val	Ser	Met		
			200				205					210					
gcc	aga	aat	gac	ccc	att	gaa	gac	tgg	agt	tca	aca	ttc	cga	caa	gta	785	
Ala	Arg	Asn	Asp	Pro	Ile	Glu	Asp	Trp	Ser	Ser	Thr	Phe	Arg	Gln	Val		
			215			220					225						
gca	gag	cgg	atg	cag	aaa	atg	cag	gag	aaa	cag	aaa	gct	ttt	gtg	ctc	833	
Ala	Glu	Arg	Met	Gln	Lys	Met	Gln	Glu	Lys	Gln	Lys	Ala	Phe	Val	Leu		
230					235					240				245			
aat	cct	gcc	atc	ggg	ccc	gag	ggg	ctc	agc	ggc	tcc	tcc	cgg	atg	aaa	881	
Asn	Pro	Ala	Ile	Gly	Pro	Glu	Gly	Leu	Ser	Gly	Ser	Ser	Arg	Met	Lys		
				250				255						260			
ggg	gga	agt	gcc	acc	aag	att	ctg	ctg	gaa	acc	ctg	tta	tta	gca	gcc	929	
Gly	Gly	Ser	Ala	Thr	Lys	Ile	Leu	Leu	Glu	Thr	Leu	Leu	Leu	Ala	Ala		
			265				270						275				
cat	aag	act	gtg	gac	cag	ggc	att	gca	gca	tct	caa	aga	tgc	ctc	ctg	977	
His	Lys	Thr	Val	Asp	Gln	Gly	Ile	Ala	Ala	Ser	Gln	Arg	Cys	Leu	Leu		
			280			285						290					
gaa	atc	ttg	cgg	aca	ttt	gag	cga	gct	cat	cag	gtg	acc	tac	agc	caa	1025	
Glu	Ile	Leu	Arg	Thr	Phe	Glu	Arg	Ala	His	Gln	Val	Thr	Tyr	Ser	Gln		
			295			300					305						
agc	ccc	aag	att	gcc	acc	ctg	atg	aag	agt	gtc	agc	acc	agt	ctg	gag	1073	

PCT/US01/04098

2367

Glu Lys Glu Gln Val Ile Pro Ile Ala Leu Leu Ser Leu Leu Phe Arg
 570 575 580

tgc tgc atc act gag gct cag gca cac ctg gct gca gct cct tct gtc 1889
 Cys Ser Ile Thr Glu Ala Gln Ala His Leu Ala Ala Ala Pro Ser Val
 585 590 595

tgt gag gct gtc agg agt gct ctt gct ggg cca ggt cag aag cgc act 1937
 Cys Glu Ala Val Arg Ser Ala Leu Ala Gly Pro Gly Gln Lys Arg Thr
 600 605 610

gcg gac ccc ctc gag atc cta gag cct gac gtt cag tga acccatgttt 1986
 Ala Asp Pro Leu Glu Ile Leu Glu Pro Asp Val Gln *
 615 620 625

ctgggtgggt gaaaggggcc caaccctgcc cacttcagcc cagcccgccc aaggggactt 2046
 gtgccagcag aacatgtggg aggaagaagc cccgtttcca gggcatccgc agcccagggt 2106
 agggagaaat attctctcca ctttggggga gagttcttgc tctcgaccta gtggtttcta 2166
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 aaa 2229

<210> 853
 <211> 1614
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (137) .. (1264)

<400> 853

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 ttctgagggc atgaagtaag aggggtctctt ccgtctggct gctggggcct cgggtctgaa 120
 gcgtctcaag cagaca atg gcc tcg gac ccc cac agc ctg gag gag ttt 169
 Met Ala Ser Asp Pro His Ser Leu Glu Glu Phe
 1 5 10

tgc tcc gac ccg cac gct gtg gca ggt gcc ctc aag tcc tat ctg cgg 217
 Cys Ser Asp Pro His Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu Arg
 15 20 25

gag ctg cca gag cct ctg atg acc ttc gac ctc tat gat gac tgg atg 265
 Glu Leu Pro Glu Pro Leu Met Thr Phe Asp Leu Tyr Asp Asp Trp Met
 30 35 40

agg gca gcc agc ctg aag gag cca ggg gcc cgg ctg cag gcc ctc caa 313
 Arg Ala Ala Ser Leu Lys Glu Pro Gly Ala Arg Leu Gln Ala Leu Gln
 45 50 55

gag gtg tgc agc cgc cta ccc ccc gag aac ctc agc aac ctc agg tac 361
 Glu Val Cys Ser Arg Leu Pro Pro Glu Asn Leu Ser Asn Leu Arg Tyr
 60 65 70 75

ctg atg aag ttc ctg gca cgg ctg gcc gag gag cag gag gtg aac aag 409
 Leu Met Lys Phe Leu Ala Arg Leu Ala Glu Glu Gln Glu Val Asn Lys

80	85	90	
atg aca ccc agc aac atc gcc ata gtc ctg gga ccc aac ttg ctg tgg Met Thr Pro Ser Asn Ile Ala Ile Val Leu Gly Pro Asn Leu Leu Trp 95 100 105			457
cca cct gag aaa gaa ggg gac cag gcc cag ctg gat gca gcc tcc gtg Pro Pro Glu Lys Glu Gly Asp Gln Ala Gln Leu Asp Ala Ala Ser Val 110 115 120			505
tct tcc atc cag gtg gtg ggc gtc gtc gag gcg ctg atc cag agc gca Ser Ser Ile Gln Val Val Gly Val Val Glu Ala Leu Ile Gln Ser Ala 125 130 135			553
gac acc ctc ttc cct gga gac atc aac ttc aac gtg tca ggc ctc ttc Asp Thr Leu Phe Pro Gly Asp Ile Asn Phe Asn Val Ser Gly Leu Phe 140 145 150 155			601
tca gct gtt acc ctc cag gac aca gtc agt gac agg ctg gcc tct gag Ser Ala Val Thr Leu Gln Asp Thr Val Ser Asp Arg Leu Ala Ser Glu 160 165 170			649
gaa ctt ccg tcc act gcc gtg ccc acc cca gcc acc acc ccg gct ccg Glu Leu Pro Ser Thr Ala Val Pro Thr Pro Ala Thr Thr Pro Ala Pro 175 180 185			697
gct ccg gct cca gct cca gct ccg gcc cca gcc ttg gct tca gca gct Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Leu Ala Ser Ala Ala 190 195 200			745
acc aag gaa agg aca gag tct gag gtg cct ccc aga cca gcc tcc ccc Thr Lys Glu Arg Thr Glu Ser Glu Val Pro Pro Arg Pro Ala Ser Pro 205 210 215			793
aag gtc acc agg agt ccc ccg gag aca gct gcc cca gtg gag gac atg Lys Val Thr Arg Ser Pro Pro Glu Thr Ala Ala Pro Val Glu Asp Met 220 225 230 235			841
gct cgg agg acc aag cgc ccg gcg cca gcc cgg ccc acc atg ccg ccc Ala Arg Arg Thr Lys Arg Pro Ala Pro Ala Arg Pro Thr Met Pro Pro 240 245 250			889
ccc cag gtc tcc ggc tcc cgc tcc tcc cct cca gcc ccg ccc ttg ccc Pro Gln Val Ser Gly Ser Arg Ser Ser Pro Pro Ala Pro Pro Leu Pro 255 260 265			937
cct ggc tct ggc agc cct ggg acc ccc caa gcc ctg ccc cga cgt ctg Pro Gly Ser Gly Ser Pro Gly Thr Pro Gln Ala Leu Pro Arg Arg Leu 270 275 280			985
gtt ggc agc agc ctc cga gcc ccc aca gtg cca ccc ccg tta ccc ccc Val Gly Ser Ser Leu Arg Ala Pro Thr Val Pro Pro Pro Leu Pro Pro 285 290 295			1033
aca ccc cct cag cct gcc cgg cgc caa agc cgg cgt tca cca gcc tcc Thr Pro Pro Gln Pro Ala Arg Arg Gln Ser Arg Arg Ser Pro Ala Ser 300 305 310 315			1081
ccc agc ccg gcc tcc cca ggt cca gcc tcc ccc agc cca gtc tct ttg Pro Ser Pro Ala Ser Pro Gly Pro Ala Ser Pro Ser Pro Val Ser Leu 320 325 330			1129
agt aac cct gca cag gtg gac ctg ggg gct gcc aca gca gag gga gga Ser Asn Pro Ala Gln Val Asp Leu Gly Ala Ala Thr Ala Glu Gly Gly 335 340 345			1177

335	340	345	
gcc cct gag gct atc agt ggg gtc ccc act ccc cca gct atc ccc cct			1225
Ala Pro Glu Ala Ile Ser Gly Val Pro Thr Pro Pro Ala Ile Pro Pro			
350	355	360	
cag ccc cgc ccc agg agc ctt gcc tca gag acc aac tga gtggctgggt			1274
Gln Pro Arg Pro Arg Ser Leu Ala Ser Glu Thr Asn *			
365	370	375	
tctccctaag cagccctcag cccccctcc ctccccacct ggccctccca ggacagctct			1334
cgccccccac aaaggggcat gggcctccag cctttgccca caagtgcctc agtgcccaact			1394
gggtcggccc ccatggccag gagggctcag gacaatcctc tatttcctga ccttttctc			1454
gtccaccctg ggcttgggga cccccccacc ggactctcca ctctccggca ggtcctaggg			1514
gagccaccgg aaggaaggag aggtttgcct gctcctacgg gactgattct tctcttgccg			1574
acatgttttt tgtaaggctg gtaaataaat tattttggac			1614

<210> 854
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (179)..(1138)

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gccgggcagg ggcctcctgg aaggaacct cctgcagcct caagcaccag gtcatgac	178
atg aca tct atc cct ttc cca ggt gac cga ctg ctg cag gtg gat gga	226
Met Thr Ser Ile Pro Phe Pro Gly Asp Arg Leu Leu Gln Val Asp Gly	
1 5 10 15	
gtg att ctg tgc ggc ctc acc cac aag cag gct gtg cag tgc ctg aag	274
Val Ile Leu Cys Gly Leu Thr His Lys Gln Ala Val Gln Cys Leu Lys	
20 25 30	
ggc cct ggg cag gtt gca aga ctg gtc tta gag aga aga gtc ccc agg	322
Gly Pro Gly Gln Val Ala Arg Leu Val Leu Glu Arg Arg Val Pro Arg	
35 40 45	
agt aca cag cag tgt cct tct gct aat gac agc atg gga gat gaa cgc	370
Ser Thr Gln Gln Cys Pro Ser Ala Asn Asp Ser Met Gly Asp Glu Arg	
50 55 60	
acg gct gtt tcc ttg gta aca gcc ttg cct ggc agg cct tcg agc tgt	418
Thr Ala Val Ser Leu Val Thr Ala Leu Pro Gly Arg Pro Ser Ser Cys	
65 70 75 80	
gtc tcg gtg aca gat ggt cct aag ttt gaa gtc aaa cta aaa aag aat	466
Val Ser Val Thr Asp Gly Pro Lys Phe Glu Val Lys Leu Lys Lys Asn	
85 90 95	

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gcc aat ggt ttg gga ttc agt ttc gtg cag atg gag aaa gag agc tgc      514
Ala Asn Gly Leu Gly Phe Ser Phe Val Gln Met Glu Lys Glu Ser Cys
      100                      105                      110

agc cat ctc aaa agt gat ctt gtg agg att aag agg ctc ttt ccg ggg      562
Ser His Leu Lys Ser Asp Leu Val Arg Ile Lys Arg Leu Phe Pro Gly
      115                      120                      125

cag cca gct gag gag aat ggg gcc att gca gct ggt gac att atc ctg      610
Gln Pro Ala Glu Glu Asn Gly Ala Ile Ala Ala Gly Asp Ile Ile Leu
      130                      135                      140

gcc gtg aat gga agg tcc acg gaa ggc ctc atc ttc cag gag gtg ctg      658
Ala Val Asn Gly Arg Ser Thr Glu Gly Leu Ile Phe Gln Glu Val Leu
      145                      150                      155                      160

cat tta ctg aga ggg gcc cca cag gaa gtc acg ctc ctc ctt tgc cga      706
His Leu Leu Arg Gly Ala Pro Gln Glu Val Thr Leu Leu Leu Cys Arg
      165                      170                      175

ccc cct cca ggt gcg ctg cct gag atg gag cag gaa tgg cag aca cct      754
Pro Pro Pro Gly Ala Leu Pro Glu Met Glu Gln Glu Trp Gln Thr Pro
      180                      185                      190

gaa ctc tca gct gac aaa gaa ttc acc agg gca aca tgt act gac tca      802
Glu Leu Ser Ala Asp Lys Glu Phe Thr Arg Ala Thr Cys Thr Asp Ser
      195                      200                      205

tgt acc agc ccc atc ctg gat caa gag gac agc tgg agg gac agt gcc      850
Cys Thr Ser Pro Ile Leu Asp Gln Glu Asp Ser Trp Arg Asp Ser Ala
      210                      215                      220

tcc cca gat gca ggg gaa ggc ctg ggt ctc agg cca gag tct tcc caa      898
Ser Pro Asp Ala Gly Glu Gly Leu Gly Leu Arg Pro Glu Ser Ser Gln
      225                      230                      235                      240

aag gcc atc aga gag gca caa tgg ggc caa aac aga gag aga cct tgg      946
Lys Ala Ile Arg Glu Ala Gln Trp Gly Gln Asn Arg Glu Arg Pro Trp
      245                      250                      255

gcc agt tcc ttg aca cat tct cct gag tcc cac cct cat tta tgc aaa      994
Ala Ser Ser Leu Thr His Ser Pro Glu Ser His Pro His Leu Cys Lys
      260                      265                      270

ctt cac caa gaa agg gat gaa tca aca ttg gcg acc tct ttg gaa aag      1042
Leu His Gln Glu Arg Asp Glu Ser Thr Leu Ala Thr Ser Leu Glu Lys
      275                      280                      285

gat gtg agg caa aac tgc tat tca gtt tgt gat atc atg aga ctt gga      1090
Asp Val Arg Gln Asn Cys Tyr Ser Val Cys Asp Ile Met Arg Leu Gly
      290                      295                      300

aga tat tcc ttc tca tct cct cta acc aga ctt tcg aca gat att ttc      1138
Arg Tyr Ser Phe Ser Ser Pro Leu Thr Arg Leu Ser Thr Asp Ile Phe
      305                      310                      315                      320

tgagcacctt ctctgcatgt ctgcagtgt gtgtaaaatg cctcgtgcc      1188

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<210> 855
 <211> 1402
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (893) .. (1231)

<400> 855

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ttcagctggc tcatccccag gggctggggg ctcttgata caatggagca gatgagccgg      180
gaggacatgc tggccatctc aacacccgtc ttgaccagtc tggatgtgcc ccctgagatg      240
atgcccaccg tcatagatga atacctagga agcaactcgg acgcacaagc caaatgccag      300
gcgttccagg aattcatggg tgacgtattc atcaatgttc ccaccgtcag tttttcaaga      360
taccttcgag attctggaag ccctgtcttt ttctatgagt tccagcatcg acccagttct      420
tttgogaaga taaaacctgc ctgggtgaag gctgatcatg gggccgaggg tgcttttgtg      480
ttcggaggtc ccttctcat ggacgagagc tcccgcctgg cctttccaga ggccacagag      540
gaggagaagc agctaagcct caccatgatg gcccagtgga cccactttgc ccggacagga      600
cctcccacac tttggggcat cgttgccact ggagcctctc ttcgggtgac gttgccctc      660
cctgctgccc ccaagctggc cccttccac tcttcagacc ttgaccagga cccaggaaa      720
caaggcaatc gctggcgggtg cgggcctctg ggccgtctc tggggttcg agaggacccc      780
acettacaga tgaggaaatt agaatcagag aggggcagta ccgtgcctga ggccacacag      840
gctgaggccc caggataagt tccttggtgt ggccctcagat ggccgtgtggg ac      895
                                     atg
                                     Met
                                     1

ctg agc aat gag gac gtg gta agg ctg gtg gtg ggg cac ctg gct gag      943
Leu Ser Asn Glu Asp Val Val Arg Leu Val Val Gly His Leu Ala Glu
                    5                      10                      15

gca gat tgg cac aag aca gac ctg gcc cag aga ccc gcc aac ttg ggg      991
Ala Asp Trp His Lys Thr Asp Leu Ala Gln Arg Pro Ala Asn Leu Gly
                    20                      25                      30

ctc atg cag agc ctg ctg ctg cag agg aaa gcc agc ggg ctc cac gag      1039
Leu Met Gln Ser Leu Leu Leu Gln Arg Lys Ala Ser Gly Leu His Glu
                    35                      40                      45

gct gac caa aat gca gcc acg cgg ctg atc aga cat gcc atc ggg aac      1087
Ala Asp Gln Asn Ala Ala Thr Arg Leu Ile Arg His Ala Ile Gly Asn
                    50                      55                      60                      65

aat gag tat ggg gag atg gag gca gag cgg ctg gcg gcg atg ctg aca      1135
Asn Glu Tyr Gly Glu Met Glu Ala Glu Arg Leu Ala Ala Met Leu Thr
                    70                      75                      80

ttg cca gag gac ttg gcg agg atg tac agg gat gat atc act gtc act      1183
Leu Pro Glu Asp Leu Ala Arg Met Tyr Arg Asp Asp Ile Thr Val Thr
                    85                      90                      95

gtg gtg tat ttt aac tca gaa tca atc ggt gca tat tac aag ggg ggt      1231

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Val Val Tyr Phe Asn Ser Glu Ser Ile Gly Ala Tyr Tyr Lys Gly Gly
 100 105 110

taagaatctc ccatacctatt gtcaagggtta acataaatgc tcttctaaaa tgtttcactt 1291

actcctaaac tagctatcca aacctatgat gtgagtgccc agacatctac atatcacctt 1351

tccttttgggt ttttgctctg agctacctca atcattctaa agctttaagt t 1402

<210> 856
 <211> 2610
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (165)..(2267)

<400> 856

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gccgacaggc atccctgag cgcctgctgg gctcttatca cgcg atg gca tcc act 176
 Met Ala Ser Thr
 1

gtg gaa gga ggc gac aca gct ctg ctc cca gaa ttc ccc agg ggg ccc 224
 Val Glu Gly Gly Asp Thr Ala Leu Leu Pro Glu Phe Pro Arg Gly Pro
 5 10 15 20

ctc gat gcc tac cga gca aga gcg tcc ttc agc tgg aag gag ctg gcg 272
 Leu Asp Ala Tyr Arg Ala Arg Ala Ser Phe Ser Trp Lys Glu Leu Ala
 25 30 35

ctg ttc acg gaa ggg gag ggc atg ctc cgc ttt aag aaa acc atc ttc 320
 Leu Phe Thr Glu Gly Glu Gly Met Leu Arg Phe Lys Lys Thr Ile Phe
 40 45 50

tca gct ctt gag aat gac cct ctt ttc gct cgt tcc cct gga gcc gat 368
 Ser Ala Leu Glu Asn Asp Pro Leu Phe Ala Arg Ser Pro Gly Ala Asp
 55 60 65

ctg tcc ttg gag aag tat cgc gag ctg aac ttc ctt cga tgc aag cgg 416
 Leu Ser Leu Glu Lys Tyr Arg Glu Leu Asn Phe Leu Arg Cys Lys Arg
 70 75 80

atc ttc gag tat gac ttc ctc agt gtc gaa gac atg ttc aag agc cct 464
 Ile Phe Glu Tyr Asp Phe Leu Ser Val Glu Asp Met Phe Lys Ser Pro
 85 90 95 100

ctg aag gtc ccc gcc ttg att cag tgc ctg ggc atg tat gac tct tct 512
 Leu Lys Val Pro Ala Leu Ile Gln Cys Leu Gly Met Tyr Asp Ser Ser
 105 110 115

ctg gct gcc aag tac ctc ctc cat agc ttg gtt ttt gga tca gca gtt 560
 Leu Ala Ala Lys Tyr Leu Leu His Ser Leu Val Phe Gly Ser Ala Val
 120 125 130

tac agt tct ggt tct gaa aga cat ctc aca tat att caa aag atc ttc 608
 Tyr Ser Ser Gly Ser Glu Arg His Leu Thr Tyr Ile Gln Lys Ile Phe

135	140	145	
agg atg gag att ttt gga tgt ttt gct ctg acc gaa tta agc cac ggc Arg Met Glu Ile Phe Gly Cys Phe Ala Leu Thr Glu Leu Ser His Gly 150 155 160			656
agt aat acc aag gcc att cgc aca act gcc cac tac gat cct gcc act Ser Asn Thr Lys Ala Ile Arg Thr Thr Ala His Tyr Asp Pro Ala Thr 165 170 175 180			704
gag gaa ttc atc ata cat tcc cct gat ttc gaa gct gcc aag ttt tgg Glu Glu Phe Ile Ile His Ser Pro Asp Phe Glu Ala Ala Lys Phe Trp 185 190 195			752
gtt ggc aac atg ggc aag aca gcc act cac gcg gtg gtg ttt gct aag Val Gly Asn Met Gly Lys Thr Ala Thr His Ala Val Val Phe Ala Lys 200 205 210			800
ctg tgt gtg cca ggg gac cag tgc cat ggg ctg cat ccc ttt atc gtg Leu Cys Val Pro Gly Asp Gln Cys His Gly Leu His Pro Phe Ile Val 215 220 225			848
cag atc cgg gac ccg aag acc ctt ctt ccc atg cct gga gtg atg gtt Gln Ile Arg Asp Pro Lys Thr Leu Leu Pro Met Pro Gly Val Met Val 230 235 240			896
ggc gac ata gga aaa aaa ctg ggg cag aac ggt ctg gat aat ggt ttc Gly Asp Ile Gly Lys Lys Leu Gly Gln Asn Gly Leu Asp Asn Gly Phe 245 250 255 260			944
gcc atg ttc cac aag gtc aga gtt cct cgc cag agc ctt ctg aac cgg Ala Met Phe His Lys Val Arg Val Pro Arg Gln Ser Leu Leu Asn Arg 265 270 275			992
atg gga gac gtc acc ccc gag ggc acc tat gtc agc ccc ttt aag gac Met Gly Asp Val Thr Pro Glu Gly Thr Tyr Val Ser Pro Phe Lys Asp 280 285 290			1040
gtc agg cag cgc ttt gga gcg tcc ctg ggg agc ctg tcc tcg ggc cgg Val Arg Gln Arg Phe Gly Ala Ser Leu Gly Ser Leu Ser Ser Gly Arg 295 300 305			1088
gtc tcc atc gtg agc ctg gcc atc ctt aac cta aag ctg gcc gtg gcc Val Ser Ile Val Ser Leu Ala Ile Leu Asn Leu Lys Leu Ala Val Ala 310 315 320			1136
atc gct ctt cgc ttc tca gcc act cgg cgt cag ttt gga ccc aca gag Ile Ala Leu Arg Phe Ser Ala Thr Arg Arg Gln Phe Gly Pro Thr Glu 325 330 335 340			1184
gag gag gaa ata cca gtg ctt gag tat cca atg cag caa tgg cgc ttg Glu Glu Glu Ile Pro Val Leu Glu Tyr Pro Met Gln Gln Trp Arg Leu 345 350 355			1232
ctt cca tat ctg gca gct gtc tac gcc tta gac cat ttc tcc aag tcg Leu Pro Tyr Leu Ala Ala Val Tyr Ala Leu Asp His Phe Ser Lys Ser 360 365 370			1280
ctc ttc ctg gac ctg gtg gag ctc cag cga gga ctt gca tcg gga gac Leu Phe Leu Asp Leu Val Glu Leu Gln Arg Gly Leu Ala Ser Gly Asp 375 380 385			1328
cgc agc gcc aga cag gca gag ctt gga cgt gag atc cac gcc ctg gca Arg Ser Ala Arg Gln Ala Glu Leu Gly Arg Glu Ile His Ala Leu Ala 390 395 400			1376

390	395	400	
tcg gcc agc aag ccc ctg gcc tcg tgg acc acc cag caa gga att cag			1424
Ser Ala Ser Lys Pro Leu Ala Ser Trp Thr Thr Gln Gln Gly Ile Gln			
405	410	415	420
gaa tgc cgg gag gcg tgt gga gga cac ggc tat ctg gcc atg aac cgg			1472
Glu Cys Arg Glu Ala Cys Gly Gly His Gly Tyr Leu Ala Met Asn Arg			
	425	430	435
ttg ggt gtc ctt aga gat gac aac gat ccc aac tgc aca tac gaa ggt			1520
Leu Gly Val Leu Arg Asp Asp Asn Asp Pro Asn Cys Thr Tyr Glu Gly			
	440	445	450
gac aac aac atc ctg ctg cag cag aca agc aac tat ttg ctg ggt ctc			1568
Asp Asn Asn Ile Leu Leu Gln Gln Thr Ser Asn Tyr Leu Leu Gly Leu			
	455	460	465
ctg gca cac cag gtc cac gat gga gct tgc ttc cgc agt ccg ctg aag			1616
Leu Ala His Gln Val His Asp Gly Ala Cys Phe Arg Ser Pro Leu Lys			
	470	475	480
tca gtg gac ttt ctg gac gcc tat ccc ggc atc ctt gac cag aag ttt			1664
Ser Val Asp Phe Leu Asp Ala Tyr Pro Gly Ile Leu Asp Gln Lys Phe			
	485	490	500
gag gtc tcc agt gtt gcc gac tgc ttg gac tct gca gtc gcc ctg gca			1712
Glu Val Ser Ser Val Ala Asp Cys Leu Asp Ser Ala Val Ala Leu Ala			
	505	510	515
gca tac aag tgg ctg gtt tgc tac ctg ctc cga gag act tat caa aaa			1760
Ala Tyr Lys Trp Leu Val Cys Tyr Leu Leu Arg Glu Thr Tyr Gln Lys			
	520	525	530
tta aac caa gag aaa aga tca gga agc agt gac ttt gaa gca agg aac			1808
Leu Asn Gln Glu Lys Arg Ser Gly Ser Ser Asp Phe Glu Ala Arg Asn			
	535	540	545
aaa tgc cag gtg tcc cac ggc cgt ccg ttg gcg ctg gcc ttc gtg gac			1856
Lys Cys Gln Val Ser His Gly Arg Pro Leu Ala Leu Ala Phe Val Asp			
	550	555	560
ctc acg gtg gtc cag agg ttc cac gag cac gtg cac cag cct tcc gtg			1904
Leu Thr Val Val Gln Arg Phe His Glu His Val His Gln Pro Ser Val			
	565	570	575
ccg ccc tcg ctg cgg gcc gtg ctg ggg cgg ctc agt gct ctg tac gcc			1952
Pro Pro Ser Leu Arg Ala Val Leu Gly Arg Leu Ser Ala Leu Ala			
	585	590	595
ctg tgg tcc ctg agc cgc cac gcg gcc ctg ctc tac cga gga gga tac			2000
Leu Trp Ser Leu Ser Arg His Ala Ala Leu Leu Tyr Arg Gly Gly Tyr			
	600	605	610
ttc tcc ggt gag cag gcg gga gaa gtg ttg gag agc gcc gtc ctg gct			2048
Phe Ser Gly Glu Gln Ala Gly Glu Val Leu Glu Ser Ala Val Leu Ala			
	615	620	625
ttg tgt tcc cag ctg aaa gac gat gca gtt gcc ctg gta gac gtg atc			2096
Leu Cys Ser Gln Leu Lys Asp Asp Ala Val Ala Leu Val Asp Val Ile			
	630	635	640
gct cct cct gac ttt gtt ctg gac tca ccg att ggc aga gcc gac ggc			2144
Ala Pro Pro Asp Phe Val Leu Asp Ser Pro Ile Gly Arg Ala Asp Gly			

645	650	655	660	
gag ctc tac aaa aac ctc tgg ggc gct gtc ctg cag gaa agc aag gtg				2192
Glu Leu Tyr Lys Asn Leu Trp Gly Ala Val Leu Gln Glu Ser Lys Val				
	665	670	675	
ttg gag cgg gca tcc tgg tgg cca gag ttt tct gtg aac aaa cct gtc				2240
Leu Glu Arg Ala Ser Trp Trp Pro Glu Phe Ser Val Asn Lys Pro Val				
	680	685	690	
ata gga agt ctg aaa tcg aag ctc tag tggga ctggcacatt cagccaagtc				2292
Ile Gly Ser Leu Lys Ser Lys Leu *				
	695	700		
taatgaaacg aagggaacta atcagacgtg gacctcaact tctgattcca gaacacgccg				2352
gagattgctg ctgctttctg agcccgccacc tgtgcgccta aactgctgat tggcctcaac				2412
tgcccaggcg gacgggaggg aggcacccgg ccggctggac taatctggga tcgcggtgat				2472
ttgcagcgtg gaaaagaaat gcagatgac atgtctacct gatgcgcgt gggttttttg				2532
ataattagaa tttcgcacat tcagttttca gggttcagct cctttctcta aagtaaacag				2592
cccattgtca gggaaaaa				2610

<210> 857
 <211> 1071
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (177) .. (878)

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gaccccttcc tcccacagcc ccttcccgcc cctcgccggg catccgccga caggtacata				120
ccaagaaatt gaattgctga gtcacaggag agatttacaa atagtgtttt ggcac				176
atg gaa cgt gta ggt tgt act tta acg aca act tac gcc cac cct aga				224
Met Glu Arg Val Gly Cys Thr Leu Thr Thr Thr Tyr Ala His Pro Arg				
1 5 10 15				
cca aca cca acc aac ttt cta cca gcc atc agt acc atg gcc tca agc				272
Pro Thr Pro Thr Asn Phe Leu Pro Ala Ile Ser Thr Met Ala Ser Ser				
20 25 30				
tac agg gac cgc ttt ccc cac tcc aat ttg acc cat agc ctg agc ctt				320
Tyr Arg Asp Arg Phe Pro His Ser Asn Leu Thr His Ser Leu Ser Leu				
35 40 45				
cct tgg aga ccc agc aca tac tac aaa gtc gcc tcc aat tcc cca agc				368
Pro Trp Arg Pro Ser Thr Tyr Tyr Lys Val Ala Ser Asn Ser Pro Ser				
50 55 60				
gtg gcc ccg tac tgc acc aga tca cag agg gtg tcc gag aat acc atg				416
Val Ala Pro Tyr Cys Thr Arg Ser Gln Arg Val Ser Glu Asn Thr Met				
65 70 75 80				

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ctt ccc ttt gtt tcc aac aga acc act ttc ttc aca aga tac aca ccg      464
Leu Pro Phe Val Ser Asn Arg Thr Thr Phe Phe Thr Arg Tyr Thr Pro
                        85                        90                        95

gat gac tgg tac agg tcc aat tta acc aac tat caa gag tcc aac act      512
Asp Asp Trp Tyr Arg Ser Asn Leu Thr Asn Tyr Gln Glu Ser Asn Thr
                        100                        105                        110

tcc cga cat aat tgc gag aaa cta aga gtg gat aca tct cgc ctg att      560
Ser Arg His Asn Ser Glu Lys Leu Arg Val Asp Thr Ser Arg Leu Ile
                        115                        120                        125

caa gac aaa tat caa caa aca aga aaa act cag gca gac aca acc caa      608
Gln Asp Lys Tyr Gln Gln Thr Arg Lys Thr Gln Ala Asp Thr Thr Gln
                        130                        135                        140

aat ctg gga gaa cgt gtc aat gac ata ggg ttt tgg aaa tct gaa atc      656
Asn Leu Gly Glu Arg Val Asn Asp Ile Gly Phe Trp Lys Ser Glu Ile
                        145                        150                        155                        160

att cat gag ttg gat gaa atg att gga gag aca aat gca ctt act gat      704
Ile His Glu Leu Asp Glu Met Ile Gly Glu Thr Asn Ala Leu Thr Asp
                        165                        170                        175

gtg aag aaa aga ctg gag cgg gct ttg atg gag act gaa gcc cct ctt      752
Val Lys Lys Arg Leu Glu Arg Ala Leu Met Glu Thr Glu Ala Pro Leu
                        180                        185                        190

cag gta gcc cga gaa tgt cta ttt cat cga gaa aag aga atg gga atc      800
Gln Val Ala Arg Glu Cys Leu Phe His Arg Glu Lys Arg Met Gly Ile
                        195                        200                        205

gac cta gtt cac gat gaa gtt gaa gca caa ctg ctg acg gta aat gtg      848
Asp Leu Val His Asp Glu Val Glu Ala Gln Leu Leu Thr Val Asn Val
                        210                        215                        220

ggg gaa atg cat cag tca cag gca gct tag t tgtaaatgta tgttgaatat      899
Gly Glu Met His Gln Ser Gln Ala Ala *
225                        230

gtagaagcaa aaaaggatgt tacataaaat gacttataag taaagcatta tcgtatcaga      959

tgctgatagc atttagcaaa gacatgtttt tcttggttat aacatatatt caatgagaat      1019

atgaaaatgc aaacgagtaa ataaagatga aaatcacttg aaaaaaaaaa aa      1071

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<210> 858
 <211> 1627
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (397)..(972)

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<400> 858
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cagcctcccc gcttcccggc gactccggga aggtcagcgc gggcagtcgg ggcgcgctcc      120
tgcggcgggg cctcgccggc aaccgggtcc ccacctgaaa ccccgctgc cactccgttc      180

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cagagggcca atagccgtgc aacctgcccg ggatggggcg ggacttatgc aaatagtgtc	240
gccttcggga ggcacatagt gatacaagag ctggaaggcg gctccggcgc agaccttgga	300
gagcacagct gccggcccgc gagccagcct cggttcccgc ggcccgcga ggctcggagc	360
catccagcga cccggcgacc ggccctcaggc cccgcc atg ggg aag acc aac agc Met Gly Lys Thr Asn Ser 1 5	414
aag ctg gcc ccc gag gtg ctg gag gac ctt gtt cag aac act gag ttc Lys Leu Ala Pro Glu Val Leu Glu Asp Leu Val Gln Asn Thr Glu Phe 10 15 20	462
agc gag cag gag ctg aag cag tgg tac aag ggc ttc ctg aag gac tgc Ser Glu Gln Glu Leu Lys Gln Trp Tyr Lys Gly Phe Leu Lys Asp Cys 25 30 35	510
ccc agc ggc atc ctc aac ctg gag gag ttt cag cag ctc tac atc aag Pro Ser Gly Ile Leu Asn Leu Glu Glu Phe Gln Gln Leu Tyr Ile Lys 40 45 50	558
ttc ttc ccc tac ggc gac gcc tcc aag ttc gcg cag cac gct ttc cgc Phe Phe Pro Tyr Gly Asp Ala Ser Lys Phe Ala Gln His Ala Phe Arg 55 60 65 70	606
acc ttc gac aag aac ggc gac ggc acc atc gac ttc cgg gag ttc atc Thr Phe Asp Lys Asn Gly Asp Gly Thr Ile Asp Phe Arg Glu Phe Ile 75 80 85	654
tgc gcc ctg tcg gtc acc tcc cgc ggc agc ttc gag cag aag ctc aac Cys Ala Leu Ser Val Thr Ser Arg Gly Ser Phe Glu Gln Lys Leu Asn 90 95 100	702
tgg gcc ttt gag atg tac gac ctg gac ggc gac ggg cgc atc acg cgc Trp Ala Phe Glu Met Tyr Asp Leu Asp Gly Asp Gly Arg Ile Thr Arg 105 110 115	750
ctg gag atg ctg gag atc atc gag gca atc tac aag atg gtg ggc acc Leu Glu Met Leu Glu Ile Ile Glu Ala Ile Tyr Lys Met Val Gly Thr 120 125 130	798
gtg atc atg atg cgc atg aac cag gac ggg ctc acg ccc cag cag cgt Val Ile Met Met Arg Met Asn Gln Asp Gly Leu Thr Pro Gln Gln Arg 135 140 145 150	846
gtg gac aag atc ttc aag aag atg gac cag gat aag gac gac cag att Val Asp Lys Ile Phe Lys Lys Met Asp Gln Asp Lys Asp Asp Gln Ile 155 160 165	894
aca ttg gag gag ttc aag gag gca gcc aag agt gac cca tcc att gtg Thr Leu Glu Glu Phe Lys Glu Ala Ala Lys Ser Asp Pro Ser Ile Val 170 175 180	942
ttg ctg ctg cag tgt gac atg cag aag tag a agctggtgag gggcagggtc Leu Leu Leu Gln Cys Asp Met Gln Lys * 185 190	993
cctggccaga aggggcatgg ccacctccca acctgatgac ctctctggct ggccctccag	1053
gaggaggggac actccagccc cctctctctgg cccaccagat cctctgcccag agcccttcct	1113
cccctccatc aagatctttg agggaccacc tcacctgca aaagagacag gtcctccagt	1173

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accctgtctt ctagccccac ctcccacttg gccagaacca atgtccattg ggcataagggg 1233
agttggcttt tgccccagga ggtgaggtta aggagttggg ggccctgggg ttctgggttag 1293
gaattctctt gatcctggga ttatgcttta tgggatgtgg tcccacaggc ctgtcacagg 1353
gccaaattgg gtctgtccat tcttgaggct ccagatccca taaagggggg ctcttcccca 1413
tcccttctac tctacctggc ccttcagcc ccagcctttg gagegttcat tcagtccttt 1473
cttcagctaa tgattactga cacctgtttg gtgctaagga tatggtcatt tacaagacac 1533
atcttgtgcc ctctggaagc tcataggggt gtgaggcaaa cttccagccg tcagggtctc 1593
agctaagcag aaggtgctgg aaggcggaat tcat 1627

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<210> 859
<211> 1371
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (117)..(1133)

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<400> 859
taagcttgcg gccgcttcta gtagtttcca ggcgctgccg ggcggctggc actaagcggg 60

cctgagggctg tggctacggc tgctccggag ctggtggcgc cgcgatagga gagccg 116
atg gcc aag tgg ggt gag gga gac cca cgc tgg atc gtg gag gag cgg 164
Met Ala Lys Trp Gly Glu Gly Asp Pro Arg Trp Ile Val Glu Glu Arg
1 5 10 15

gcg gac gcc acc aac gtc aac aac tgg cac tgg acg gag aga gat gct 212
Ala Asp Ala Thr Asn Val Asn Asn Trp His Trp Thr Glu Arg Asp Ala
20 25 30

tca aat tgg tcc acg gat aag ctg aaa aca ctg ttc ttg gca gtg cag 260
Ser Asn Trp Ser Thr Asp Lys Leu Lys Thr Leu Phe Leu Ala Val Gln
35 40 45

gtt caa aat gaa gaa ggc aag tgt gag gtg acg gaa gtg agt aag ctt 308
Val Gln Asn Glu Glu Gly Lys Cys Glu Val Thr Glu Val Ser Lys Leu
50 55 60

gat gga gag gca tcc att aac aat cgc aaa ggg aaa ctt atc ttc ttt 356
Asp Gly Glu Ala Ser Ile Asn Asn Arg Lys Gly Lys Leu Ile Phe Phe
65 70 75 80

tat gaa tgg agc gtc aaa cta aac tgg aca ggt act tct aag tca gga 404
Tyr Glu Trp Ser Val Lys Leu Asn Trp Thr Gly Thr Ser Lys Ser Gly
85 90 95

gta cag tac aaa gga cat gtg gag atc ccc aat ttg tct gat gaa aac 452
Val Gln Tyr Lys Gly His Val Glu Ile Pro Asn Leu Ser Asp Glu Asn
100 105 110

agc gtg gat gaa gtg gag att agt gtg agc ctt gcc aaa gat gag cct 500
Ser Val Asp Glu Val Glu Ile Ser Val Ser Leu Ala Lys Asp Glu Pro
115 120 125

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gac aca aat ctc gtg gcc tta atg aag gaa gaa ggg gtg aaa ctt cta 548
 Asp Thr Asn Leu Val Ala Leu Met Lys Glu Glu Gly Val Lys Leu Leu
 130 135 140

aga gaa gca atg gga att tac atc agc acc ctc aaa aca gag ttc acc 596
 Arg Glu Ala Met Gly Ile Tyr Ile Ser Thr Leu Lys Thr Glu Phe Thr
 145 150 155 160

cag ggc atg atc tta cct aca atg aat gga gag tca gta gac cca gtg 644
 Gln Gly Met Ile Leu Pro Thr Met Asn Gly Glu Ser Val Asp Pro Val
 165 170 175

ggg cag cca gca ctg aaa act gag gag cgc aag gct aag cct gct cct 692
 Gly Gln Pro Ala Leu Lys Thr Glu Glu Arg Lys Ala Lys Pro Ala Pro
 180 185 190

tca aaa acc cag gcc aga cct gtt gga gtc aaa atc ccc act tgt aag 740
 Ser Lys Thr Gln Ala Arg Pro Val Gly Val Lys Ile Pro Thr Cys Lys
 195 200 205

atc act ctt aag gaa acc ttc ctg acg tca cca gag gag ctc tat aga 788
 Ile Thr Leu Lys Glu Thr Phe Leu Thr Ser Pro Glu Glu Leu Tyr Arg
 210 215 220

gtg ttt acc acc caa gag ctg gtg cag gcc ttt acc cat gct cct gca 836
 Val Phe Thr Thr Gln Glu Leu Val Gln Ala Phe Thr His Ala Pro Ala
 225 230 235 240

aca tta gaa gca gac aga ggt gga aag ttc cac atg gta gat ggc aac 884
 Thr Leu Glu Ala Asp Arg Gly Gly Lys Phe His Met Val Asp Gly Asn
 245 250 255

gtc tct ggg gaa ttt act gat ctg gtc cct gag aaa cat att gtg atg 932
 Val Ser Gly Glu Phe Thr Asp Leu Val Pro Glu Lys His Ile Val Met
 260 265 270

aag tgg agg ttt aaa tct tgg cca gag gga cac ttt gcc acc atc acc 980
 Lys Trp Arg Phe Lys Ser Trp Pro Glu Gly His Phe Ala Thr Ile Thr
 275 280 285

ttg acc ttc atc gac aag aac gga gag act gag ctg tgc atg gaa ggt 1028
 Leu Thr Phe Ile Asp Lys Asn Gly Glu Thr Glu Leu Cys Met Glu Gly
 290 295 300

cga ggc atc cct gct cct gag gaa gag cgg aca cga cag ggc tgg cag 1076
 Arg Gly Ile Pro Ala Pro Glu Glu Glu Arg Thr Arg Gln Gly Trp Gln
 305 310 315 320

cgg tac tac ttt gag ggc att aaa cag acc ttt ggc tat ggc gca cgc 1124
 Arg Tyr Tyr Phe Glu Gly Ile Lys Gln Thr Phe Gly Tyr Gly Ala Arg
 325 330 335

tta ttt tag ggccagc ggcaggggac tccagcctgc tggacaacttc agtccagctc 1180
 Leu Phe *

tctcctgact ggggcttgcg actcacagga ttgcatcgtc ccagctgcta acttggggcc 1240

gggggccctc ccttcacat ataccttggg tttgtgcatg ttttctgctg ggtgggttca 1300

gagggcaatt tctcttttat gtgtacatat gctaaataaa cataatttaa aaaacaaaaa 1360

aaaaaaaaaa a 1371

<210> 860
 <211> 1036
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(933)

<400> 860

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Met Ser Tyr Leu Lys Gln Pro Pro Tyr Ala Val Asn Gly Leu Ser Leu	
1 5 10 15	
acc act tcg ggt atg gac ttg ctg cac ccc tcc gtg ggc tac ccg ggt	96
Thr Thr Ser Gly Met Asp Leu Leu His Pro Ser Val Gly Tyr Pro Gly	
20 25 30	
ttg cct tct gag gaa gca gtc cca ggg cat tta ctg acc aag cag aga	144
Leu Pro Ser Glu Glu Ala Val Pro Gly His Leu Leu Thr Lys Gln Arg	
35 40 45	
aca ggg gtt ggg aaa acc acc ccc cgg aaa cag cgc cgg gag agg acg	192
Thr Gly Val Gly Lys Thr Thr Pro Arg Lys Gln Arg Arg Glu Arg Thr	
50 55 60	
acg ttc act cgg gcg cag cta gat gtg ctg gaa gca ctg ttt gcc aag	240
Thr Phe Thr Arg Ala Gln Leu Asp Val Leu Glu Ala Leu Phe Ala Lys	
65 70 75 80	
acc cgg tac cca gac atc ttc atg cga gag gag gtg gca ctg aaa atc	288
Thr Arg Tyr Pro Asp Ile Phe Met Arg Glu Glu Val Ala Leu Lys Ile	
85 90 95	
aac ttg ccc gag tcg agg gtg cag gta tgg ttt aag aat cga aga gct	336
Asn Leu Pro Glu Ser Arg Val Gln Val Trp Phe Lys Asn Arg Arg Ala	
100 105 110	
aag tgc cgc caa caa cag caa caa cag cag aat gga ggt caa aac aaa	384
Lys Cys Arg Gln Gln Gln Gln Gln Gln Gln Asn Gly Gly Gln Asn Lys	
115 120 125	
gtg aga cct gcc aaa aag aag aca tct cca gct cgg gaa gtg agt tca	432
Val Arg Pro Ala Lys Lys Lys Thr Ser Pro Ala Arg Glu Val Ser Ser	
130 135 140	
gag agt gga aca agt ggc caa ttc act ccc ccc tct agc acc tca gtc	480
Glu Ser Gly Thr Ser Gly Gln Phe Thr Pro Pro Ser Ser Thr Ser Val	
145 150 155 160	
ccg acc att gcc agc agc agt gct cct gtg tct atc tgg agc cca gct	528
Pro Thr Ile Ala Ser Ser Ser Ala Pro Val Ser Ile Trp Ser Pro Ala	
165 170 175	
tcc atc tcc cca ctg tca gat ccc ttg tcc acc tcc tct tcc tgc atg	576
Ser Ile Ser Pro Leu Ser Asp Pro Leu Ser Thr Ser Ser Ser Cys Met	
180 185 190	
cag agg tcc tat ccc atg acc tat act cag gct tca ggt tat agt caa	624
Gln Arg Ser Tyr Pro Met Thr Tyr Thr Gln Ala Ser Gly Tyr Ser Gln	

195	200	205	
gga tat gct ggc tca act tcc tac ttt ggg ggc atg gac tgt gga tca			672
Gly Tyr Ala Gly Ser Thr Ser Tyr Phe Gly Gly Met Asp Cys Gly Ser			
210	215	220	
tat ttg acc cct atg cat cac cag ctt ccc gga cca ggg gcc aca ctc			720
Tyr Leu Thr Pro Met His His Gln Leu Pro Gly Pro Gly Ala Thr Leu			
225	230	235	240
agt ccc atg ggt acc aat gca gtc acc agc cat ctc aat cag tcc cca			768
Ser Pro Met Gly Thr Asn Ala Val Thr Ser His Leu Asn Gln Ser Pro			
245	250	255	
gct tct ctt tcc acc cag gga tat gga gct tca agc ttg ggt ttt aac			816
Ala Ser Leu Ser Thr Gln Gly Tyr Gly Ala Ser Ser Leu Gly Phe Asn			
260	265	270	
tca acc act gat tgc ttg gat tat aag gac caa act gcc tcc tgg aag			864
Ser Thr Thr Asp Cys Leu Asp Tyr Lys Asp Gln Thr Ala Ser Trp Lys			
275	280	285	
ctt aac ttc aat gct gac tgc ttg gat tat aaa gat cag aca tcc tcg			912
Leu Asn Phe Asn Ala Asp Cys Leu Asp Tyr Lys Asp Gln Thr Ser Ser			
290	295	300	
tgg aaa ttc cag gtt ttg tga ag acctgtagaa cctctttttg tgggtgattt			965
Trp Lys Phe Gln Val Leu *			
305	310		
ttaaatatac tgggctggac attccagttt tagccaggca ttggttaaaa gagttagatg			1025
ggatgatgcc g			1036

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 <211> 2623
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (93)..(1457)

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aagcaggctg gtaccggtcc ggaattcccg gg atg gcg cag cgg gac tgg acc	113
Met Ala Gln Arg Asp Trp Thr	
1 5	
tgg gtg ccg agc gga gcc gct gcc atg ggc ctg ggc gtc agc gct gag	161
Trp Val Pro Ser Gly Ala Ala Met Gly Leu Gly Val Ser Ala Glu	
10 15 20	
cag ccc gca ggc ggc gcc gag ggc ttc cac ctc cac ggg gtg cag gag	209
Gln Pro Ala Gly Gly Ala Glu Gly Phe His Leu His Gly Val Gln Glu	
25 30 35	
aac tcc cca gcc cag cag gcg ggc ctg gag ccc tac ttt gac ttc atc	257
Asn Ser Pro Ala Gln Gln Ala Gly Leu Glu Pro Tyr Phe Asp Phe Ile	
40 45 50 55	

atc acc att ggg cac tcg agg ctg aac aag gag aat gac acc ctg aag Ile Thr Ile Gly His Ser Arg Leu Asn Lys Glu Asn Asp Thr Leu Lys 60 65 70	305
gca cta ctg aaa gcc aat gtg gag aag ccc gtg aag ctg gag gtg ttc Ala Leu Leu Lys Ala Asn Val Glu Lys Pro Val Lys Leu Glu Val Phe 75 80 85	353
aat atg aag acc atg agg gtg cgc gag gtg gag gtg gtg ccc agc aac Asn Met Lys Thr Met Arg Val Arg Glu Val Glu Val Val Pro Ser Asn 90 95 100	401
atg tgg ggc ggc cag ggc cta ctg ggt gcc agt gtg cgc ttc tgc agc Met Trp Gly Gly Gln Gly Leu Gly Ala Ser Val Arg Phe Cys Ser 105 110 115	449
ttc cgc agg gcc agt gag cag gtg tgg cat gtg ctg gat gtg gaa cca Phe Arg Arg Ala Ser Glu Gln Val Trp His Val Leu Asp Val Glu Pro 120 125 130 135	497
tct tca cct gct gcc ctt gcc ggc ctg cgc ccc tac aca gac tat gtg Ser Ser Pro Ala Ala Leu Ala Gly Leu Arg Pro Tyr Thr Asp Tyr Val 140 145 150	545
gtt ggt tcg gac cag att ctc cag gag tcc gag gac ttc ttt acg ctc Val Gly Ser Asp Gln Ile Leu Gln Glu Ser Glu Asp Phe Phe Thr Leu 155 160 165	593
atc gag tct cat gag ggg aag ccc ttg aag ctg atg gtg tat aac tcc Ile Glu Ser His Glu Gly Lys Pro Leu Lys Leu Met Val Tyr Asn Ser 170 175 180	641
aag tca gac tcc tgc cgg gag gtg act gta act ccc aac gca gcc tgg Lys Ser Asp Ser Cys Arg Glu Val Thr Val Thr Pro Asn Ala Ala Trp 185 190 195	689
ggt gga gag ggc agt ctg gga tgt ggc att ggc tat ggg tat cta cac Gly Gly Glu Gly Ser Leu Gly Cys Gly Ile Gly Tyr Gly Tyr Leu His 200 205 210 215	737
cgg atc cca act cag ccc ccc agc tac cac aag aag cca cct ggc acc Arg Ile Pro Thr Gln Pro Pro Ser Tyr His Lys Lys Pro Pro Gly Thr 220 225 230	785
cca cca cct tct gct cta cca ctt ggt gcc cca cca cct gat gct cta Pro Pro Pro Ser Ala Leu Pro Leu Gly Ala Pro Pro Pro Asp Ala Leu 235 240 245	833
cca cct gga ccc acc ccc gag gac tct cct tcc ctg gag aca ggt tcc Pro Pro Gly Pro Thr Pro Glu Asp Ser Pro Ser Leu Glu Thr Gly Ser 250 255 260	881
agg cag agt gac tac atg gag gcc ctg ctg cag gca cct ggc tcc tcc Arg Gln Ser Asp Tyr Met Glu Ala Leu Leu Gln Ala Pro Gly Ser Ser 265 270 275	929
atg gag gat ccc ctt cct ggg cct ggg agt ccc agc cac agt gct cca Met Glu Asp Pro Leu Pro Gly Pro Gly Ser Pro Ser His Ser Ala Pro 280 285 290 295	977
gac cct gat gga ctt ccc cat ttc atg gag act cct ctt cag ccc cca Asp Pro Asp Gly Leu Pro His Phe Met Glu Thr Pro Leu Gln Pro Pro 300 305 310	1025

cct cca gtg cag cga gtt atg gac cca ggc ttc ctg gac gtg tcg gga Pro Pro Val Gln Arg Val Met Asp Pro Gly Phe Leu Asp Val Ser Gly 315 320 325	1073
att tct ctc ttg gac aac agc aat gcc agt gtg tgg ccc agc ctg ccc Ile Ser Leu Leu Asp Asn Ser Asn Ala Ser Val Trp Pro Ser Leu Pro 330 335 340	1121
tct tcc aca gaa ctg acc acc aca gct gtc tca acc tca ggg cca gag Ser Ser Thr Glu Leu Thr Thr Thr Ala Val Ser Thr Ser Gly Pro Glu 345 350 355	1169
gac atc tgc tcc agc agc agt tct cat gag cgg ggt ggt gag gct aca Asp Ile Cys Ser Ser Ser Ser Ser His Glu Arg Gly Gly Glu Ala Thr 360 365 370 375	1217
tgg tct ggg tca gag ttt gag gtc tcc ttc ctg gac agc cca ggt gcc Trp Ser Gly Ser Glu Phe Glu Val Ser Phe Leu Asp Ser Pro Gly Ala 380 385 390	1265
caa gcc cag gcg gac cac ctg cct cag ctg act ctt cct gac agt ctc Gln Ala Gln Ala Asp His Leu Pro Gln Leu Thr Leu Pro Asp Ser Leu 395 400 405	1313
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 ggaagccccc tcctcagccc tgcggctcct ggggtcgtg ctgcatcccg cacgcctcca 180
 ccggctgcag accc atg gcc gag cgc ggg gaa ctc gac ttg acc ggc gcc 230
 Met Ala Glu Arg Gly Glu Leu Asp Leu Thr Gly Ala
 1 5 10
 aaa cag aac aca gga gtg tgg cta gtc aag gtt cct aaa tat ttg tca 278
 Lys Gln Asn Thr Gly Val Trp Leu Val Lys Val Pro Lys Tyr Leu Ser
 15 20 25
 cag caa tgg gct aaa gcc tct gga aga ggt gaa gtt ggg aaa ctg cgg 326
 Gln Gln Trp Ala Lys Ala Ser Gly Arg Gly Glu Val Gly Lys Leu Arg
 30 35 40
 att gcc aag act caa gga agg act gag gtg tca ttt act ttg aat gag 374
 Ile Ala Lys Thr Gln Gly Arg Thr Glu Val Ser Phe Thr Leu Asn Glu
 45 50 55 60
 gat ctt gca aat att cat gat att ggt gga aaa cca gct tca gtc agt 422
 Asp Leu Ala Asn Ile His Asp Ile Gly Gly Lys Pro Ala Ser Val Ser
 65 70 75
 gct cct aga gaa cat cca ttt gtc ttg caa agt gtt gga gga cag aca 470
 Ala Pro Arg Glu His Pro Phe Val Leu Gln Ser Val Gly Gly Gln Thr
 80 85 90
 tta aca gta ttt act gag agc tca tca gat aag ctg tca ttg gaa gga 518
 Leu Thr Val Phe Thr Glu Ser Ser Ser Asp Lys Leu Ser Leu Glu Gly
 95 100 105
 ata gtg gta caa aga gct gaa tgc cga cca gct gcc agt gaa aac tac 566
 Ile Val Val Gln Arg Ala Glu Cys Arg Pro Ala Ala Ser Glu Asn Tyr
 110 115 120

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atg cga tta aaa aga ttg caa ata gaa gag tct tcc aaa cca gtg agg      614
Met Arg Leu Lys Arg Leu Gln Ile Glu Glu Ser Ser Lys Pro Val Arg
125                      130                      135                      140

cta tca caa cag ctg gac aaa gtt gta aca acc aat tac aaa cct gtt      662
Leu Ser Gln Gln Leu Asp Lys Val Val Thr Thr Asn Tyr Lys Pro Val
145                      150                      155

gct aat cat caa tac aat atc gaa tat gaa agg aaa aag aaa gaa gac      710
Ala Asn His Gln Tyr Asn Ile Glu Tyr Glu Arg Lys Lys Lys Glu Asp
160                      165                      170

gga aag cga gct cga gct gat aaa caa cat gtt tta gac atg cta ttt      758
Gly Lys Arg Ala Arg Ala Asp Lys Gln His Val Leu Asp Met Leu Phe
175                      180                      185

tca gcc ttt gag aaa cat caa tac tat aat ctt aag gac ttg gtg gac      806
Ser Ala Phe Glu Lys His Gln Tyr Tyr Asn Leu Lys Asp Leu Val Asp
190                      195                      200

atc aca aaa caa cct gtg gtg tac ctg aag gaa atc tta aaa gaa att      854
Ile Thr Lys Gln Pro Val Val Tyr Leu Lys Glu Ile Leu Lys Glu Ile
205                      210                      215                      220

ggt gtt cag aat gta aaa ggg atc cac aaa aac aca tgg gag ctg aag      902
Gly Val Gln Asn Val Lys Gly Ile His Lys Asn Thr Trp Glu Leu Lys
225                      230                      235

cca gag tac aga cac tat caa gga gaa gaa aag agt gac taa gaagact      951
Pro Glu Tyr Arg His Tyr Gln Gly Glu Glu Lys Ser Asp *
240                      245                      250

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gaaggcttga acaccgtatg ttaatagggg ttaagtgaca gtactttgat ttctctcggt 1071
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 <213> Homo sapiens

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 <222> (190) .. (354)

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 ataattcaat actatggggc agctacctgg gcacaagatg ggtcacgggg atactgcact 180
 cctatttac atg ctt aac cac atc ata agg ttg cag gca gta ctt gaa 228
 Met Leu Asn His Ile Ile Arg Leu Gln Ala Val Leu Glu
 1 5 10
 atc atc atg aat gaa aga gca aat gca tta gat tta ctg gcc cag caa 276
 Ile Ile Met Asn Glu Arg Ala Asn Ala Leu Asp Leu Leu Ala Gln Gln
 15 20 25
 acc aca aaa atg aga aat gct aac tat cag aac aga tta gct tta gat 324
 Thr Thr Lys Met Arg Asn Ala Asn Tyr Gln Asn Arg Leu Ala Leu Asp
 30 35 40 45
 tac ctc cta gcc cac gaa gga gga gta tga g gaaagttcag tctaactaat 375
 Tyr Leu Leu Ala His Glu Gly Gly Val *
 50 55
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 aaattagccc atattccagt tcacactttg aaagggg 472

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<220>
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 <222> (50)..(1180)

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 Glu Arg Gly Arg Lys Arg Pro Cys Gly Pro Gly Glu His Gly Gln Arg
 5 10 15
 att gag tgg cga aaa tgg aag caa cag aag aaa gag gag aaa aaa aaa 151
 Ile Glu Trp Arg Lys Trp Lys Gln Gln Lys Lys Glu Glu Lys Lys Lys
 20 25 30
 tgg aag gat ctc aag ctg atg aaa aaa ctg gag cgg cag cgg gca cag 199
 Trp Lys Asp Leu Lys Leu Met Lys Lys Leu Glu Arg Gln Arg Ala Gln
 35 40 45 50
 gag gaa cag gca aag cgc ctg gaa gag gag gag gca gcg gca gag aag 247
 Glu Glu Gln Ala Lys Arg Leu Glu Glu Glu Glu Ala Ala Ala Glu Lys
 55 60 65
 gag gac cgc ggg cgg ccc tac aca ctg agc gta gcc ctg ccg ggc tcc 295
 Glu Asp Arg Gly Arg Pro Tyr Thr Leu Ser Val Ala Leu Pro Gly Ser
 70 75 80

atc ctg gac aat gct cag tcg ccg gag ctt cgc acc tac ttg gcc ggt Ile Leu Asp Asn Ala Gln Ser Pro Glu Leu Arg Thr Tyr Leu Ala Gly 85 90 95	343
cag att gcc aga gcc tgt gcc atc ttc tgt gtg gat gag atc gtg gtg Gln Ile Ala Arg Ala Cys Ala Ile Phe Cys Val Asp Glu Ile Val Val 100 105 110	391
ttt gat gag gag ggc cag gat gcc aag act gtg gag ggg gaa ttc aca Phe Asp Glu Glu Gly Gln Asp Ala Lys Thr Val Glu Gly Glu Phe Thr 115 120 125 130	439
gga gtt ggg aag aag ggg cag gcg tgc gta cag ctg gcc cgg atc ctg Gly Val Gly Lys Lys Gly Gln Ala Cys Val Gln Leu Ala Arg Ile Leu 135 140 145	487
cag tac ctg gag tgt cca cag tac ctg agg aag gcg ttc ttc ccc aag Gln Tyr Leu Glu Cys Pro Gln Tyr Leu Arg Lys Ala Phe Phe Pro Lys 150 155 160	535
cac cag gat cta cag ttt gca ggg ctc ctg aac ccc ctg gac agc ccc His Gln Asp Leu Gln Phe Ala Gly Leu Leu Asn Pro Leu Asp Ser Pro 165 170 175	583
cac cac atg cgt cag gat gag gaa tcc gag ttc cga gag ggc atc gtg His His Met Arg Gln Asp Glu Glu Ser Glu Phe Arg Glu Gly Ile Val 180 185 190	631
gtg gat cgg ccc acc cgg cca ggc cac ggc tcc ttt gtc aac tgt ggc Val Asp Arg Pro Thr Arg Pro Gly His Gly Ser Phe Val Asn Cys Gly 195 200 205 210	679
atg aaa aag gag gtg aag att gac aag aac ctg gag ccc ggg ctt cgg Met Lys Lys Glu Val Lys Ile Asp Lys Asn Leu Glu Pro Gly Leu Arg 215 220 225	727
gtg act gtg cga ctg aac cag cag cag cac cca gac tgc aag acc tac Val Thr Val Arg Leu Asn Gln Gln Gln His Pro Asp Cys Lys Thr Tyr 230 235 240	775
cat ggc aaa gtg gta tca tcg cag gac cct cgc acc aaa gct ggt ctc His Gly Lys Val Val Ser Ser Gln Asp Pro Arg Thr Lys Ala Gly Leu 245 250 255	823
tac tgg ggc tac acc gtc cga ctg gct tcc tgc ctc agt gct gtg ttt Tyr Trp Gly Tyr Thr Val Arg Leu Ala Ser Cys Leu Ser Ala Val Phe 260 265 270	871
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gag cgc ggc tca gat gtg gct tct gcc cag ctt ccc aac ttc agg cat Glu Arg Gly Ser Asp Val Ala Ser Ala Gln Leu Pro Asn Phe Arg His 295 300 305	967
gct ctt gtg gtg ttc ggg ggc ctc cag ggt ctg gaa gct gga gcg gat Ala Leu Val Val Phe Gly Gly Leu Gln Gly Leu Glu Ala Gly Ala Asp 310 315 320	1015
gct gac ccc aac ctg gag gtg gct gaa ccc agt gtc ctc ttt gac ctg Ala Asp Pro Asn Leu Glu Val Ala Glu Pro Ser Val Leu Phe Asp Leu 325 330 335	1063

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Tyr Val Asn Thr Cys Pro Gly Gln Gly Ser Arg Thr Ile Arg Thr Glu	
340 345 350	
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Glu Ala Ile Leu Ile Ser Leu Ala Ala Leu Gln Pro Gly Leu Thr Gln	
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Ala Gly Ala Arg His Thr *	
375	
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 aataaacttg ctcatcaagg acaacttctt tcttataatt cttgtctgca ggc atg 296
 Met
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 tct aat ttt act cat tat gcc tat ctg ctt atg ata gag tca ctg atg 344
 Ser Asn Phe Thr His Tyr Ala Tyr Leu Leu Met Ile Glu Ser Leu Met
 5 10 15
 ttg ggg aaa gtt ccc ccg cat gtc ccc agt cat cat ttc ata ttt cat 392
 Leu Gly Lys Val Pro Pro His Val Pro Ser His His Phe Ile Phe His
 20 25 30
 gat gat ggg agt gcc aga cag aag gga gag agt gat tac aag gtc atc 440
 Asp Asp Gly Ser Ala Arg Gln Lys Gly Glu Ser Asp Tyr Lys Val Ile
 35 40 45
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 Ile Gln Gln Trp Phe Ser Lys Ser Gly Pro Trp Thr Thr Ser Ser Asn
 50 55 60 65
 gtt acc tgg ggc ttg tta gaa ctg caa caa agc att tct gaa tca gct 536
 Val Thr Trp Gly Leu Leu Glu Leu Gln Gln Ser Ile Ser Glu Ser Ala
 70 75 80
 gtt tta acc att cct cca gga gat tct ggt gca ggc tca aat ttg ata 584
 Val Leu Thr Ile Pro Pro Gly Asp Ser Gly Ala Gly Ser Asn Leu Ile
 85 90 95
 acc atg ttt cta cgt aac aga aaa gaa aca gat ctg tgc agt ggg aga 632
 Thr Met Phe Leu Arg Asn Arg Lys Glu Thr Asp Leu Cys Ser Gly Arg
 100 105 110
 agt aaa gtg aac aga gga tgg aat tct ggc aga tgc aaa caa agg ggc 680
 Ser Lys Val Asn Arg Gly Trp Asn Ser Gly Arg Cys Lys Gln Arg Gly
 115 120 125
 aag act gag cag cct gga gag ccc ttg gaa cat gtg tat gtg act ata 728
 Lys Thr Glu Gln Pro Gly Glu Pro Leu Glu His Val Tyr Val Thr Ile
 130 135 140 145
 aaa cat gct gta gcc ctg gaa tcc cga cat caa aag gga gag ctt cag 776
 Lys His Ala Val Ala Leu Glu Ser Arg His Gln Lys Gly Glu Leu Gln
 150 155 160
 tgc ctg ata aaa atg tgc att cct ctt agc aaa cca ctc caa atg ttc 824
 Cys Leu Ile Lys Met Cys Ile Pro Leu Ser Lys Pro Leu Gln Met Phe
 165 170 175
 ttt tct cca ccc cac tgg gaa gct tgg ctg cag aga gta cag caa ctt 872
 Phe Ser Pro Pro His Trp Glu Ala Trp Leu Gln Arg Val Gln Gln Leu
 180 185 190
 gcg aaa aac aca aga tac ttc aga caa aga ctg cag gaa atg gga ttc 920
 Ala Lys Asn Thr Arg Tyr Phe Arg Gln Arg Leu Gln Glu Met Gly Phe
 195 200 205

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att atc tat ggc aat gag aat gct tct gtt gtt cct ctg ctt ctt tat      968
Ile Ile Tyr Gly Asn Glu Asn Ala Ser Val Val Pro Leu Leu Leu Tyr
210                      215                      220                      225

atg cct ggt aaa gta gcg gct ttt gca agg cat atg cta gag aaa aaa      1016
Met Pro Gly Lys Val Ala Ala Phe Ala Arg His Met Leu Glu Lys Lys
                230                      235                      240

att gga gtg gtg gtc gtg gga ttt cca gcc act ccc ctc gca gaa gct      1064
Ile Gly Val Val Val Val Gly Phe Pro Ala Thr Pro Leu Ala Glu Ala
                245                      250                      255

cgg gct cgg ttt tgt gtt tca gcg gca cat acc cgg gag atg tta gac      1112
Arg Ala Arg Phe Cys Val Ser Ala Ala His Thr Arg Glu Met Leu Asp
                260                      265                      270

acg gtt tta gaa gct ctt gat gaa atg ggt gat ctc ttg caa ctg aaa      1160
Thr Val Leu Glu Ala Leu Asp Glu Met Gly Asp Leu Leu Gln Leu Lys
                275                      280                      285

tat tcc cgg cac aag aag tca gca cgt cct gag ctc tat gat gag acg      1208
Tyr Ser Arg His Lys Lys Ser Ala Arg Pro Glu Leu Tyr Asp Glu Thr
290                      295                      300                      305

agc ttt gaa ctc gaa gat taa gt ttactgggtcc tgaatgacac ataaagactt      1261
Ser Phe Glu Leu Glu Asp *
                310

tgcgagaaag acctccctcc ttgcctcaca aggaatataa atggatttct ccccttctct      1321

ca                                                                    1323

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 <222> (571)..(858)

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accctgtcg tatagaaaat cccaagtaag gtacctgccg tcggcagatc tgagctttct      180
tcttgacac ctaataacca cagtcctcca gacctgtgc ggatagtaaa tccaagtaa      240
ggtaccttct gctggaagat ctgagctttc ttcttgga cctaaaacc acagtctcc      300
agtgaaggat ccagtgagat tttccagggt aacggtcata atcgctact ggtccaacgt      360
tcagaagtaa cacaggcacc tggacaatac acagtagatg tggaaggaca cggttgtaca      420
tttatccagg ccacccttaa gtacaatgtt ctctaccta agaaggcatc tggattttct      480
ctttccttgg aaatagtaaa gaactactct tcgactgctt ttgacctcac agtgacctc      540

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aaatacactg gaattcgcaa taaatccagt      atg gtg gtt ata gat gta aaa      591
Met Val Val Ile Asp Val Lys
      1                      5

atg cta tca gga ttt act cca acc atg tca tcc att gaa gag ctt gaa      639
Met Leu Ser Gly Phe Thr Pro Thr Met Ser Ser Ile Glu Glu Leu Glu
      10                      15                      20

aac aag ggc caa gtg atg aag act gaa gtc aag aat gac cat gtt ctt      687
Asn Lys Gly Gln Val Met Lys Thr Glu Val Lys Asn Asp His Val Leu
      25                      30                      35

ttc tac ttg gaa aat ggt ttt ggt cga gca gac agt ttc cct ttt tct      735
Phe Tyr Leu Glu Asn Gly Phe Gly Arg Ala Asp Ser Phe Pro Phe Ser
      40                      45                      50                      55

gtt gag cag agc aac ctt gtg ttc aac att cag cca gcc cca gcc atg      783
Val Glu Gln Ser Asn Leu Val Phe Asn Ile Gln Pro Ala Pro Ala Met
      60                      65                      70

gtc tac gat tac tat gaa aaa gaa gaa tat gcc cta gct ttt tac aac      831
Val Tyr Asp Tyr Tyr Glu Lys Glu Glu Tyr Ala Leu Ala Phe Tyr Asn
      75                      80                      85

atc gac agt agt tca gtt tcc gag tga gacaa agcaattact agaagagttg      883
Ile Asp Ser Ser Ser Val Ser Glu *
      90                      95

gagaagcatt tcttgtaaca aactgattct tctgtatcaa acctggaaaa aaatcatgaa      943

ccatctgaca tcgtgaacag tctgcagtgg gctatgggttt cttgtcaagt cttatttctt      1003

tatcatccca ttaaattgttg tcattttgca aa      1035

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ccggctcctg tcagtgcggt gactgcgctg ggaaac      atg gcg acc gag gga atg      114
Met Ala Thr Glu Gly Met
      1                      5

atc ctt act aac cac gac cat caa atc cgt gtc gga gtc ctt aca gtg      162
Ile Leu Thr Asn His Asp His Gln Ile Arg Val Gly Val Leu Thr Val
      10                      15                      20

agt gat agt tgc ttc agg aat ctt gca gaa gac cgc agt ggg ata aat      210
Ser Asp Ser Cys Phe Arg Asn Leu Ala Glu Asp Arg Ser Gly Ile Asn
      25                      30                      35

ctc aaa gat ctc gta caa gat cct tct ttg ttg ggt ggg act ata tca      258
Leu Lys Asp Leu Val Gln Asp Pro Ser Leu Leu Gly Gly Thr Ile Ser
      40                      45                      50

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gca tac aag ata gta cca gat gaa ata gaa gaa atc aag gaa acc ctg Ala Tyr Lys Ile Val Pro Asp Glu Ile Glu Glu Ile Lys Glu Thr Leu 55 60 65 70	306
ata gat tgg tgt gat gaa aag gaa ctt aat ttg ata tta aca act gga Ile Asp Trp Cys Asp Glu Lys Glu Leu Asn Leu Ile Leu Thr Thr Gly 75 80 85	354
gga aca gga ttt gca cca cga gat gtc act cca gag gcc aca aaa gaa Gly Thr Gly Phe Ala Pro Arg Asp Val Thr Pro Glu Ala Thr Lys Glu 90 95 100	402
gta ata gaa cgg gaa gca cca ggg atg gcc ctg gca atg ctg atg gga Val Ile Glu Arg Glu Ala Pro Gly Met Ala Leu Ala Met Leu Met Gly 105 110 115	450
tca ctt aat gtt aca cct ctg ggc atg ctc tct agg cct gta tgt gga Ser Leu Asn Val Thr Pro Leu Gly Met Leu Ser Arg Pro Val Cys Gly 120 125 130	498
atc aga ggg aaa acg ctc ata att aac ctg cca ggt agc aag aaa gga Ile Arg Gly Lys Thr Leu Ile Ile Asn Leu Pro Gly Ser Lys Lys Gly 135 140 145 150	546
tct cag gaa tgc ttt caa ttc ata ctg cca gct cta cct cat gcc att Ser Gln Glu Cys Phe Gln Phe Ile Leu Pro Ala Leu Pro His Ala Ile 155 160 165	594
gac ctt tta cgt gat gcc att gta aaa gta aag gag gtg cat gat gaa Asp Leu Leu Arg Asp Ala Ile Val Lys Val Lys Glu Val His Asp Glu 170 175 180	642
ctt gaa gat ttg cct tcc cca cct ccc cct ctt tcc cct cct cct act Leu Glu Asp Leu Pro Ser Pro Pro Pro Pro Leu Ser Pro Pro Pro Thr 185 190 195	690
acc agc ccc cat aaa cag aca gaa gac aaa gga gtt caa tgt gag gaa Thr Ser Pro His Lys Gln Thr Glu Asp Lys Gly Val Gln Cys Glu Glu 200 205 210	738
gag gaa gaa gag aag aaa gac agt ggt gtt gct tca aca gaa gat agt Glu Glu Glu Glu Lys Lys Asp Ser Gly Val Ala Ser Thr Glu Asp Ser 215 220 225 230	786
tcc tca tca cat ata act gca gca gcc att gct gcc aag att cca gac Ser Ser Ser His Ile Thr Ala Ala Ala Ile Ala Ala Lys Ile Pro Asp 235 240 245	834
tcc atc att tct cgt ggt gtt cag gtg ctc cca cga gac aca gcc tcc Ser Ile Ile Ser Arg Gly Val Gln Val Leu Pro Arg Asp Thr Ala Ser 250 255 260	882
ctc agc act act cct tca gaa tcg cct cgt gct cag gct aca tct cgc Leu Ser Thr Thr Pro Ser Glu Ser Pro Arg Ala Gln Ala Thr Ser Arg 265 270 275	930
ctc tct aca gct tcc tgc cca aca cca aaa gtc cag tcc agg tgc agc Leu Ser Thr Ala Ser Cys Pro Thr Pro Lys Val Gln Ser Arg Cys Ser 280 285 290	978
agc aag gag aac att ctc aga gcc agt cac agt gct gtc gat atc acc Ser Lys Glu Asn Ile Leu Arg Ala Ser His Ser Ala Val Asp Ile Thr 295 300 305 310	1026

aag gtg gct aga aga cat cgc atg tct cct ttt cct ctg aca tct atg Lys Val Ala Arg Arg His Arg Met Ser Pro Phe Pro Leu Thr Ser Met 315 320 325	1074
gac aaa gcc ttt atc aca gtc ctg gag atg act ccg gtg ctt ggg aca Asp Lys Ala Phe Ile Thr Val Leu Glu Met Thr Pro Val Leu Gly Thr 330 335 340	1122
gaa atc atc aat tac cga gat gga atg ggg cga gtc ctt gct caa gat Glu Ile Ile Asn Tyr Arg Asp Gly Met Gly Arg Val Leu Ala Gln Asp 345 350 355	1170
gta tat gca aaa gac aat tta ccc ccc ttc cca gca tca gta aaa gat Val Tyr Ala Lys Asp Asn Leu Pro Pro Phe Pro Ala Ser Val Lys Asp 360 365 370	1218
ggc tat gct gtc cga gct gct gat ggc cca gga gat cgt ttc atc att Gly Tyr Ala Val Arg Ala Ala Asp Gly Pro Gly Asp Arg Phe Ile Ile 375 380 385 390	1266
ggg gaa tcc caa gct ggt gaa cag cca act cag aca gta atg cca gga Gly Glu Ser Gln Ala Gly Glu Gln Pro Thr Gln Thr Val Met Pro Gly 395 400 405	1314
caa gtc atg cgg gtt aca aca ggt gct cca ata ccc tgc ggt gct gat Gln Val Met Arg Val Thr Thr Gly Ala Pro Ile Pro Cys Gly Ala Asp 410 415 420	1362
gca gta gta caa gtg gaa gat acc gaa ctt atc agg gaa tca gat gat Ala Val Val Gln Val Glu Asp Thr Glu Leu Ile Arg Glu Ser Asp Asp 425 430 435	1410
ggc act gaa gaa ctt gaa gtg cga att ctg gtg caa gct cgg cca ggc Gly Thr Glu Glu Leu Glu Val Arg Ile Leu Val Gln Ala Arg Pro Gly 440 445 450	1458
caa gat atc aga ccc atc ggc cat gac att aaa aga ggg gaa tgt gtt Gln Asp Ile Arg Pro Ile Gly His Asp Ile Lys Arg Gly Glu Cys Val 455 460 465 470	1506
ttg gcc aaa gga acc cac atg ggc ccc tca gag att ggt ctt ctg gca Leu Ala Lys Gly Thr His Met Gly Pro Ser Glu Ile Gly Leu Leu Ala 475 480 485	1554
act gta ggt gtc aca gag gtt gaa gtt aat aag ttt cca gtg gtt gca Thr Val Gly Val Thr Glu Val Glu Val Asn Lys Phe Pro Val Val Ala 490 495 500	1602
gtc atg tca aca ggg aat gag ctg cta aat cct gaa gat gac ctc tta Val Met Ser Thr Gly Asn Glu Leu Leu Asn Pro Glu Asp Asp Leu Leu 505 510 515	1650
cca ggg aag att cga gac agc aat cgt tca act ctt cta gca aca att Pro Gly Lys Ile Arg Asp Ser Asn Arg Ser Thr Leu Leu Ala Thr Ile 520 525 530	1698
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cca gat gac tta ctc aat gcc ttg aat gag ggt atc agt cgt gct gat Pro Asp Asp Leu Leu Asn Ala Leu Asn Glu Gly Ile Ser Arg Ala Asp 555 560 565	1794

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Val Ile Ile Thr Ser Gly Gly Val Ser Met Gly Glu Lys Asp Tyr Leu	
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Lys Gln Val Leu Asp Ile Asp Leu His Ala Gln Ile His Phe Gly Arg	
585 590 595	
gtt ttt atg aaa cca ggc ttg cca aca aca ttt gca act ttg gat att	1938
Val Phe Met Lys Pro Gly Leu Pro Thr Thr Phe Ala Thr Leu Asp Ile	
600 605 610	
gat ggt gta aga aaa ata atc ttt gca cta cct ggg aat cct gta tcg	1986
Asp Gly Val Arg Lys Ile Phe Ala Leu Pro Gly Asn Pro Val Ser	
615 620 625 630	
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Ala Val Val Thr Cys Asn Leu Phe Val Val Pro Ala Leu Arg Lys Met	
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Gln Gly Ile Leu Asp Pro Arg Pro Thr Ile Ile Lys Ala Arg Leu Ser	
650 655 660	
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Cys Asp Val Lys Leu Asp Pro Arg Pro Glu Tyr His Arg Cys Ile Leu	
665 670 675	
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Thr Trp His His Gln Glu Pro Leu Pro Trp Ala Gln Ser Thr Gly Asn	
680 685 690	
caa atg agc agc cgt ctg atg agc atg cgc agt gcc aat gga ttg ttg	2226
Gln Met Ser Ser Arg Leu Met Ser Met Arg Ser Ala Asn Gly Leu Leu	
695 700 705 710	
atg cta cct cca aag aca gaa cag tac gtg gag ctc cac aaa ggc gag	2274
Met Leu Pro Pro Lys Thr Glu Gln Tyr Val Glu Leu His Lys Gly Glu	
715 720 725	
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Val Val Asp Val Met Val Ile Gly Arg Leu *	
730 735	
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tctcgcccca atagcctcac ggcacagtac tcttgggcag taactggaca ccttttattt	2925

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 gaggcagag atg gcg ggc cga gag gcc ctg tca ctg ggc aca gag gcc 168
 Met Ala Gly Arg Glu Ala Leu Ser Leu Gly Thr Glu Ala
 1 5 10
 gag ctg ccg aac agc ctg ccg ggc gat gac cag gat gag tgc ctt ctc 216
 Glu Leu Pro Asn Ser Leu Pro Gly Asp Asp Gln Asp Glu Cys Leu Leu
 15 20 25
 ctc ccg gga gag ctg tgc cag cac ctt tgc atc aat act gtg ggt tct 264
 Leu Pro Gly Glu Leu Cys Gln His Leu Cys Ile Asn Thr Val Gly Ser
 30 35 40 45
 tac cac tgt gcc tgc ttt cct ggc ttc tca ctg cag gac gat ggc cgc 312
 Tyr His Cys Ala Cys Phe Pro Gly Phe Ser Leu Gln Asp Asp Gly Arg
 50 55 60
 act tgc cgc cca gag ggt cac cct cca cag ccg gaa gcc cca cag gag 360
 Thr Cys Arg Pro Glu Gly His Pro Pro Gln Pro Glu Ala Pro Gln Glu
 65 70 75
 cct gca ctg aag tca gaa ttt tcc cag gtg gcc tct aac acc atc ccg 408
 Pro Ala Leu Lys Ser Glu Phe Ser Gln Val Ala Ser Asn Thr Ile Pro
 80 85 90
 ctg cca ctg ccg cag ccc aat acc tgc aaa gac aat gga ccc tgc aag 456
 Leu Pro Leu Pro Gln Pro Asn Thr Cys Lys Asp Asn Gly Pro Cys Lys
 95 100 105
 cag gtg tgc agc act gtt ggg ggc tca gcc ata tgc tcc tgt ttt ccc 504
 Gln Val Cys Ser Thr Val Gly Gly Ser Ala Ile Cys Ser Cys Phe Pro
 110 115 120 125
 ggc tat gcc atc atg gcg gat ggc gtg tcc tgt gaa gac caa gac gag 552
 Gly Tyr Ala Ile Met Ala Asp Gly Val Ser Cys Glu Asp Gln Asp Glu
 130 135 140

tgc ctg atg ggt gct cac gat tgt agc cgg cga cag ttc tgt gtg aac	600
Cys Leu Met Gly Ala His Asp Cys Ser Arg Arg Gln Phe Cys Val Asn	
145 150 155	
acc ctg gga tcc ttc tac tgt gtc aac cac aca gtg ctc tgt gcc gat	648
Thr Leu Gly Ser Phe Tyr Cys Val Asn His Thr Val Leu Cys Ala Asp	
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ggc tat atc ctc aat gcg cac agg aag tgc gtg gac atc aac gag tgt	696
Gly Tyr Ile Leu Asn Ala His Arg Lys Cys Val Asp Ile Asn Glu Cys	
175 180 185	
gtg acg gac ctg cac acg tgc agc cgg ggc gag cac tgt gtg aac aca	744
Val Thr Asp Leu His Thr Cys Ser Arg Gly Glu His Cys Val Asn Thr	
190 195 200 205	
ctg ggc tcc ttc cac tgc tac aag gca ctc acc tgt gag cca ggc tat	792
Leu Gly Ser Phe His Cys Tyr Lys Ala Leu Thr Cys Glu Pro Gly Tyr	
210 215 220	
gcc ctc aag gat ggc gag tgc gaa gac gtg gat gag tgt gcg atg ggc	840
Ala Leu Lys Asp Gly Glu Cys Glu Asp Val Asp Glu Cys Ala Met Gly	
225 230 235	
acg cac acc tgc cag ccg ggc ttc ttg tgc cag aac acc aag ggc tcc	888
Thr His Thr Cys Gln Pro Gly Phe Leu Cys Gln Asn Thr Lys Gly Ser	
240 245 250	
ttc tac tgc cag gcc agg cag cgc tgc atg gat ggc ttc ctg cag gat	936
Phe Tyr Cys Gln Ala Arg Gln Arg Cys Met Asp Gly Phe Leu Gln Asp	
255 260 265	
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Pro Glu Gly Asn Cys Val Asp Ile Asn Glu Cys Thr Ser Leu Ser Glu	
270 275 280 285	
cca tgt cgg cca ggc ttc agc tgc atc aac acg gtg ggc tcc tac acg	1032
Pro Cys Arg Pro Gly Phe Ser Cys Ile Asn Thr Val Gly Ser Tyr Thr	
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tgc cag agg aac ccg ctg atc tgc gcg cgc ggc tac cac gcc agc gat	1080
Cys Gln Arg Asn Pro Leu Ile Cys Ala Arg Gly Tyr His Ala Ser Asp	
305 310 315	
gat ggg acc aag tgt gtg gac gtg aat gag tgt gag aca ggt gtg cac	1128
Asp Gly Thr Lys Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His	
320 325 330	
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Arg Cys Gly Glu Gly Gln Val Cys His Asn Leu Pro Gly Ser Tyr Arg	
335 340 345	
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Cys Asp Cys Lys Ala Gly Phe Gln Arg Asp Ala Phe Gly Arg Gly Cys	
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Ile Asp Val Asn Glu Cys Trp Ala Ser Pro Gly Arg Leu Cys Gln His	
370 375 380	
acg tgt gag aac aca ctc ggc tcc tac cgc tgt tcc tgc gcc tcc ggg	1320
Thr Cys Glu Asn Thr Leu Gly Ser Tyr Arg Cys Ser Cys Ala Ser Gly	
385 390 395	

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Phe Leu Leu Ala Ala Asp Gly Lys Arg Cys Glu Asp Val Asn Glu Cys	
400 405 410	
gag gcc cag cgc tgc agc cag gag tgt gcc aac atc tat ggc tcc tac	1416
Glu Ala Gln Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr	
415 420 425	
cag tgc tac tgc cgc cag ggc tac cag ctg gct gag gat ggg cac acc	1464
Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr	
430 435 440 445	
tgc aca gac atc gac gag tgt gct caa ggc gcc ggc atc ctc tgc acc	1512
Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr	
450 455 460	
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Phe Arg Cys Leu Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu	
465 470 475	
cag ggc tac acc atg acg gcc aac ggg agg tcc tgc aag gac gtg gat	1608
Gln Gly Tyr Thr Met Thr Ala Asn Gly Arg Ser Cys Lys Asp Val Asp	
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gag tgt gca ctg ggt acc cac aac tgt tcc gag gct gag acc tgc cac	1656
Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His	
495 500 505	
aac atc cag ggt agc ttc cgc tgc ctg cgc ttc gag tgt cct ccc aac	1704
Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Glu Cys Pro Pro Asn	
510 515 520 525	
tat gtc caa gtc tcc aaa acg aag tgc gag cgc acc acg tgc cat gac	1752
Tyr Val Gln Val Ser Lys Thr Lys Cys Glu Arg Thr Thr Cys His Asp	
530 535 540	
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Phe Leu Glu Cys Gln Asn Ser Pro Ala Arg Ile Thr His Tyr Gln Leu	
545 550 555	
aac ttc cag acg ggc ctc ctg gtg cct gcg cat atc ttc cgc att ggc	1848
Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly	
560 565 570	
ccc gcg cca gcc ttc aca ggg gac acc atc gcc ctg aac atc atc aag	1896
Pro Ala Pro Ala Phe Thr Gly Asp Thr Ile Ala Leu Asn Ile Ile Lys	
575 580 585	
ggc aat gag gag ggc tac ttt ggc acg cgc agg ctc aat gcc tac acg	1944
Gly Asn Glu Glu Gly Tyr Phe Gly Thr Arg Arg Leu Asn Ala Tyr Thr	
590 595 600 605	
ggt gtg gtc tac ctg cag cgg gcc gtg ctg gag ccc cgg gac ttt gcc	1992
Gly Val Val Tyr Leu Gln Arg Ala Val Leu Glu Pro Arg Asp Phe Ala	
610 615 620	
ctg gat gtg gag atg aag ctc tgg agg cag ggc tcc gtc acc acc ttc	2040
Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe	
625 630 635	
ctg gcc aag atg cac atc ttc ttc acc acc ttt gcc ctg tga ggtgcc	2089
Leu Ala Lys Met His Ile Phe Phe Thr Thr Phe Ala Leu *	
640 645 650	

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 gaggcagag atg gcg ggc cga gag gcc ctg tca ctg ggc aca gag gcc 168
 Met Ala Gly Arg Glu Ala Leu Ser Leu Gly Thr Glu Ala
 1 5 10
 gag ctg ccg aac agc ctg ccg ggc gat gac cag gat gag tgc ctt ctc 216
 Glu Leu Pro Asn Ser Leu Pro Gly Asp Asp Gln Asp Glu Cys Leu Leu
 15 20 25
 ctc ccg gga gag ctg tgc cag cac ctt tgc atc aat act gtg ggt tct 264
 Leu Pro Gly Glu Leu Cys Gln His Leu Cys Ile Asn Thr Val Gly Ser
 30 35 40 45
 tac cac tgt gcc tgc ttt cct ggc ttc tca ctg cag gac gat ggc cgc 312
 Tyr His Cys Ala Cys Phe Pro Gly Phe Ser Leu Gln Asp Asp Gly Arg
 50 55 60
 act tgc cgc cca gag ggt cac cct cca cag ccg gaa gcc cca cag gag 360
 Thr Cys Arg Pro Glu Gly His Pro Pro Gln Pro Glu Ala Pro Gln Glu
 65 70 75
 cct gca ctg aag tca gaa ttt tcc cag gtg gcc tct aac acc atc ccg 408
 Pro Ala Leu Lys Ser Glu Phe Ser Gln Val Ala Ser Asn Thr Ile Pro
 80 85 90
 ctg cca ctg ccg cag ccc aat acc tgc aaa gac aat gga ccc tgc aag 456
 Leu Pro Leu Pro Gln Pro Asn Thr Cys Lys Asp Asn Gly Pro Cys Lys
 95 100 105
 cag gtg tgc agc act gtt ggg ggc tca gcc ata tgc tcc tgt ttt ccc 504

Gln Val Cys Ser Thr Val Gly Gly Ser Ala Ile Cys Ser Cys Phe Pro	
110 115 120 125	
ggc tat gcc atc atg gcg gat ggc gtg tcc tgt gaa gac atc aac gag	552
Gly Tyr Ala Ile Met Ala Asp Gly Val Ser Cys Glu Asp Ile Asn Glu	
130 135 140	
tgt gtg acg gac ctg cac acg tgc agc cgg ggc gag cac tgt gtg aac	600
Cys Val Thr Asp Leu His Thr Cys Ser Arg Gly Glu His Cys Val Asn	
145 150 155	
aca ctg ggc tcc ttc cac tgc tac aag gca ctc acc tgt gag cca ggc	648
Thr Leu Gly Ser Phe His Cys Tyr Lys Ala Leu Thr Cys Glu Pro Gly	
160 165 170	
tat gcc ctc aag gat ggc gag tgc gaa gac gtg gat gag tgt gcg atg	696
Tyr Ala Leu Lys Asp Gly Glu Cys Glu Asp Val Asp Glu Cys Ala Met	
175 180 185	
ggc acg cac acc tgc cag ccg ggc ttc ttg tgc cag aac acc aag ggc	744
Gly Thr His Thr Cys Gln Pro Gly Phe Leu Cys Gln Asn Thr Lys Gly	
190 195 200 205	
tcc ttc tac tgc cag gcc agg cag cgc tgc atg gat ggc ttc ctg cag	792
Ser Phe Tyr Cys Gln Ala Arg Gln Arg Cys Met Asp Gly Phe Leu Gln	
210 215 220	
gat cct gaa ggc aac tgt gtg gac atc aac gag tgc acg tca ctg tcc	840
Asp Pro Glu Cys Asn Cys Val Asp Ile Asn Glu Cys Thr Ser Leu Ser	
225 230 235	
gag cca tgt cgg cca ggc ttc agc tgc atc aac acg gtg ggc tcc tac	888
Glu Pro Cys Arg Pro Gly Phe Ser Cys Ile Asn Thr Val Gly Ser Tyr	
240 245 250	
acg tgc cag agg aac ccg ctg atc tgc gcg cgc ggc tac cac gcc agc	936
Thr Cys Gln Arg Asn Pro Leu Ile Cys Ala Arg Gly Tyr His Ala Ser	
255 260 265	
gat gat ggg acc aag tgt gtg gac gtg aat gag tgt gag aca ggt gtg	984
Asp Asp Gly Thr Lys Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val	
270 275 280 285	
cac cgc tgc ggt gag ggc caa gtg tgc cac aac ctc cct ggc tcc tac	1032
His Arg Cys Gly Glu Gly Gln Val Cys His Asn Leu Pro Gly Ser Tyr	
290 295 300	
cgc tgt gac tgc aaa gcc ggc ttt cag cgg gat gcc ttc ggc cgg ggc	1080
Arg Cys Asp Cys Lys Ala Gly Phe Gln Arg Asp Ala Phe Gly Arg Gly	
305 310 315	
tgc atc gac gtg aat gag tgc tgg gcc tcg cca ggc cgc ctg tgc cag	1128
Cys Ile Asp Val Asn Glu Cys Trp Ala Ser Pro Gly Arg Leu Cys Gln	
320 325 330	
cac acg tgt gag aac aca ctc ggc tcc tac cgc tgt tcc tgc gcc tcc	1176
His Thr Cys Glu Asn Thr Leu Gly Ser Tyr Arg Cys Ser Cys Ala Ser	
335 340 345	
ggg ttc ctg cta gca gcg gac ggc aag cgc tgt gaa gac gtg aat gag	1224
Gly Phe Leu Leu Ala Ala Asp Gly Lys Arg Cys Glu Asp Val Asn Glu	
350 355 360 365	
tgt gag gcc cag cgc tgc agc cag gag tgt gcc aac atc tat ggc tcc	1272